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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:51:14 ; Search time 5.46546 Seconds
(without alignment)
1149.648 Million cell updates/sec

Title: US-10-644-277-149
Perfect score: 405
Sequence: 1 QPDAINAPVTCYNFTNRKI.....QKWQDSMDHLDKQTQTPKT 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6 COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCITUS COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	76	1	US-08-716-188-2
2	405	100.0	76	1	US-08-615-232A-5
3	405	100.0	76	2	US-08-470-323-5
4	405	100.0	76	2	US-09-195-457-5
5	405	100.0	76	2	US-09-291-038-5
6	405	100.0	76	2	US-09-043-861-31
7	405	100.0	78	1	US-08-330-163-12
8	405	100.0	78	1	US-08-482-111-12
9	405	100.0	78	2	US-09-567-225-14
10	405	100.0	99	1	US-08-127-499A-35
11	405	100.0	99	1	US-08-482-847-35
12	405	100.0	99	1	US-08-347-492B-8
13	405	100.0	99	1	US-08-480-449-19
14	405	100.0	99	1	US-08-479-126B-5
15	405	100.0	99	1	US-08-421-144A-5
16	405	100.0	99	1	US-08-726-830A-5
17	405	100.0	99	1	US-08-660-542-19
18	405	100.0	99	1	US-08-798-143-8
19	405	100.0	99	2	US-07-927-391-24
20	405	100.0	99	2	US-08-995-156A-5
21	405	100.0	99	2	US-09-044-856A-5
22	405	100.0	99	2	US-09-044-855A-5
23	405	100.0	99	2	US-08-679-493A-152
24	405	100.0	99	2	US-08-479-603-19
25	405	100.0	99	2	US-09-419-281-5
26	405	100.0	99	2	US-09-366-887A-10
27	405	100.0	99	2	US-08-939-107-19

28	405	100.0	99	2	US-09-545-894-5	Sequence 5, Appli
29	405	100.0	99	2	US-09-067-447B-19	Sequence 19, Appl
30	405	100.0	99	2	US-09-517-204-10	Sequence 10, Appl
31	405	100.0	99	2	US-08-437-306-2	Sequence 2, Appli
32	405	100.0	99	2	US-08-479-620-19	Sequence 19, Appl
33	405	100.0	99	2	US-10-054-967-5	Sequence 5, Appli
34	405	100.0	99	2	US-10-141-965-5	Sequence 5, Appli
35	405	100.0	99	4	PCT-US96-10087-5	Sequence 5, Appli
36	405	100.0	99	6	5212073-2	Patent No. 5212073
37	400	98.8	76	1	US-07-956-862A-1	Sequence 1, Appli
38	400	98.8	76	1	US-08-250-958-1	Sequence 1, Appli
39	400	98.8	76	1	US-08-235-659-1	Sequence 1, Appli
40	400	98.8	78	4	PCT-US95-00605-1	Sequence 1, Appli
41	398	98.3	99	2	US-09-834-795A-28	Sequence 28, Appl
42	362	89.4	68	2	US-09-463-458A-30	Sequence 30, Appl
43	362	89.4	69	2	US-09-463-458A-31	Sequence 31, Appl
44	362	89.4	69	2	US-09-463-458A-32	Sequence 32, Appl
45	358	88.4	68	2	US-09-463-458A-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-08-716-188-2
; Sequence 2, Application US/08716188
; Patent No. 5908629
; GENERAL INFORMATION:
; APPLICANT: KELLY, RODNEY W
; TITLE OF INVENTION: USE OF MCP-1 FOR INDUCING RIPENING OF
; TITLE OF INVENTION: THE CERVIX
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,188
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/00733
; FILING DATE: 31-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9406463.1
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-716-188-2

Query Match 100.0%; Score 405; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 7.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 2

US-08-615-232A-5
; Sequence 5, Application US/08615232A
; Patent No. 5993814
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,232A
; FILING DATE: 13-AUG-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9318984
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: GB 9408602
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 550-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-615-232A-5

Query Match 100.0%; Score 405; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 7.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 3

US-08-470-323-5

; Sequence 5, Application US/08470323A
; Patent No. 6031080
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/08/470,323A
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: PCT/GB94/02006
; EARLIER FILING DATE: 1994-09-14
; EARLIER APPLICATION NUMBER: GB 9318984.3
; EARLIER FILING DATE: 1993-09-14
; EARLIER APPLICATION NUMBER: GB 94086902.2
; EARLIER FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
; US-08-470-323-5

Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 7.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 4

US-09-195-457-5
; Sequence 5, Application US/09195457
; Patent No. 6605702
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/09/195,457
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/470,323
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/GB94/02006
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: GB 9318984.3
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: GB 94086902.2
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
; US-09-195-457-5

Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 7.3e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTKT 76
Db 61 QDSMDHLDKQTPTKT 76

RESULT 5

US-09-291-038-5
; Sequence 5, Application US/09291038

; Patent No. 6635251

; GENERAL INFORMATION:

; APPLICANT: WILLIAMS, TIMOTHY J.

; JOSE, PETER J.

; GRIFFITHS-JOHNSON, DAVID A.

; HSUAN, JOHN J.

; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/291,038

; FILING DATE: 14-Apr-1999

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/615,232A

; FILING DATE: 13-AUG-1996

; APPLICATION NUMBER: GB 9318984

; FILING DATE: 14-SEP-1993

; APPLICATION NUMBER: GB 9408602

; FILING DATE: 29-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: WILSON, MARY J.

; REGISTRATION NUMBER: 32,955

; REFERENCE/DOCKET NUMBER: 550-32

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 816-4000

; TELEFAX: (703) 816-4100

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 76 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-291-038-5

Query Match 100.0%; Score 405; DB 2; Length 76;

Best Local Similarity 100.0%; Pred. No. 7.3e-47;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 QDSMDHLDKQTPTKT 76

Db

61 QDSMDHLDKQTPTKT 76

RESULT 6

US-09-043-861-31

; Sequence 31, Application US/09043861

; Patent No. 6793917

; GENERAL INFORMATION:

; APPLICANT: IMAI, Toshio

; APPLICANT: YOSHIDA, Tetsuya

; APPLICANT: YOSHIE, Osamu

; TITLE OF INVENTION: TYPE CC CHEMOKINE-LIKE PROTEIN

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/043,861

; FILING DATE: 27-MAR-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/JP96/02801

; FILING DATE: 27-SEP-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 56044/1996

; FILING DATE: 13-MAR-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: JP 249457/1995

; FILING DATE: 27-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wegner, Harold C.

; REGISTRATION NUMBER: 25,258

; REFERENCE/DOCKET NUMBER: 74129/432

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399

; INFORMATION FOR SEQ ID NO: 31:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 76 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-043-861-31

Query Match 100.0%; Score 405; DB 2; Length 76;

Best Local Similarity 100.0%; Pred. No. 7.3e-47;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QPDAINAPVTCYNTNRKISVQLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTPTKT 76

Db 61 QDSMDHLDKQTPTKT 76

RESULT 7

US-08-330-163-12

; Sequence 12, Application US/08330163

; Patent No. 5656724

; GENERAL INFORMATION:

; APPLICANT: Daly, Thomas J.

; APPLICANT: Larosa, Gregory J.

; TITLE OF INVENTION: Chemokine-Like Proteins and Methods of

; TITLE OF INVENTION: Use

; NUMBER OF SEQUENCES: 46

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson

; STREET: 225 Franklin Street

Tue Feb 7 10:19:30 2006

; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,163
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 00231/080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-330-163-12

Query Match 100.0%; Score 405; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 62

QY 61 QDSMDHLDKQTPTPKT 76
DB 63 QDSMDHLDKQTPTPKT 78

RESULT 9
US-09-567-225-14
; Sequence 14, Application US/09567225
; Patent No. 6713052
; GENERAL INFORMATION:
; APPLICANT: White, John R.
; APPLICANT: Pelus, Louis
; APPLICANT: Li, Haodong
; APPLICANT: Kreider, Brant L.
; TITLE OF INVENTION: No. 6713052el Chemokine for Mobilizing Stem Cells
; FILE REFERENCE: 1488.1550004
; CURRENT APPLICATION NUMBER: US/09/567,225
; CURRENT FILING DATE: 2000-10-09
; PRIOR APPLICATION NUMBER: US 09/225,501
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: US 60/006,051
; PRIOR FILING DATE: 1995-10-24
; PRIOR APPLICATION NUMBER: US 08/740,033
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 78
; TYPE: PRT
; ORGANISM: MCP-1
; US-09-567-225-14

Query Match 100.0%; Score 405; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
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QY 61 QDSMDHLDKQTPTPKT 76
DB 63 QDSMDHLDKQTPTPKT 78

RESULT 10
US-08-127-499A-35
; Sequence 35, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES

; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 78 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-482-111-12

Query Match 100.0%; Score 405; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 3 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 62

QY 61 QDSMDHLDKQTPTPKT 76
DB 63 QDSMDHLDKQTPTPKT 78

RESULT 9
US-09-567-225-14
; Sequence 14, Application US/09567225
; Patent No. 6713052
; GENERAL INFORMATION:
; APPLICANT: White, John R.
; APPLICANT: Pelus, Louis
; APPLICANT: Li, Haodong
; APPLICANT: Kreider, Brant L.
; TITLE OF INVENTION: No. 6713052el Chemokine for Mobilizing Stem Cells
; FILE REFERENCE: 1488.1550004
; CURRENT APPLICATION NUMBER: US/09/567,225
; CURRENT FILING DATE: 2000-10-09
; PRIOR APPLICATION NUMBER: US 09/225,501
; PRIOR FILING DATE: 1999-01-06
; PRIOR APPLICATION NUMBER: US 60/006,051
; PRIOR FILING DATE: 1995-10-24
; PRIOR APPLICATION NUMBER: US 08/740,033
; PRIOR FILING DATE: 1996-10-23
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 78
; TYPE: PRT
; ORGANISM: MCP-1
; US-09-567-225-14

Query Match 100.0%; Score 405; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3 QPDAINAPVTCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 62

QY 61 QDSMDHLDKQTPTPKT 76
DB 63 QDSMDHLDKQTPTPKT 78

RESULT 10
US-08-127-499A-35
; Sequence 35, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES


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;
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; SEQUENCE CHARACTERISTICS:
; INFORMATION FOR SEQ ID NO: 35:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
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; US-08-127-499A-35
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; Query Match 100.0%; Score 405; DB 1; Length 99;
; Best Local Similarity 100.0%; Pred. No. 1e-46;
; Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Db 24 QPDAINAPVTCVNFYTKISVQRLASVYRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 83
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; Qy 61 QDSMDHLDKQTQTPKT 76
; Db 84 QDSMDHLDKQTQTPKT 99
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; RESULT 11
; US-08-482-847-35
; Sequence 35, Application US/08482847
; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
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; US-08-482-847-35
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; Query Match 100.0%; Score 405; DB 1; Length 99;
; Best Local Similarity 100.0%; Pred. No. 1e-46;
; Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 1 QPDAINAPVTCVNFYTKISVQRLASVYRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 60
; Db 24 QPDAINAPVTCVNFYTKISVQRLASVYRRITSSKCPKEAVIFKTIYAKEICADPKQKWV 83
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; Qy 61 QDSMDHLDKQTQTPKT 76
; Db 84 QDSMDHLDKQTQTPKT 99
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; RESULT 12
; US-08-347-492B-8
; Sequence 8, Application US/08347492B
; Patent No. 5602008
; GENERAL INFORMATION:
; APPLICANT: Wilde, Craig G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Bandman, Olga
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
; TITLE OF INVENTION: PRODUCTION AND USES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,492B
; FILING DATE: 29-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/303,241
; FILING DATE: 07-SEP-1994
; APPLICATION NUMBER: 08/320,011
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33,954
; REFERENCE/DOCKET NUMBER: PF-0024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
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/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ IMMEDIATE SOURCE:
/ LIBRARY: GENBANK
/ CLONE: GI 487124
/ US-08-347-492B-8

Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 83

QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 13
US-08-480-449-19
; Sequence 19, Application US/08480449
; Patent No. 5688927
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,449
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Gass, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/32779
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "Hu MCP-1"
; US-08-480-449-19

Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 14
US-08-479-126B-5
; Sequence 5, Application US/08479126B
; Patent No. 5866373
; GENERAL INFORMATION:
; APPLICANT: LI, HAODONG
; APPLICANT: RUBEN, STEVEN M
; APPLICANT: SUTTON, GRANGER G III
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN MONOCYTE
; TITLE OF INVENTION: CHEMOTACTIC PROTEIN-4 (AS AMENDED)
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,126B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,425
; FILING DATE: 21-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05384
; FILING DATE: 16-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0340001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-479-126B-5

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Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 24 QPDAINAPVTCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 83

QY 61 QDSMDHLDKQTQTPKT 76
DB 84 QDSMDHLDKQTQTPKT 99

RESULT 15
US-08-421-144A-5
; Sequence 5, Application US/08421144A
; Patent No. 5874211
; GENERAL INFORMATION:

APPLICANT: BANDMAN, OLGA
APPLICANT: COLEMAN, ROGER
APPLICANT: STUART, SUSAN G.
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,144A
FILING DATE: 13-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PF-0031 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-421-144A-5

Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 1e-46;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 QDSMDHLDKQTQPTKT 76
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Search completed: February 3, 2006, 09:53:35
Job time : 6.56546 secs

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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:53:49 ; Search time 16.4394 Seconds
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Title: US-10-644-277-149

Perfect score: 405

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA_Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	405	100.0	76	3	US-09-792-793A-20
3	405	100.0	76	4	US-10-339-778-3
4	405	100.0	76	4	US-10-276-971-1
5	405	100.0	76	4	US-10-375-209A-20
6	405	100.0	76	4	US-10-332-038A-5
7	405	100.0	76	4	US-10-668-733-7
8	405	100.0	76	4	US-10-668-733-14
9	405	100.0	76	4	US-10-393-804A-1
10	405	100.0	76	4	US-10-243-795-7
11	405	100.0	76	5	US-10-872-198-102
12	405	100.0	76	5	US-10-839-017-8
13	405	100.0	76	5	US-10-644-277-149
14	405	100.0	76	5	US-10-332-039A-5
15	405	100.0	76	5	US-10-833-656-3
16	405	100.0	76	5	US-10-822-134-5
17	405	100.0	76	5	US-10-981-936-42
18	405	100.0	76	6	US-11-021-951-102
19	405	100.0	78	4	US-10-803-960-14
20	405	100.0	98	4	US-10-449-831A-210
21	405	100.0	99	2	US-08-927-939-16
22	405	100.0	99	4	US-10-057-275-9
23	405	100.0	99	4	US-10-033-067-4
24	405	100.0	99	4	US-10-141-965-5
25	405	100.0	99	4	US-10-146-496-9
26	405	100.0	99	4	US-10-054-967-5
27	405	100.0	99	4	US-10-293-705-8

28	405	100.0	99	4	US-10-170-385-395	Sequence 395, Appl
29	405	100.0	99	4	US-10-116-275-222	Sequence 222, Appl
30	405	100.0	99	4	US-10-440-464-62	Sequence 62, Appl
31	405	100.0	99	4	US-10-764-649-18	Sequence 18, Appl
32	405	100.0	99	5	US-10-733-878-515	Sequence 515, Appl
33	405	100.0	99	5	US-10-852-335A-141	Sequence 141, Appl
34	405	100.0	99	5	US-10-852-335A-148	Sequence 148, Appl
35	405	100.0	99	5	US-10-833-656-1	Sequence 1, Appl
36	405	100.0	99	5	US-10-773-446-130	Sequence 130, Appl
37	405	100.0	99	5	US-10-818-952-19	Sequence 19, Appl
38	405	100.0	99	6	US-11-035-998-5	Sequence 5, Appl
39	405	100.0	122	4	US-10-339-778-2	Sequence 2, Appl
40	405	100.0	133	4	US-10-449-831A-214	Sequence 214, Appl
41	405	100.0	325	3	US-09-792-793A-71	Sequence 71, Appl
42	405	100.0	325	4	US-10-375-209A-71	Sequence 71, Appl
43	405	100.0	327	3	US-09-792-793A-72	Sequence 72, Appl
44	405	100.0	327	4	US-10-375-209A-72	Sequence 72, Appl
45	405	100.0	332	3	US-09-792-793A-73	Sequence 73, Appl

ALIGNMENTS

RESULT 1

US-09-195-457-5
; Sequence 5, Application US/09195457
; Patent No. US20020081623A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/09/195,457
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/470,323
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/GB94/02006
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: GB 9318984.3
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: GB 94086902.2
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-09-195-457-5

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Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 QDSMDHLKQTQTPKT 76
Db 61 QDSMDHLKQTQTPKT 76

RESULT 2

US-09-792-793A-20
; Sequence 20, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Cogging, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; OTHER INFLAMMATORY CONDITIONS AND DISORDERS

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; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792,793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-09-792-793A-20

Query Match          100.0%; Score 405; DB 3; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 3
US-10-339-778-3
; Sequence 3, Application US/10339778
; Publication No. US20030129214A1
; GENERAL INFORMATION:
; APPLICANT: Bornstein, P.
; TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDICAL DEVICE
; FILE REFERENCE: UMOTL-1-20275
; CURRENT APPLICATION NUMBER: US/10/339,778
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,560
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-339-778-3

Query Match          100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 4
US-10-276-971-1
; Sequence 1, Application US/10276971
; Publication No. US20030162737A1
; GENERAL INFORMATION:
; APPLICANT: Egaehira Kensuke
; APPLICANT: Yoshikazu Yonemitsu
; APPLICANT: Katsuo Sueishi
; APPLICANT: Yasuhiro Ikeda
; APPLICANT: Yoshiyuki Inada
; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
; FILE REFERENCE: 2733 US0P
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; CURRENT APPLICATION NUMBER: US/10/276,971
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Human
US-10-276-971-1

Query Match          100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 5
US-10-375-209A-20
; Sequence 20, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggins, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601E
; CURRENT APPLICATION NUMBER: US/10/375,209A
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-10-375-209A-20

Query Match          100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 6
US-10-332-038A-5
; Sequence 5, Application US/10332038A
; Publication No. US20040077835A1
; GENERAL INFORMATION:
; APPLICANT: Gryphon Therapeutics, Inc.
; APPLICANT: Offord, Robin
; APPLICANT: Gaertner, Hubert
; APPLICANT: Hartley, Oliver
; TITLE OF INVENTION: Chemokine Receptor Modulators, Production and Use
; FILE REFERENCE: 03504.271
; CURRENT APPLICATION NUMBER: US/10/332,038A
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: US 60/217,683
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 28
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-332-038A-5

Query Match      100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 7
US-10-668-733-7
; Sequence 7, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT APPLICATION NUMBER: US/10/668,733
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 60/412,866
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; NAME/KEY: misc feature
; LOCATION: (75)-(75)
; OTHER INFORMATION: The Lysine at position 75 is biotinylated
US-10-668-733-7

Query Match      100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 8
US-10-668-733-14
; Sequence 14, Application US/10668733
; Publication No. US20040138422A1
; GENERAL INFORMATION:
; APPLICANT: Demotz et al.
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT APPLICATION NUMBER: US/10/668,733
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 60/412,866
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 14
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-668-733-14

Query Match      100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 9
US-10-393-804A-1
; Sequence 1, Application US/10393804A
; Publication No. US20040185450A1
; GENERAL INFORMATION:
; APPLICANT: Heavner, George
; APPLICANT: Das, Anuk
; TITLE OF INVENTION: MCP-1 MUTANT PROTEINS, ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0290NP
; CURRENT APPLICATION NUMBER: US/10/393,804A
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/367,932
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-804A-1

Query Match      100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTQTPKT 76
Db 61 QDSMDHLDKQTQTPKT 76

RESULT 10
US-10-243-795-7
; Sequence 7, Application US/10243795
; Publication No. US20040197303A1
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
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US-10-243-795-7
Query Match      100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTPT 76
Db 61 QDSMDHLDKQTPTPT 76

RESULT 11
US-10-872-198-102
; Sequence 102, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VORTSMEIER
; APPLICANT: Ulrich Kettling
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2004-05-18
; PRIOR FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2003-11-11
; PRIOR FILING DATE: 2003-11-10
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-102

Query Match      100.0%; Score 405; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTPT 76
Db 61 QDSMDHLDKQTPTPT 76

RESULT 12
US-10-839-017-8
; Sequence 8, Application US/10839017
; Publication No. US20050058635A1
; GENERAL INFORMATION:
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROJ, ANDRE J.
; APPLICANT: SCHILLING, STEPHAN
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL CYCLASE
; FILE REFERENCE: 20488-53

US-10-243-795-7
Query Match      100.0%; Score 405; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTPT 76
Db 61 QDSMDHLDKQTPTPT 76

RESULT 11
US-10-872-198-102
; Sequence 102, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VORTSMEIER
; APPLICANT: Ulrich Kettling
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2004-05-18
; PRIOR FILING DATE: 2004-02-11
; PRIOR FILING DATE: 2003-11-11
; PRIOR FILING DATE: 2003-11-10
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-102

Query Match      100.0%; Score 405; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTPT 76
Db 61 QDSMDHLDKQTPTPT 76

RESULT 12
US-10-839-017-8
; Sequence 8, Application US/10839017
; Publication No. US20050058635A1
; GENERAL INFORMATION:
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROJ, ANDRE J.
; APPLICANT: SCHILLING, STEPHAN
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL CYCLASE
; FILE REFERENCE: 20488-53

US-10-644-277-149
Query Match      100.0%; Score 405; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTPT 76
Db 61 QDSMDHLDKQTPTPT 76

RESULT 13
US-10-644-277-149
; Sequence 149, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; FILE REFERENCE: ABGENIX.091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-149

Query Match      100.0%; Score 405; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.4e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

Qy 61 QDSMDHLDKQTPTPT 76
Db 61 QDSMDHLDKQTPTPT 76

RESULT 14
US-10-332-039A-5
; Sequence 5, Application US/10332039A
; Publication No. US20050089970A1
; GENERAL INFORMATION:
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; APPLICANT: Gryphon Therapeutics, Inc.
; APPLICANT: Bradburne, James
; APPLICANT: Kochendoerfer, Gerd
; APPLICANT: Wilken, Jill
; TITLE OF INVENTION: Polymer-Modified Bioactive Synthetic Chemokines and Methods for
; TITLE OF INVENTION: their Manufacture and Use
; FILE REFERENCE: 03504.270
; CURRENT APPLICATION NUMBER: US/10/332,039A
; CURRENT FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US60/217,683
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-332-039A-5

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	Query Match	100.0%	Score 405;	DB 5;	Length 76;
	Best Local Similarity	100.0%;	Pred. NO. 1.4e-41;		
	Matches 76;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QPDAINAPVTCCYCNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKIICADPKQKW	60		
Db	1	QPDAINAPVTCCYCNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKIICADPKQKW	60		
Qy	61	QDSMDHLDKTOTQTPKT	76		
Db	61	QDSMDHLDKTOTQTPKT	76		

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RESULT 15
US-10-833-656-3
; Sequence 3, Application US/10833656
; Publication No. US20050148507A1
; GENERAL INFORMATION:
; APPLICANT: Wandl, Robert
; APPLICANT: Necina, Roman
; APPLICANT: Doods, Henri
; APPLICANT: Lenter, Martin
; APPLICANT: Seidler, Randolph
; TITLE OF INVENTION: Method for the production of an N-terminally modified
; FILE OF INVENTION: Chemoractic factor
; FILE REFERENCE: Case 1/1492
; CURRENT APPLICATION NUMBER: US/10/833,656
; CURRENT FILING DATE: 2004-04-28
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-833-656-3

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	Query Match	100.0%;	Score 405;	DB 5;	Length 76;	
	Best Local Similarity	100.0%;	Pred. NO. 1.4e-41;			
	Matches 76; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
Oy	1 QPDAINAPVTCCNFTNRKISVORLASYYRRITSSKCPKEAVIPKTIYAKEICADPPQKWV	60				
Dd	1 QPDAINAPVTCCNFTNRKISVORLASYYRRITSSKCPKEAVIPKTIYAKEICADPPQKWV	60				
Oy	61 QDSMDHLDKQTQTPKT	76				
Dd	61 QDSMDHLDKQTQTPKT	76				

Search completed: February 3, 2006, 10:00:25
Job time : 17.4394 secs

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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:57:44 : Search time 2.06569 Seconds
(without alignments)
431.127 Million cell updates/sec

Title: US-10-644-277-149

Perfect score: 405

Sequence: 1 QPDAINAPVTCYNTNRKISVQLASVLRITSSKCPKEAVIFKTIIVAKETICADPKOKWV 76

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Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:*

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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/2/pubpaa/US03_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	99	7 US-11-043-788-8	Sequence 8, Appli
2	273	67.4	74	6 US-10-509-292-1	Sequence 1, Appli
3	273	67.4	97	6 US-10-995-561-900	Sequence 900, App
4	218	53.8	65	7 US-11-043-788-9	Sequence 9, Appli
5	176.5	43.6	73	6 US-10-329-472-7	Sequence 7, Appli
6	145.5	35.9	93	7 US-11-186-284-179	Sequence 179, App
7	133.5	33.0	92	7 US-11-224-076-3	Sequence 3, Appli
8	125	30.9	134	6 US-10-329-472-2	Sequence 2, Appli
9	125	30.9	134	6 US-10-821-234-1597	Sequence 1597, App
10	122.5	30.2	66	7 US-11-175-690-287	Sequence 287, App
11	122.5	30.2	68	7 US-11-175-690-285	Sequence 285, App
12	122.5	30.2	68	7 US-11-175-690-286	Sequence 286, App
13	122.5	30.2	672	7 US-11-175-690-200	Sequence 200, App
14	122.5	30.2	688	7 US-11-175-690-198	Sequence 198, App
15	122.5	30.2	693	7 US-11-175-690-199	Sequence 199, App
16	118.5	29.3	94	6 US-10-131-826A-322	Sequence 322, Appli
17	99.5	24.6	254	6 US-10-997-747-3	Sequence 3, Appli
18	84.5	20.9	122	6 US-10-512-109-13	Sequence 13, Appli
19	78.5	19.4	28	6 US-10-509-292-44	Sequence 44, Appli
20	76	18.8	21	6 US-10-509-292-23	Sequence 23, Appli
21	76	18.8	28	6 US-10-509-292-42	Sequence 42, Appli
22	76	18.8	28	6 US-10-509-292-43	Sequence 43, Appli
23	76	18.8	28	6 US-10-509-292-45	Sequence 45, Appli
24	71	17.5	20	6 US-10-509-292-24	Sequence 24, Appli
25	70	17.3	19	6 US-10-509-292-25	Sequence 25, Appli

ALIGNMENTS

RESULT 1

US-11-043-788-8

; Sequence 8, Application US/11043788

; Publication No. US20060014166A1

; GENERAL INFORMATION:

; APPLICANT: Compugen Ltd

; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS

; FILE REFERENCE: 1847.1006

; CURRENT APPLICATION NUMBER: US/11/043,788

; CURRENT FILING DATE: 2005-01-27

; NUMBER OF SEQ ID NOS: 506

; SEQ ID NO 8

; LENGTH: 99

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-043-788-8

Query Match 100.0%; Score 405; DB 7; Length 99;

Best Local Similarity 100.0%; Pred. No. 3e-45;

Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQLASVLRITSSKCPKEAVIFKTIIVAKETICADPKOKWV 60

Db 24 QPDAINAPVTCYNTNRKISVQLASVLRITSSKCPKEAVIFKTIIVAKETICADPKOKWV 83

Qy 61 QDSMDHLDKQTQTPKT 76

Db 84 QDSMDHLDKQTQTPKT 99

RESULT 2

US-10-509-292-1

; Sequence 1, Application US/10509292

; Publication No. US20050287159A1

; GENERAL INFORMATION:

; APPLICANT: Mercia Pharma LLC

; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin

; FILE REFERENCE: MERPH.001

; CURRENT APPLICATION NUMBER: US/10/509,292

; PRIOR FILING DATE: 2004-09-23

; PRIOR APPLICATION NUMBER: US 60/367,591

; PRIOR FILING DATE: 2002-03-25

; NUMBER OF SEQ ID NOS: 61

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 1

; LENGTH: 74

;	TYPE: PRT																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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```
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-179

Query Match      35.9%; Score 145.5; DB 7; Length 93;
Best Local Similarity 40.3%; Pred. No. 5.6e-12;
Matches 27; Conservative 16; Mismatches 23; Indels 1; Gaps 1;

Qy 2 PDAINAPVTCYNTNRKISVQRLASVYRITSSKCPKEAVIFKTIIVAKEICADPKQKWVQ 61
Db 25 PLAADTPTACCFSTSRQIPQNFIAIDYFE-TSSQCKSPSVIFLTGRGQVCADPSEEWVQ 83
Qy 62 DSMDHL 68
Db 84 KYVSDLE 90

RESULT 7
US-11-224-076-3
; Sequence 3, Application US/11224076
; Publication No. US20060008882A1
; GENERAL INFORMATION:
; APPLICANT: Wei et al.
; FILE REFERENCE: PF401D1
; CURRENT APPLICATION NUMBER: US/11/224,076
; PRIOR FILING DATE: 2005-09-13
; PRIOR APPLICATION NUMBER: US/10/114,482
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 09/195,106
; PRIOR FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 60/066,369
; PRIOR FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-11-224-076-3

Query Match      33.0%; Score 133.5; DB 7; Length 92;
Best Local Similarity 37.3%; Pred. No. 1.9e-10;
Matches 25; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

Qy 2 PDAINAPVTCYNTNRKISVQRLASVYRITSSKCPKEAVIFKTIIVAKEICADPKQKWVQ 61
Db 25 PIGSDPTSCCFSTSRKIHNFWDYFE-TSSLCSPQAVVFLTKGRGQICADPSEEPVN 83
Qy 62 DSMDHL 68
Db 84 EYVNDLE 90

RESULT 8
US-10-329-472-2
; Sequence 2, Application US/10329472
; Publication No. US2005024888A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human Chemokine Beta-9
; FILE REFERENCE: PFI31P2D1

; CURRENT APPLICATION NUMBER: US/10/329,472
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: US 08/793,381
; PRIOR FILING DATE: 1997-05-19
; PRIOR APPLICATION NUMBER: PCT/US95/06260
; PRIOR FILING DATE: 1996-02-29
; PRIOR APPLICATION NUMBER: US 08/294,251
; PRIOR FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-329-472-2

Query Match      30.9%; Score 125; DB 6; Length 134;
Best Local Similarity 41.2%; Pred. No. 3.6e-09;
Matches 28; Conservative 12; Mismatches 24; Indels 4; Gaps 3;

Qy 11 CCYNFTNRKISVQRLASVYRITSS-KCPKEAVIF--KTIIVAKEICADPKQKWVQSDMDHL 67
Db 31 CCLKYSQKIPAKVVRYSYRKQEPSLGCISIPAILFLPKRSQAEICADPKELWVQQLMQHL 90
Qy 68 DKQTQTPK 75
Db 91 DK-TPSPQ 97

RESULT 9
US-10-821-234-1597
; Sequence 1597, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1597
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1597

Query Match      30.9%; Score 125; DB 6; Length 134;
Best Local Similarity 41.2%; Pred. No. 3.6e-09;
Matches 28; Conservative 12; Mismatches 24; Indels 4; Gaps 3;

Qy 11 CCYNFTNRKISVQRLASVYRITSS-KCPKEAVIF--KTIIVAKEICADPKQKWVQSDMDHL 67
Db 31 CCLKYSQKIPAKVVRYSYRKQEPSLGCISIPAILFLPKRSQAEICADPKELWVQQLMQHL 90
Qy 68 DKQTQTPK 75
Db 91 DK-TPSPQ 97

RESULT 10
US-11-175-690-287
; Sequence 287, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
```

QY 8 PVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWQD 62
DB 7 PSECCFTYTYTKIPQRIMDYE-TNSQCSKPGIVFITKRGHSVCTNPSDKWQD 60

RESULT 12

US-11-175-690-286
; Sequence 286, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 286
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-286

Query Match 30.2%; Score 122.5; DB 7; Length 68;
Best Local Similarity 40.0%; Pred. No. 3.5e-09;
Matches 22; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

QY 8 PVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWQD 62
DB 7 PSECCFTYTYTKIPQRIMDYE-TNSQCSKPGIVFITKRGHSVCTNPSDKWQD 60

RESULT 13

US-11-175-690-200
; Sequence 200, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746

; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 287
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-287

Query Match 30.2%; Score 122.5; DB 7; Length 66;
Best Local Similarity 40.0%; Pred. No. 3.4e-09;
Matches 22; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

QY 8 PVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWQD 62
DB 5 PSECCFTYTYTKIPQRIMDYE-TNSQCSKPGIVFITKRGHSVCTNPSDKWQD 58

RESULT 11

US-11-175-690-285
; Sequence 285, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 285
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-285

Query Match 30.2%; Score 122.5; DB 7; Length 68;
Best Local Similarity 40.0%; Pred. No. 3.5e-09;
Matches 22; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

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; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-200

```

Query Match	30.2%	Score 122.5;	DB 7;	Length 672;
Best Local Similarity	40.0%;	Pred. NO. 4.7e-08;		
Matches 22; Conservative	9;	Mismatches 23;	Indels 1;	Gaps 1;

```

RESULT 14
US-11-175-690-198
; Sequence 198, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/441,305
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/453,201
; PRIOR FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 60/467,222
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: US 60/472,816
; PRIOR FILING DATE: 2003-05-23
; PRIOR APPLICATION NUMBER: US 60/476,267
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/505,172
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: US 60/506,746
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 568
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 198
; LENGTH: 688
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-175-690-198

```

Query Match	30.2%	Score 122.5;	DB 7;	Length 688;
Best Local Similarity	40.0%;	Pred. No. 4.8e-08;		
Matches	22; Conservative	9; Mismatches	23; Indels	1; Gaps
Qy	8	PVTCCTNFRNRKISVLRSLASRYRITSKCPKEAVIFKTIIVAKELICADPKQKVVQD	62	
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
Db	26	PBSCCTTYTKIPRIIRIMDYER-TNSQCSKPGVIFIKRGHSVCTNPSDKVVQD	79	
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:
	:	:	:	:

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RESULT 15
US-11-175-690-199
; Sequence 199, Application US/11175690
; Publication No. US20060014254A1
; GENERAL INFORMATION:
; APPLICANT: Haseltine et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF605
; CURRENT APPLICATION NUMBER: US/11/175,690
; CURRENT FILING DATE: 2005-07-07
; PRIOR APPLICATION NUMBER: PCT/US04/001369
; PRIOR FILING DATE: 2004-01-20

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, PRIOR APPLICATION NUMBER: US 60/441,305
, PRIOR FILING DATE: 2003-01-22
, PRIOR APPLICATION NUMBER: US 60/453,201
, PRIOR FILING DATE: 2003-03-11
, PRIOR APPLICATION NUMBER: US 60/467,222
, PRIOR FILING DATE: 2003-05-02
, PRIOR APPLICATION NUMBER: US 60/472,816
, PRIOR FILING DATE: 2003-05-23
, PRIOR APPLICATION NUMBER: US 60/476,267
, PRIOR FILING DATE: 2003-06-06
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, PRIOR FILING DATE: 2003-09-24
, PRIOR APPLICATION NUMBER: US 60/506,746
, PRIOR FILING DATE: 2003-09-30
, NUMBER OF SEQ ID NOS: 568
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 199
, LENGTH: 693
, TYPE: PR7
, ORGANISM: Homo sapiens
US-11-175-690-199

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Query Match	30.2%	Score 122.5;	DB 7;	Length 693;
Best Local Similarity	40.0%;	Pred. No. 4.8e-08;		
Matches	22; Conservative	9; Mismatches 23;	Indels 1; Gaps 1;	

Search completed: February 3, 2006, 10:00:35
Job time : 3.06569 secs

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OM protein - protein search, using sw model

Run on: February 6, 2006, 14:21:14 ; Search time 196 Seconds

(without alignments)
35.868 Million cell updates/sec

Title: US-10-644-277-149_COPY_20_35

Perfect score: 73

Sequence: 1 ISVQLASRYRITSSK 16

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : A_Geneseq21.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	23	3 AAB15851	Aab15851 Chemokine
2	73	100.0	23	4 AAY72689	Aay72689 Human mon
3	73	100.0	24	4 AAY72682	Aay72682 Human mon
4	73	100.0	26	4 AAY72683	Aay72683 Human mon
5	73	100.0	26	8 ADM71779	Adm71779 Chemokine
6	73	100.0	26	8 ADM71742	Adm71742 Chemokine
7	73	100.0	26	8 ADM71778	Adm71778 Chemokine
8	73	100.0	35	8 ADM71727	Adm71727 Chemokine
9	73	100.0	35	8 ADM71718	Adm71718 Chemokine
10	73	100.0	35	8 ADM71720	Adm71720 Chemokine
11	73	100.0	35	8 ADM71736	Adm71736 Chemokine
12	73	100.0	35	8 ADM71741	Adm71741 Chemokine
13	73	100.0	35	8 ADM71725	Adm71725 Chemokine
14	73	100.0	35	8 ADM71726	Adm71726 Chemokine
15	73	100.0	35	8 ADM71719	Adm71719 Chemokine
16	73	100.0	35	8 ADM71723	Adm71723 Chemokine
17	73	100.0	35	8 ADM71730	Adm71730 Chemokine
18	73	100.0	35	8 ADM71722	Adm71722 Chemokine
19	73	100.0	35	8 ADM71728	Adm71728 Chemokine
20	73	100.0	35	8 ADM71734	Adm71734 Chemokine
21	73	100.0	35	8 ADM71735	Adm71735 Chemokine
22	73	100.0	35	8 ADM71740	Adm71740 Chemokine
23	73	100.0	35	8 ADM71733	Adm71733 Chemokine
24	73	100.0	35	8 ADM71780	Adm71780 Chemokine

25	73	100.0	35	8 ADM71721	Adm71721 Chemokine
26	73	100.0	35	8 ADM71724	Adm71724 Chemokine
27	73	100.0	35	8 ADM71731	Adm71731 Chemokine
28	73	100.0	35	8 ADM71739	Adm71739 Chemokine
29	73	100.0	35	8 ADM71729	Adm71729 Chemokine
30	73	100.0	35	8 ADM71732	Adm71732 Chemokine
31	73	100.0	35	8 ADM71737	Adm71737 Chemokine
32	73	100.0	35	8 ADM71738	Adm71738 Chemokine
33	73	100.0	41	8 ADM71745	Adm71745 Chemokine
34	73	100.0	41	8 ADM71783	Adm71783 Chemokine
35	73	100.0	65	9 AEB70238	Aeb70238 Small ind
36	73	100.0	66	2 AAW13598	Aaw13598 Monocyte
37	73	100.0	67	2 AAW13599	Aaw13599 Monocyte
38	73	100.0	68	2 AAW13597	Aaw13597 Monocyte
39	73	100.0	68	2 AAW95037	Aaw95037 MCP-1 ana
40	73	100.0	68	2 AAW95035	Aaw95035 MCP-1 ana
41	73	100.0	68	2 AAW95036	Aaw95036 MCP-1 ana
42	73	100.0	68	8 ADN36565	Adn36565 Chemokine
43	73	100.0	68	8 ADS75933	Ads75933 Monocyte
44	73	100.0	69	2 AAR87678	Aar87678 des(2-8)
45	73	100.0	69	2 AAW13596	Aaw13596 Monocyte
46	73	100.0	69	5 AAM53049	Aam53049 Human mut
47	73	100.0	69	7 ADD14999	Add14999 Truncated
48	73	100.0	69	8 ADN36567	Adn36567 Chemokine
49	73	100.0	69	8 ADT95562	Adt95562 Monocyte
50	73	100.0	74	8 ADR90677	Adr90677 Human mon
51	73	100.0	75	8 ADU04446	Adu04446 Human mon
52	73	100.0	76	1 AAP90292	Aap90292 Peptide f
53	73	100.0	76	2 AAR28660	Aar28660 MCF. 3/20
54	73	100.0	76	2 AAR53398	Aar53398 Sense MCP
55	73	100.0	76	2 AAR87677	Aar87677 (3-Ala) M
56	73	100.0	76	2 AAR87680	Aar87680 Monocyte
57	73	100.0	76	2 AAW09374	Aaw09374 Monocyte
58	73	100.0	76	2 AAW11131	Aaw11131 Mature hu
59	73	100.0	76	2 AAW40175	Aaw40175 Macrophag
60	73	100.0	76	3 AAY69030	Aay69030 Amino aci
61	73	100.0	76	3 AAB12818	Aab12818 Human gli
62	73	100.0	76	5 AAO20010	Aao20010 Human che
63	73	100.0	76	5 AAO14143	Aao14143 Human MCP
64	73	100.0	76	5 AAM53048	Aam53048 Human mon
65	73	100.0	76	7 ADC89673	Adc89673 Human mat
66	73	100.0	76	7 ADD14998	Add14998 Human mon
67	73	100.0	76	7 ADE80852	Adc80852 huMCP1 ch
68	73	100.0	76	7 ADE06777	Ade06777 Human MCP
69	73	100.0	76	8 ADK52443	Adk52443 Human MCP
70	73	100.0	76	8 ADM70376	Adm70376 Human MCP
71	73	100.0	76	8 ADS19898	Ads19898 Modified
72	73	100.0	76	8 ADS19905	Ads19905 Human che
73	73	100.0	76	8 ADS75929	Ads75929 Monocyte
74	73	100.0	76	8 ADR70694	Adr70694 Macrophag
75	73	100.0	76	8 ADR70705	Adr70705 Macrophag
76	73	100.0	76	8 ADR70702	Adr70702 Macrophag
77	73	100.0	76	8 ADR70703	Adr70703 Macrophag
78	73	100.0	76	8 ADR70691	Adr70691 Human mac
79	73	100.0	76	8 ADR70696	Adr70696 Macrophag
80	73	100.0	76	8 ADR70704	Adr70704 Macrophag
81	73	100.0	76	8 ADR70692	Adr70692 Macrophag
82	73	100.0	76	8 ADR70695	Adr70695 Macrophag
83	73	100.0	76	8 ADR70700	Adr70700 Macrophag
84	73	100.0	76	8 ADR70693	Adr70693 Macrophag
85	73	100.0	76	8 ADR70698	Adr70698 Macrophag
86	73	100.0	76	8 ADR70706	Adr70706 Macrophag
87	73	100.0	76	8 ADR70697	Adr70697 Macrophag
88	73	100.0	76	8 ADR70699	Adr70699 Macrophag
89	73	100.0	76	8 ADR70701	Adr70701 Macrophag
90	73	100.0	76	8 ADU24450	Adu24450 Novel glu
91	73	100.0	76	8 ADU46724	Adu46724 CCL2, sub
92	73	100.0	76	9 ADV90272	Adv90272 Protease-
93	73	100.0	76	9 ADV91968	Adv91968 Human mat
94	73	100.0	76	9 ADZ58559	Adz58559 Mature hu
95	73	100.0	76	9 ADZ58560	Adz58560 Mature hu
96	73	100.0	76	9 ADZ58558	Adz58558 Mature hu
97	73	100.0	76	9 ADZ58557	Adz58557 Mature hu

98	73	100.0	76	9	ADZ71380	Adz71380 N-termina	171	56	76.7	74	5	ABB80912	Abb80912 Human eot
99	73	100.0	76	9	AEA16549	Aea16549 Human mon	172	56	76.7	74	5	AAO14141	Aao14141 Human eot
100	73	100.0	76	9	AEb92582	Aeb92582 Glutamin	173	56	76.7	74	5	ADC89677	Adc89677 Human eot
101	73	100.0	77	2	AAR66859	Aar66859 Mature MC	174	56	76.7	74	7	ADF42623	Adf42623 Mature hu
102	73	100.0	77	2	AY14222	AY14222 Chemokine	175	56	76.7	74	8	ADJ66688	Adj66688 Human mat
103	73	100.0	77	2	ADC89671	Adc89671 Human MCP	176	56	76.7	74	8	ADO32082	Ado32082 Eotaxin p
104	73	100.0	77	7	ADC89672	Adc89672 Human MCP	177	56	76.7	74	8	ADR40246	Adr40246 Human mat
105	73	100.0	91	8	ADN36564	Adn36564 Chemokine	178	56	76.7	74	8	ADSL19902	Adsl19902 Modified
106	73	100.0	92	8	ADN36566	Adn36566 Chemokine	179	56	76.7	74	8	ADSL19899	Adsl19899 Modified
107	73	100.0	98	1	ADJ36261	Adj36261 Self-coal	180	56	76.7	74	8	ADSL19906	Adsl19906 Human che
108	73	100.0	99	1	AP95387	Ap95387 Human mon	181	56	76.7	74	8	ADR90676	Adr90676 Human eot
109	73	100.0	99	2	AAR6398	Aar6398 Human MCP	182	56	76.7	74	8	ADSL18178	Adsl18178 Mature hu
110	73	100.0	99	2	AAR28663	Aar28663 MCF_3/20	183	56	76.7	74	9	ADV90271	Adv90271 Protease-
111	73	100.0	99	2	AAR73914	Aar73914 Human mon	184	56	76.7	82	2	AAW44721	Aaw44721 Amino aci
112	73	100.0	99	2	AAR70800	Aar70800 Chemoattr	185	56	76.7	82	2	AAW00667	Aaw00667 Pancreas
113	73	100.0	99	2	AAW40174	Aaw40174 Macrophag	186	56	76.7	97	2	AAW10099	Aaw10099 Human eot
114	73	100.0	99	2	AAW26176	Aay26176 Monocyte	187	56	76.7	97	2	AAW14990	Aaw14990 Human eot
115	73	100.0	99	2	AAW48391	Aay48391 Human pro	188	56	76.7	97	3	AAW15794	Aaw15794 Human che
116	73	100.0	99	3	AAW5785	Aab15785 Human che	189	56	76.7	97	5	ABG94303	Abg94303 Human eot
117	73	100.0	99	4	AAW97914	Aab97914 Human mon	190	56	76.7	97	5	ABG80913	Abg80913 Human eot
118	73	100.0	99	5	AAW52440	Aam52440 HIV_Nef1	191	56	76.7	97	5	ABG80615	Abg80615 Human sec
119	73	100.0	99	5	AAW77179	Aau77179 Human sma	192	56	76.7	97	5	ABG94303	Abg94303 Human eot
120	73	100.0	99	5	ABW80901	Abb80901 Human MCP	193	56	76.7	97	5	ABG80913	Abg80913 Human eot
121	73	100.0	99	5	ABP65214	Abp65214 Hypoxia-r	194	56	76.7	97	5	ABG80615	Abg80615 Human sec
122	73	100.0	99	5	ADG47764	Adg47764 Monocyte	195	56	76.7	97	7	ADC38694	Adc38694 Human che
123	73	100.0	99	6	ABP96799	Adp96799 Human COP	196	56	76.7	97	7	ADK17210	Adk17210 Human eot
124	73	100.0	99	7	ABU10502	Abu10502 Human MCP	197	56	76.7	97	8	ADR40248	Adr40248 Human ful
125	73	100.0	99	7	ADN95634	Adn95634 Human MCP	198	56	76.7	323	3	AAW69058	Aay69058 A chemoki
126	73	100.0	99	7	ADN95634	Adn95634 Human BEC	199	56	76.7	323	3	AAW69059	Aay69059 A chemoki
127	73	100.0	99	7	ADN95618	Adn95618 Human mon	200	52	71.2	70	8	AAW70251	Aay70251 A chemoki
128	73	100.0	99	8	ADN95618	Adn95618 Human mon	201	52	71.2	73	2	AAW70251	Aay70251 A chemoki
129	73	100.0	99	8	ADN04746	Adn04746 Antipeori	202	52	71.2	73	2	AAW70251	Aay70251 A chemoki
130	73	100.0	99	8	ADN04746	Adn04746 Antipeori	203	52	71.2	73	2	AAW70251	Aay70251 A chemoki
131	73	100.0	99	8	ADP75932	Adp75932 Chemokine	204	52	71.2	73	2	AAW70251	Aay70251 A chemoki
132	73	100.0	99	8	ADQ76210	Adq76210 Chemokine	205	52	71.2	73	2	AAW70251	Aay70251 A chemoki
133	73	100.0	99	8	ADQ09330	Adq09330 Human SCY	206	52	71.2	73	2	AAW70251	Aay70251 A chemoki
134	73	100.0	99	8	ADQ09330	Adq09330 Human SCY	207	52	71.2	73	2	AAW70251	Aay70251 A chemoki
135	73	100.0	99	8	ADQ09330	Adq09330 Human SCY	208	52	71.2	73	2	AAW70251	Aay70251 A chemoki
136	73	100.0	99	8	ADP24779	Adp24779 PRO poly	209	52	71.2	73	2	AAW70251	Aay70251 A chemoki
137	73	100.0	99	8	ADP24779	Adp24779 PRO poly	210	52	71.2	73	2	AAW70251	Aay70251 A chemoki
138	73	100.0	99	8	ADU04444	Adu04444 Human sma	211	52	71.2	73	2	AAW70251	Aay70251 A chemoki
139	73	100.0	99	8	ADT75242	Adt75242 Human sma	212	52	71.2	73	2	AAW70251	Aay70251 A chemoki
140	73	100.0	99	8	ADU50779	Adu50779 Human mon	213	52	71.2	73	2	AAW70251	Aay70251 A chemoki
141	73	100.0	99	9	ADV70217	Adv70217 Tumor-ass	214	52	71.2	73	2	AAW70251	Aay70251 A chemoki
142	73	100.0	99	9	ADV70217	Adv70217 Tumor-ass	215	52	71.2	73	2	AAW70251	Aay70251 A chemoki
143	73	100.0	99	9	AEA89981	Aea89981 Human mon	216	50	68.5	77	2	AAW70251	Aay70251 A chemoki
144	73	100.0	99	9	AEb94408	Aeb94408 Human C-C	217	49	67.1	74	2	AAW70251	Aay70251 A chemoki
145	73	100.0	99	9	AEb70237	Aeb70237 Small ind	218	49	67.1	74	2	AAW70251	Aay70251 A chemoki
146	73	100.0	99	9	AEb70237	Aeb70237 Small ind	219	49	67.1	74	2	AAW70251	Aay70251 A chemoki
147	73	100.0	122	7	ADU14997	Adu14997 Human mon	220	49	67.1	74	2	AAW70251	Aay70251 A chemoki
148	73	100.0	133	8	ADJ36265	Adj36265 Self-coal	221	49	67.1	74	2	AAW70251	Aay70251 A chemoki
149	73	100.0	325	3	AAW69049	Aay69049 A chemoki	222	49	67.1	74	2	AAW70251	Aay70251 A chemoki
150	73	100.0	327	3	AAW69049	Aay69049 A chemoki	223	49	67.1	74	2	AAW70251	Aay70251 A chemoki
151	73	100.0	331	9	ADZ58561	Adz58561 Mature hu	224	49	67.1	74	2	AAW70251	Aay70251 A chemoki
152	73	100.0	332	3	AAW69051	Aay69051 A chemoki	225	49	67.1	74	2	AAW70251	Aay70251 A chemoki
153	73	100.0	23	4	AAW72692	Aay72692 Human mon	226	49	67.1	74	2	AAW70251	Aay70251 A chemoki
154	68	93.2	23	4	AAW72693	Abg11504 Novel hum	227	49	67.1	74	2	AAW70251	Aay70251 A chemoki
155	65	89.0	44	4	AAW72693	Aay72693 Human mon	228	47	64.4	60	8	AAW70251	Aay70251 A chemoki
156	65	89.0	76	2	AAW87676	Aar87676 (24-Arg)	229	47	64.4	60	8	AAW70251	Aay70251 A chemoki
157	63	86.3	19	4	AAW72690	Aay72690 Human mon	230	47	64.4	60	8	AAW70251	Aay70251 A chemoki
158	63	86.3	23	4	AAW72690	Aay72690 Human mon	231	47	64.4	60	8	AAW70251	Aay70251 A chemoki
159	61	83.6	76	2	AAW87675	Aar87675 (28-Asp)	232	47	64.4	60	8	AAW70251	Aay70251 A chemoki
160	61	83.6	76	2	AAW87675	Aar87675 (28-Asp)	233	47	64.4	60	8	AAW70251	Aay70251 A chemoki
161	59	80.8	23	4	AAW72691	Aay72691 Human mon	234	47	64.4	60	8	AAW70251	Aay70251 A chemoki
162	58	79.5	23	4	AAW72684	Aay72684 Human mon	235	47	64.4	60	8	AAW70251	Aay70251 A chemoki
163	56	76.7	37	5	ABB80908	Abb80908 Human eot	236	47	64.4	60	8	AAW70251	Aay70251 A chemoki
164	56	76.7	37	8	ADR40241	Adr40241 Human eot	237	47	64.4	60	8	AAW70251	Aay70251 A chemoki
165	56	76.7	73	7	ADN080854	Adn080854 Eotaxin c	238	47	64.4	60	8	AAW70251	Aay70251 A chemoki
166	56	76.7	73	7	ADN080877	Adn080877 Eotaxin c	239	47	64.4	60	8	AAW70251	Aay70251 A chemoki
167	56	76.7	73	9	ADW22565	Adw22565 Human mat	240	47	64.4	60	8	AAW70251	Aay70251 A chemoki
168	56	76.7	74	3	AAW69023	Aay69023 Amino aci	241	47	64.4	60	8	AAW70251	Aay70251 A chemoki
169	56	76.7	74	5	AAO20001	Aao20001 74-mer pr	242	47	64.4	60	8	AAW70251	Aay70251 A chemoki
170	56	76.7	74	5	AAO20008	Aao20008 Human che	243	47	64.4	60	8	AAW70251	Aay70251 A chemoki

244	47	64.4	76	9	AEB92585	Aeb92585	Glutamine
245	47	64.4	77	2	AAy14224	Aay14224	Chemokine
246	47	64.4	77	3	AAy69064	Aay69064	Amino aci
247	47	64.4	91	8	ADN36560	Adn36560	Chemokine
248	47	64.4	92	8	ADN36562	Adn36562	Chemokine
249	47	64.4	99	2	AAr70801	Aar70801	Chemoattr
250	47	64.4	99	3	AAb15787	Aab15787	Human che
251	47	64.4	99	5	AAO19999	Aao19999	99-nex pr
252	47	64.4	99	5	ABP65245	Abp65245	Hypoxia-r
253	47	64.4	99	5	ADZ58696	Adz58696	Human MCP
254	47	64.4	99	7	ADC78915	Adc78915	Human MCP
255	47	64.4	99	7	ADP65189	Adp65189	Human sma
256	47	64.4	99	8	ADJ66686	Adj66686	Human MCP
257	47	64.4	99	8	ADQ32080	Adq32080	Chemokine
258	47	64.4	99	8	ADO47924	Ado47924	Human che
259	47	64.4	99	8	ADP24078	Adp24078	PRO poly
260	47	64.4	99	9	ADW20994	Adw20994	Human MCP
261	47	64.4	109	4	AAU27814	Aau27814	Full-leng
262	47	64.4	109	5	AAm52441	Aam52441	HIV Nef1
263	47	64.4	109	5	AAO21490	Aao21490	Small ind
264	47	64.4	110	5	ABB80904	Abb80904	Human MCP
265	47	64.4	110	8	ADR40234	Adr40234	Human eot
266	47	64.4	133	8	ADU24453	Adu24453	Novel glu
267	47	64.4	137	2	AAy29893	Aay29893	Human MCP
268	47	64.4	143	4	AAO12965	Aao12965	Human pol
269	47	64.4	151	2	AAy29898	Aay29898	Human MCP
270	47	64.4	325	3	AAy69052	Aay69052	A chemoki
271	47	64.4	327	3	AAy69053	Aay69053	DNA encod
272	47	64.4	332	3	AAy69054	Aay69054	A chemoki
273	47	64.4	348	2	AAy29903	Aay29903	Human MCP
274	47	64.4	359	2	AAy29913	Aay29913	Human MCP
275	47	64.4	361	2	AAy29912	Aay29912	Human MCP
276	47	64.4	471	5	AAE23958	Aae23958	MCP3-HIV
277	47	64.4	601	2	AAy29901	Aay29901	Human IP-
278	47	64.4	931	5	AAE23965	Aae23965	MCP3-gp16
279	46	63.0	70	5	AAO19998	Aao19998	70-mex pr
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282	46	63.0	70	9	ADW20993	Adw20993	Eotaxin m
283	46	63.0	148	7	ADD46369	Add46369	Rat Prote
284	45	61.6	92	5	ABB80905	Abb80905	Murine MC
285	45	61.6	92	8	ADR40235	Adr40235	Mouse eot
286	45	61.6	97	2	AAr70803	Aar70803	Growth fa
287	45	61.6	97	5	ADZ58695	Adz58695	Mouse MCP
288	45	61.6	156	2	AAy29907	Aay29907	Murine MCP
289	45	61.6	171	2	AAy29909	Aay29909	Murine MC
290	44	60.3	71	2	AAy07238	Aay07238	Truncated
291	44	60.3	71	2	AAy07234	Aay07234	Truncated
292	44	60.3	72	2	AAr70804	Aar70804	Chemoattr
293	44	60.3	76	3	AAy69031	Aay69031	Amino aci
294	44	60.3	76	5	AAg78390	Aag78390	Human che
295	44	60.3	76	5	AAg68353	Aag68353	Human mon
296	44	60.3	76	5	AAO21099	Aao21099	Protein o
297	44	60.3	76	5	AAO21109	Aao21109	MCP-2 che
298	44	60.3	76	6	ABB99533	Abb99533	Human aci
299	44	60.3	76	7	ADC98686	Adc98686	Human MCP
300	44	60.3	76	7	ADC89674	Adc89674	Human MCP
301	44	60.3	76	7	ADE80844	Ade80844	MCP2 chem
302	44	60.3	76	7	ADR80873	Adr80873	MCP2 chem
303	44	60.3	76	8	ADU24449	Adu24449	Novel glu
304	44	60.3	76	8	ADU46723	Adu46723	CCL8, sub
305	44	60.3	76	9	ADZ71379	Adz71379	N-termina
306	44	60.3	76	9	AEA41185	Aea41185	MCP-2 gly
307	44	60.3	76	9	AEb92581	Aeb92581	Glutamine
308	44	60.3	77	3	AAb15786	Aab15786	Human che
309	44	60.3	77	3	ABB80903	Abb80903	Human MCP
310	44	60.3	77	5	AAg78395	Aag78395	Mouse/hum
311	44	60.3	77	5	AAg68358	Aag68358	Chimeric
312	44	60.3	77	6	ABB99538	Abb99538	Amino aci
313	44	60.3	77	6	ADR40233	Adr40233	Human eot
314	44	60.3	78	7	ADC98691	Adc98691	Human mmd
315	44	60.3	94	5	AAg78393	Aag78393	Mouse/hum

317	44	60.3	94	5	AAg68356	Aag68356	Chimeric
318	44	60.3	94	6	ABB99536	Abb99536	Amino aci
319	44	60.3	94	7	ADC98689	Adc98689	Human mcl
320	44	60.3	95	4	ABB11828	Abb11828	Human che
321	44	60.3	99	2	AAy07237	Aay07237	Wild type
322	44	60.3	99	2	AAy07233	Aay07233	C-C chemo
323	44	60.3	99	2	AAy05300	Aay05300	Human MCP
324	44	60.3	99	5	ADZ58702	Adz58702	Human MCP
325	44	60.3	99	8	ADQ20008	Adq20008	Human eot
326	44	60.3	99	8	ADP55086	Adp55086	Human PRO
327	44	60.3	109	2	AAr24353	Aar24353	Cytokine
328	44	60.3	109	2	AAW26655	Aaw26655	Human bet
329	44	60.3	109	2	AAW42072	Aaw42072	Human MC
330	44	60.3	109	5	ABP65253	Abp65253	Hypoxia-r
331	44	60.3	109	5	ABG35167	Abg35167	Reference
332	44	60.3	109	5	ABG35169	Abg35169	Polymorph
333	44	60.3	109	5	ABG35168	Abg35168	Polymorph
334	44	60.3	109	5	ADZ58742	Adz58742	Human MCP
335	44	60.3	109	7	ADZ58765	Adz58765	Human MCP
336	44	60.3	109	8	ABM81857	Abm81857	Tumour-as
337	43	58.9	9	2	AAy14255	Aay14255	Chemokine
338	43	58.9	9	3	AAb15842	Aab15842	Human che
339	43	58.9	10	2	AAy14280	Aay14280	Chemokine
340	43	58.9	10	3	AAb15835	Aab15835	Human che
341	43	58.9	15	2	AAy14234	Aay14234	Chemokine
342	43	58.9	15	3	AAb18354	Aab18354	Human che
343	43	58.9	15	3	AAb15852	Aab15852	Human che
344	43	58.9	15	3	AAb15772	Aab15772	Human che
345	43	58.9	16	3	AAb15857	Aab15857	Human che
346	43	58.9	17	2	AAy14273	Aay14273	Chemokine
347	43	58.9	17	2	AAy14258	Aay14258	Chemokine
348	43	58.9	17	2	AAy14286	Aay14286	Chemokine
349	42	57.5	17	3	AAb15841	Aab15841	Human che
350	42	57.5	14	4	AAy72697	Aay72697	Human mon
351	42	57.5	301	6	AAb93760	Aab93760	Human pro
352	42	57.5	301	6	ABU00303	Abu00303	Human nov
353	42	57.5	352	4	ABG03657	Abg03657	Novel hum
354	42	57.5	771	6	AAU65531	Aau65531	Propionib
355	42	57.5	771	6	ABM62050	Abm62050	Propionib
356	42	57.5	1480	6	ABM65520	Abm65520	Propionib
357	41	56.2	18	4	AAy72700	Aay72700	Human mon
358	41	56.2	18	4	AAy72696	Aay72696	Human mon
359	41	56.2	321	7	ABO79927	AbO79927	Pseudomon
360	41	56.2	356	7	ABO83985	AbO83985	Pseudomon
361	41	56.2	919	8	ADL26748	Adl26748	Human syn
362	41	56.2	931	4	ABG18567	Abg18567	Novel hum
363	41	56.2	1908	4	ABG18569	Abg18569	Novel hum
364	40	54.8	475	9	ABE39330	Aeb39330	L. pneumo
365	40	54.8	491	9	ABE35895	Aeb35895	L. pneumo
366	40	54.8	492	8	ADK67290	Adk67290	Acidovor
367	39	53.4	12	8	ADS18308	AdS18308	Human eot
368	39	53.4	12	8	ADS18307	AdS18307	Human eot
369	39	53.4	12	8	ADS18309	AdS18309	Human eot
370	39	53.4	375	9	ABE54572	Aeb54572	Vibrio vu
371	39	53.4	1307	8	ADU02646	Adu02646	Novel hum
372	38	52.1	14	4	AAy72699	Aay72699	Human mon
373	38	52.1	44	7	ADF70122	Adf70122	Acma-type
374	38	52.1	179	8	ADX74488	Adx74488	Plant ful
375	38	52.1	223	7	ADC87129	Adc87129	Human GPC
376	38	52.1	311	4	AAg73016	Aag73016	Olfactory
377	38	52.1	342	4	AAg72843	Aag72843	Human olf
378	38	52.1	423	5	AAE22839	Aae22839	Human pho
379	38	52.1	547	7	ABM85898	Abm85898	Rice abio
380	38	52.1	564	9	AEA20320	Aea20320	Novel hum
381	38	52.1	802	5	AAE22843	Aae22843	Human pho
382	38	52.1	818	7	ADB61634	Adb61634	Human 818
383	38	52.1	1026	5	ABB07497	Abb07497	Human lip
384	38	52.1	1045	7	ADC10174	Adc10174	Human NOV
385	37	50.7	14	4	AAy72698	Aay72698	Human mon
386	37	50.7	197	6	ABU29465	Abu29465	Protein e
387	37	50.7	198	7	ADH86543	Adh86543	Enterococ
388	37	50.7	241	1	AAp90060	Aap90060	N-termina
389	37	50.7	241	2	AAW26128	Aaw26128	Flagellin

390	37	50.7	248	5	ABB06152	Human NS	463	36	49.3	762	4	AAB94398	Human pro
391	37	50.7	317	1	AAP70303	Sequence	464	36	49.3	789	6	ABU23388	Protein e
392	37	50.7	349	4	AAB49636	Escherich	465	36	49.3	844	8	ADO61905	Transcrip
393	37	50.7	369	1	AAP70309	Sequence	466	36	49.3	905	4	ABG05208	Novel hum
394	37	50.7	387	1	AAP70307	Sequence	467	36	49.3	1003	4	ABG23021	Novel hum
395	37	50.7	395	1	AAP70308	Sequence	468	36	49.3	1022	6	ABU27718	Protein e
396	37	50.7	414	1	AAP70313	Sequence	469	36	49.3	1134	6	ABU45323	Protein e
397	37	50.7	425	1	AAP70315	Sequence	470	36	49.3	1148	4	AU434541	E. coli c
398	37	50.7	436	4	AAB49637	Escherich	471	36	49.3	1148	4	AU382233	Salmonell
399	37	50.7	447	1	AAP70314	Sequence	472	36	49.3	1148	6	AU47974	Protein e
400	37	50.7	476	8	ADX71308	Plant ful	473	36	49.3	1148	6	ABU31825	Protein e
401	37	50.7	498	1	AAP70302	Sequence	474	36	49.3	1148	6	ABU28601	Protein e
402	37	50.7	498	4	AAB49641	Escherich	475	36	49.3	1152	6	ABM67058	Photornab
403	37	50.7	500	2	AAR90303	Thioredox	476	36	49.3	1154	7	ABO61207	Protein e
404	37	50.7	527	9	ABM96031	M. xanthu	477	36	49.3	1166	6	ABU40581	Human tra
405	37	50.7	550	9	ABM96031	Microbial	478	36	49.3	1172	5	AU96983	Human tra
406	37	50.7	557	9	ABM91490	Escherich	479	36	49.3	1172	5	AU97451	Human tra
407	37	50.7	565	4	AAB49642	Escherich	480	36	49.3	1172	8	ADL16938	Human tra
408	37	50.7	568	4	AAB49639	Escherich	481	36	49.3	1173	7	ADF07680	Bacterial
409	37	50.7	570	4	AAB49640	Escherich	482	36	49.3	1173	7	ADU98137	Human ion
410	37	50.7	588	4	AAB49638	Escherich	483	36	49.3	1204	9	ADU98137	Human ion
411	37	50.7	595	3	RAY52370	Escherich	484	36	49.3	1211	8	ADU98137	Human ion
412	37	50.7	605	4	AAB49643	Escherich	485	36	49.3	1235	5	ADU98137	Human ion
413	37	50.7	1078	4	ABG21954	Novel hum	486	36	49.3	1235	7	ADU98137	Human ion
414	37	50.7	1265	5	ABP73331	Candida a	487	36	49.3	1262	4	ABG20674	Novel hum
415	37	50.7	1309	4	ABG30366	Novel hum	488	36	49.3	1262	4	ABG20674	Novel hum
416	37	50.7	1443	8	ADN21466	Bacterial	489	36	49.3	1322	7	ABR82700	Human cal
417	36.5	50.0	220	6	AAM53626	Propionib	490	36	49.3	1349	7	ABR82700	Human cal
418	36	49.3	23	4	AAU00933	Propionib	491	36	49.3	1349	7	ABR82700	Human cal
419	36	49.3	44	4	AAU00933	Propionib	492	36	49.3	1430	8	ADU98137	Human ion
420	36	49.3	44	4	ABM44250	Novel hum	493	36	49.3	1507	4	ABG30343	Novel hum
421	36	49.3	44	4	ABM77987	Human bra	494	36	49.3	1585	4	ABG10815	Novel hum
422	36	49.3	44	4	AAM65289	Human bra	495	36	49.3	1585	4	ABG10815	Novel hum
423	36	49.3	44	5	ABG47003	Human pep	496	36	49.3	1598	4	ABG06618	Novel hum
424	36	49.3	54	4	AAU45504	Propionib	497	36	49.3	1614	2	AAR75917	Polycyveti
425	36	49.3	54	6	ABM42023	Propionib	498	36	49.3	1614	2	AAR75917	Polycyveti
426	36	49.3	57	4	AAU56117	Propionib	499	36	49.3	1647	4	ABG04001	Novel hum
427	36	49.3	57	6	ABM52636	Propionib	500	36	49.3	1680	8	ADJ35146	Xylanase
428	36	49.3	118	4	AAG66777	Human ILF	501	36	49.3	3001	5	AAE18944	Human PKD
429	36	49.3	118	4	AAG66777	Human ILF	502	36	49.3	3001	5	AAE18944	Human PKD
430	36	49.3	131	4	ABG16963	Novel hum	503	36	49.3	3313	4	AU301034	Novel hum
431	36	49.3	139	4	AAO05874	Human pol	504	36	49.3	3858	5	ABP69242	Human pol
432	36	49.3	158	8	ADY06335	Plant ful	505	36	49.3	4292	4	ABG17060	Novel hum
433	36	49.3	159	8	ADY22993	Plant ful	506	36	49.3	4299	6	ABU52622	Human NOV
434	36	49.3	209	8	AAW39178	Human PKD	507	36	49.3	4302	2	AAW00870	Polycyveti
435	36	49.3	209	8	ABO58792	Human gen	508	36	49.3	4302	2	AAW33396	Human PKD
436	36	49.3	217	8	ADT56318	Plant pol	509	36	49.3	4302	2	AAW33396	Human PKD
437	36	49.3	223	3	AAW24244	Aspergill	510	36	49.3	4302	2	AAW33396	Human PKD
438	36	49.3	228	8	ABR86058	Aspergill	511	36	49.3	4302	2	AAW33396	Human PKD
439	36	49.3	257	9	ABM94771	M. xanthu	512	36	49.3	4302	2	AAW33396	Human PKD
440	36	49.3	281	8	ADX67927	Plant ful	513	36	49.3	4302	2	AAW33396	Human PKD
441	36	49.3	282	7	ABM87880	Rice abio	514	36	49.3	4303	3	AAE18943	Human PKD
442	36	49.3	290	5	ABB92940	Herbicida	515	36	49.3	4303	3	AAE18943	Human PKD
443	36	49.3	331	4	ABB59867	Drosophil	516	36	49.3	4303	5	AAE18935	Human PKD
444	36	49.3	331	8	ADU08051	Fly poly	517	36	49.3	4303	5	AAE18935	Human PKD
445	36	49.3	345	6	ABU48718	Protein e	518	36	49.3	4303	5	AAE18935	Human PKD
446	36	49.3	348	6	ABM67677	Photornab	519	36	49.3	4303	5	AAE18935	Human PKD
447	36	49.3	355	5	ADT117237	Human NOV	520	36	49.3	4303	5	AAE18935	Human PKD
448	36	49.3	417	7	ABO70979	Pseudomon	521	36	49.3	4303	5	AAE18935	Human PKD
449	36	49.3	447	4	ABG30346	Novel hum	522	36	49.3	4303	5	AAE18935	Human PKD
450	36	49.3	462	5	ADT117234	Human NOV	523	36	49.3	4303	5	AAE18935	Human PKD
451	36	49.3	479	7	ABO79945	Pseudomon	524	36	49.3	4303	5	AAE18935	Human PKD
452	36	49.3	489	7	ADC37575	Human nuc	525	36	49.3	4303	5	AAE18935	Human PKD
453	36	49.3	496	5	ADT117235	Human NOV	526	36	49.3	4303	5	AAE18935	Human PKD
454	36	49.3	496	7	ADJ70341	Human hea	527	36	49.3	4304	5	AAE18935	Human PKD
455	36	49.3	521	5	ADT117233	Human NOV	528	36	49.3	4304	5	AAE18935	Human PKD
456	36	49.3	521	9	ADY15832	PRO poly	529	36	49.3	4339	2	AAR75916	Polycyveti
457	36	49.3	531	8	ADT60843	Plant pol	530	36	49.3	4339	2	AAR75916	Polycyveti
458	36	49.3	542	4	AAB94571	Human pro	531	36	49.3	4725	4	ABG23837	Novel hum
459	36	49.3	590	7	ABO74701	Pseudomon	532	36	49.3	4725	4	ABG23837	Novel hum
460	36	49.3	643	4	ABB11071	Human pol	533	36	49.3	4977	4	ABG17057	Novel hum
461	36	49.3	664	4	ABG04272	Novel hum	534	36	49.3	6685	4	ABG23030	Novel hum
462	36	49.3	664	4	ABG05550	Novel hum	535	35.5	48.6	37	4	ABB39431	Peptide #
								35.5	48.6	37	4	AAM32956	Peptide #

536	35.5	48.6	37	4	ABB24203	Abb24203 Protein #	609	35	47.9	129	7	ABO79747	AbO79747 Pseudomon
537	35.5	48.6	37	4	AM72725	Aam72725 Human bon	610	35	47.9	141	2	AAy19767	Aay19767 SEQ ID NO
538	35.5	48.6	37	4	AM60112	Aam60112 Human bra	611	35	47.9	146	8	ADx73014	Adx73014 Plant ful
539	35.5	48.6	37	4	ABG54423	Abg54423 Human liv	612	35	47.9	209	8	ADb29805	AdB29805 Bacterial
540	35.5	48.6	37	5	ABG42549	Abg42549 Human pep	613	35	47.9	219	4	ABb69309	ABb69309 Drosophil
541	35.5	48.6	64	3	AAy95578	Aay95578 Human che	614	35	47.9	260	8	ADx91046	Adx91046 Plant ful
542	35.5	48.6	64	5	AAE15784	Aae15784 Human che	615	35	47.9	274	9	ABm92570	ABm92570 M. xanthu
543	35.5	48.6	65	3	AAy95577	Aay95577 Human che	616	35	47.9	283	8	ADn21526	ADn21526 Bacterial
544	35.5	48.6	65	3	AAE15783	Aae15783 Human che	617	35	47.9	287	5	ABb49876	ABb49876 Listeria
545	35.5	48.6	66	3	AAy95567	Aay95567 Human che	618	35	47.9	287	6	AAE33353	AAE33353 Listeria
546	35.5	48.6	66	5	AAE15782	Aae15782 Human che	619	35	47.9	334	4	ABb70737	ABb70737 Drosophil
547	35.5	48.6	67	3	AAy95566	Aay95566 Human che	620	35	47.9	343	5	ABp73327	ABp73327 Candida a
548	35.5	48.6	67	5	AAE15781	Aae15781 Human che	621	35	47.9	344	2	AAr47213	AAr47213 Lipase mo
549	35.5	48.6	68	5	AAE15780	Aae15780 Human che	622	35	47.9	352	6	ABO14679	ABO14679 Novel hum
550	35.5	48.6	69	3	AAy95565	Aay95565 Human che	623	35	47.9	353	7	ADM26624	ADM26624 Hyperther
551	35.5	48.6	69	5	AAE15779	Aae15779 Human che	624	35	47.9	358	6	ABR62336	ABr62336 Thermoasc
552	35.5	48.6	70	3	AAy95564	Aay95564 Human che	625	35	47.9	358	8	ADx94179	ADx94179 Plant ful
553	35.5	48.6	71	2	AAE15778	Aae15778 Human che	626	35	47.9	415	7	ADf07717	ADf07717 Bacterial
554	35.5	48.6	71	2	AAW23675	Aaw23675 Drol3+ ch	627	35	47.9	424	6	ABO14680	ABO14680 Novel hum
555	35.5	48.6	71	3	AAy95563	Aay95563 Human che	628	35	47.9	450	7	ADM05405	ADM05405 Human pro
556	35.5	48.6	71	5	AAE15785	Aae15785 Human che	629	35	47.9	450	9	AEb39376	AEb39376 L. pneumo
557	35.5	48.6	72	3	AAy95562	Aay95562 Human che	630	35	47.9	453	9	AEb35942	AEb35942 L. pneumo
558	35.5	48.6	72	3	AAy95576	Aay95576 Human che	631	35	47.9	455	6	ABm68247	ABm68247 Photorhab
559	35.5	48.6	72	5	AAE15786	Aae15786 Human che	632	35	47.9	466	5	ADl17236	ADl17236 Murine NO
560	35.5	48.6	73	3	AAy95575	Aay95575 Human che	633	35	47.9	469	6	ABO14678	ABO14678 Novel hum
561	35.5	48.6	73	3	AAE15787	Aae15787 Human che	634	35	47.9	469	6	ABR61426	ABr61426 Syrian ha
562	35.5	48.6	74	5	AAE15788	Aae15788 Human che	635	35	47.9	469	7	ADJ68407	ADj68407 Human hea
563	35.5	48.6	74	7	ADe80851	Ade80851 MCP4 chem	636	35	47.9	469	8	ADN03839	ADn03839 Antipsori
564	35.5	48.6	74	7	ADe80851	Ade80851 MCP4 chem	637	35	47.9	469	8	ADQ30583	ADq30583 Pancreas
565	35.5	48.6	75	2	AAW23673	Aaw23673 Bac 3 che	638	35	47.9	469	7	ADY54941	ADy54941 Chronic v
566	35.5	48.6	75	2	AAW56690	Aaw56690 Chemokine	639	35	47.9	470	7	ADJ69473	ADj69473 Human hea
567	35.5	48.6	75	3	AAy69033	Aay69033 Amino aci	640	35	47.9	470	8	ABM80386	ABm80386 Tumour-as
568	35.5	48.6	75	3	AAy95574	Aay95574 Human che	641	35	47.9	473	8	ADN19556	ADn19556 Bacterial
569	35.5	48.6	75	3	AAy95561	Aay95561 Human che	642	35	47.9	485	8	ADU07677	ADu07677 Amino aci
570	35.5	48.6	75	5	AAE15789	Aae15789 Human che	643	35	47.9	490	4	ABG07778	ABg07778 Novel hum
571	35.5	48.6	75	7	ADC89676	Adc89676 Human MCP	644	35	47.9	490	4	ABG08484	ABg08484 Novel hum
572	35.5	48.6	76	3	AAy95573	Aay95573 Human che	645	35	47.9	505	6	ABU33273	ABu33273 Protein e
573	35.5	48.6	77	2	AAW23672	Aaw23672 Bac 2 che	646	35	47.9	506	9	AEb36481	AEb36481 L. pneumo
574	35.5	48.6	77	2	AAy95572	Aay95572 Human che	647	35	47.9	506	9	AEb39884	AEb39884 L. pneumo
575	35.5	48.6	78	3	AAy95571	Aay95571 Human che	648	35	47.9	507	8	ADN20926	ADn20926 Bacterial
576	35.5	48.6	79	2	AAW23674	Aaw23674 Drol1/2 c	649	35	47.9	515	8	ADx94287	ADx94287 Plant ful
577	35.5	48.6	79	3	AAy95570	Aay95570 Human che	650	35	47.9	550	8	ADx66701	ADx66701 Plant ful
578	35.5	48.6	80	3	AAy95569	Aay95569 Human che	651	35	47.9	552	8	ADx93413	ADx93413 Plant ful
579	35.5	48.6	81	3	AAy95568	Aay95568 Human che	652	35	47.9	646	4	ABG25254	ABg25254 Novel hum
580	35.5	48.6	82	2	AAW23671	Aaw23671 Bac 1 che	653	35	47.9	702	4	ABG18349	ABg18349 Novel hum
581	35.5	48.6	82	2	AAW17665	Aaw17665 Stem cell	654	35	47.9	716	4	ABG35880	ABg35880 Novel hum
582	35.5	48.6	98	2	AAW93087	Aaw93087 Human che	655	35	47.9	730	6	ABU29945	ABu29945 Protein e
583	35.5	48.6	98	2	AAW23670	Aaw23670 Human che	656	35	47.9	730	7	ADC95125	ADC95125 E. faeciu
584	35.5	48.6	98	2	AAW30191	Aaw30191 Monocyte	657	35	47.9	749	4	ABG05779	ABg05779 Novel hum
585	35.5	48.6	98	2	AAW56087	Aaw56087 Human mon	658	35	47.9	808	8	ADL33463	ADl33463 Feetuca a
586	35.5	48.6	98	2	AAy41164	Aay41164 Human che	659	35	47.9	808	8	ADG63031	ADg63031 Transcrip
587	35.5	48.6	98	3	AAE15831	Aae15831 Human che	660	35	47.9	811	4	ABG29434	ABg29434 Novel hum
588	35.5	48.6	98	3	AAE15808	Aae15808 Human che	661	35	47.9	924	4	ABG25166	ABg25166 Novel hum
589	35.5	48.6	98	3	AAy95534	Aay95534 Human che	662	35	47.9	1257	7	ABO68544	ABO68544 Pseudomon
590	35.5	48.6	98	4	AAE31795	Aae31795 Amino aci	663	35	47.9	1402	5	ABP66040	ABp66040 Bifidobac
591	35.5	48.6	98	5	AAO19997	Aao19997 Protein o	664	35	47.9	1717	4	ABG20672	ABg20672 Novel hum
592	35.5	48.6	98	5	AAE15751	Aae15751 Human che	665	34.5	47.3	211	3	AAG41341	AAg41341 Arabidops
593	35.5	48.6	98	5	AAU77180	Aau77180 Human che	666	34.5	47.3	219	3	AAG41340	AAg41340 Arabidops
594	35.5	48.6	98	7	ADD46371	Ad46371 Human Pro	667	34.5	47.3	221	3	AAG41339	AAg41339 Arabidops
595	35.5	48.6	98	7	ADN39903	ADn39903 Cancer/an	668	34.5	47.3	411	8	ADN18521	ADn18521 Bacterial
596	35.5	48.6	98	8	ADJ66672	Adj66672 Human che	669	34.5	46.6	18	9	ADV22825	ADv22825 HCV H77 1
597	35.5	48.6	98	8	ADO32066	Ado32066 Chemokine	670	34	46.6	22	2	AAU84628	AAu84628 HCV HepC1
598	35.5	48.6	98	8	ADQ20884	Adq20884 Human sof	671	34	46.6	30	5	AAU84627	AAu84627 HCV HepC1
599	35.5	48.6	98	9	ADW20982	Adw20982 Human che	672	34	46.6	30	5	AAU84627	AAu84627 HCV HepC1
600	35.5	48.6	106	4	ABG13572	ABg13572 Novel hum	673	34	46.6	48	8	ADU04144	ADu04144 HCV type
601	35	47.9	18	4	AAy72701	Aay72701 Human mon	674	34	46.6	58	7	ADC23277	ADC23277 Conserved
602	35	47.9	72	4	AAU39893	Aau39893 Propionib	675	34	46.6	58	7	ADC23101	ADC23101 Conserved
603	35	47.9	72	6	ABM36412	ABm36412 Propionib	676	34	46.6	72	4	AAm85498	AAm85498 Human imm
604	35	47.9	83	6	ABU39737	ABu39737 Protein e	677	34	46.6	72	5	ADU04170	ADu04170 HCV secon
605	35	47.9	85	4	AAU50390	Aau50390 Propionib	678	34	46.6	73	8	ABB80911	ABb80911 Murine eo
606	35	47.9	85	6	ABM46909	ABm46909 Propionib	679	34	46.6	73	8	ADR40245	ADr40245 Mouse mat
607	35	47.9	121	5	ABP34551	ABp34551 Human ORF	680	34	46.6	82	8	ADU04116	ADu04116 HCV type
608	35	47.9	121	9	ABM91642	ABm91642 M. xanthu	681	34	46.6	83	6	ABU23471	ABu23471 Protein e

609	35	47.9	129	7	ABO79747	AbO79747 Pseudomon
610	35	47.9	141	2	AAy19767	Aay19767 SEQ ID NO
611	35	47.9	146	8	ADx73014	Adx73014 Plant ful
612	35	47.9	209	8	ADs29805	AdS29805 Bacterial
613	35	47.9	219	4	ABb69309	ABb69309 Drosophi
614	35	47.9	260	8	ADx91046	Adx91046 Plant ful
615	35	47.9	274	9	ABm92570	ABm92570 M. xanthu
616	35	47.9	283	8	ADn21526	ADn21526 Bacterial
617	35	47.9	287	5	ABb49876	ABb49876 Listeria
618	35	47.9	287	6	AAE33353	AAE33353 Listeria
619	35	47.9	334	4	ABb70737	ABb70737 Drosophi
620	35	47.9	343	5	ABp73327	ABp73327 Candida a
621	35	47.9	344	2	AAr47213	AAr47213 Lipase mo
622	35	47.9	352	6	ABO14679	ABO14679 Novel hum
623	35	47.9	353	7	ADM26624	ADM26624 Hyperther
624	35	47.9	355	6	ABR62336	ABr62336 Thermoasc
625	35	47.9	358	8	ADx94179	ADx94179 Plant ful
626	35	47.9	415	7	ADf07717	ADf07717 Bacterial
627	35	47.9	424	6	ABO14680	ABO14680 Novel hum
628	35	47.9	450	7	ADM05405	ADM05405 Human pro
629	35	47.9	450	9	AEb39376	AEb39376 L. pneumo
630	35	47.9	453	9	AEb35942	L. pneumo
631	35	47.9	455	6	ABm68247	ABm68247 Photorhab
632	35	47.9	466	5	ADl17236	ADl17236 Murine NO
633	35	47.9	469	6	ABO14678	ABO14678 Novel hum
634	35	47.9	469	6	ABR61426	ABr61426 Syrian ha
635	35	47.9	469	7	ADJ68407	ADj68407 Human hea
636	35	47.9	469	8	ADN03839	ADn03839 Antipsori
637	35	47.9	469	8	ADQ30583	ADq30583 Pancreas
638	35	47.9	469	9	ADY54941	ADy54941 Chronic v
639	35	47.9	470	7	ADJ69473	ADj69473 Human hea
640	35	47.9	470	8	ABM80386	ABm80386 Tumour-as
641	35	47.9	473	8	ADN19556	ADn19556 Bacterial
642	35	47.9	485	8	ADU07677	Amino aci
643	35	47.9	490	4	ABG07778	Novel hum
644	35	47.9	490	4	ABG08484	Novel hum
645	35	47.9	505	6	ABU33273	Protein e
646	35	47.9	506	9	AEb36481	L. pneumo
647	35	47.9	506	9	AEb39884	L. pneumo
648	35	47.9	507	8	ADN20926	Bacterial
649	35	47.9	515	8	ADx94287	Plant ful
650	35	47.9	550	8	ADx66701	Plant ful
651	35	47.9	552	8	ADx93413	Plant ful
652	35	47.9	646	4	ABG25254	Novel hum
653	35	47.9	702	4	ABG18349	Novel hum
654	35	47.9	716	4	ABG25880	Novel hum
655	35	47.9	730	6	ABU29945	Protein e
656	35	47.9	730	7	ADc95125	Novel hum
657	35	47.9	749	4	ABG05779	Novel hum
658	35	47.9	808	8	ADL33463	Festuca a
659	35	47.9	808	8	ADG63031	Arabidops
660	35	47.9	811	4	ABG29434	Novel hum
661	35	47.9	924	4	ABG25166	Novel hum
662	35	47.9	1257	7	ABO68544	Pseudomon
663	35	47.9	1402	5	ABP66040	Bifidobac
664	35	47.9	1717	4	ABG20672	Novel hum
665	34.5	47.3	211	3	AGC411341	Arabidops
666	34.5	47.3	221	3	AGC411339	Arabidops
667	34.5	47.3	431	8	ADN18521	Bacterial
668	34.5	47.3	431	8	ADV22825	HCV H77 i
669	34	46.6	18	9	ADV22825	HCV H77 i
670	34	46.6	22	2	AAr25133	mokk-C4
671	34	46.6	30	5	AAU84628	HCV HepC1
672	34	46.6	30	5	AAU84627	HCV HepC1
673	34	46.6	48	8	ADU04144	HCV type
674	34	46.6	58	7	ADc23277	Conserved
675	34	46.6	58	7	ADc23101	Conserved
676	34	46.6	72	4	AAm85498	Human lmm
677	34	46.6	72	5	ADU04170	HCV secon
678	34	46.6	73	5	ABE80311	Murine eo
679	34	46.6	73	8	ADR40245	Mouse mat
680	34	46.6	82	8	ADU04116	HCV type
681	34	46.6	83	6	ABU23471	Protein e

682	34	46.6	84	4	AUA42321	Aau42321	Propionib	755	34	46.6	421	9	ADW71301	Adw71301	Hepatitis
683	34	46.6	84	6	ABM38840	Abm38840	Propionib	756	34	46.6	425	8	ADL72980	Adl72980	Hepatitis
684	34	46.6	84	7	ADK17255	Adk17255	Mouse eot	757	34	46.6	434	8	AAR79219	Aar79219	pHCV418-e
685	34	46.6	91	5	ABB77256	Abb77256	HCV bait	758	34	46.6	440	4	ABG25855	Abg25855	Novel hum
686	34	46.6	91	7	ABO80300	Abo80300	Pseudomon	759	34	46.6	441	2	AAR79230	Aar79230	pHCV429-e
687	34	46.6	96	7	ADK17286	Adk17286	Virus-lik	760	34	46.6	447	2	AAR79229	Aar79229	pHCV435-e
688	34	46.6	97	5	ABG94306	Abg94306	Mouse eot	761	34	46.6	453	2	AAR79225	Aar79225	pHCV441-e
689	34	46.6	97	5	ABB80897	Abb80897	Murine eo	762	34	46.6	454	3	AAG44669	Aag44669	Zea may
690	34	46.6	97	5	ABG80618	Abg80618	Mouse che	763	34	46.6	473	6	ADA54368	Ada54368	Human pro
691	34	46.6	97	8	ADK17213	Adk17213	Mouse eot	764	34	46.6	473	7	ADJ70685	Adj70685	Human hea
692	34	46.6	97	8	ADR40228	Adr40228	Mouse ful	765	34	46.6	484	3	AG44668	Ag44668	Zea may
693	34	46.6	98	5	ABB80898	Abb80898	Murine eo	766	34	46.6	488	6	ABJ18750	Abj18750	Pseudomon
694	34	46.6	98	8	ADR40229	Adr40229	Mouse ful	767	34	46.6	488	9	ADJ72216	Adj72216	S. enteri
695	34	46.6	105	3	AAG33281	Aag33281	Zea may	768	34	46.6	490	2	AAR79224	Aar79224	pHCV420-e
696	34	46.6	125	3	AAG33280	Aag33280	Zea may	769	34	46.6	493	4	AAB31432	Aab31432	Amino aci
697	34	46.6	144	2	AAR33398	Aar33398	HC-J1 E2/	770	34	46.6	497	4	AAE00443	Aae00443	HCV HVR1-
698	34	46.6	145	7	ADF59171	Adf59171	Human pol	771	34	46.6	497	4	AAE00444	Aae00444	HCV HVR1-
699	34	46.6	145	8	ADX171954	Adx171954	Human pol	772	34	46.6	504	3	AAG44667	Aag44667	Zea may
700	34	46.6	156	4	AAB84198	Abb84198	Amino aci	773	34	46.6	504	3	AAB15522	Abi15522	S. muench
701	34	46.6	165	4	ABB64384	Abb64384	Human pro	774	34	46.6	503	2	AAR24086	Aar24086	NANB hepa
702	34	46.6	166	4	ABB69534	Abb69534	Protein e	775	34	46.6	513	2	AAR24086	Aar24086	HCV polyp
703	34	46.6	174	2	AAR34441	Aar34441	Sequence	776	34	46.6	527	2	AAR25136	Aar25136	APP-HCV-E
704	34	46.6	208	6	ABU35518	Abu35518	Human cor	777	34	46.6	537	2	AAR40114	Aar40114	Oil-aseoc
705	34	46.6	239	4	AG65305	Ag66305	Human cor	778	34	46.6	606	8	ADJ49459	Adj49459	Oil-aseoc
706	34	46.6	246	6	ABU97224	Abu97224	Protein e	779	34	46.6	608	4	ABB67704	Abb67704	Drosophil
707	34	46.6	250	5	AAU97220	Aau97220	Hepatitis	780	34	46.6	608	7	ADC96075	Adc96075	E. faeciu
708	34	46.6	266	3	ABA42726	Aab42726	Human ORF	781	34	46.6	608	8	ADJ50410	Adj50410	Oil-aseoc
709	34	46.6	271	3	AAU57069	Aay57069	Calbindin	782	34	46.6	614	8	ADJ10456	Adj10456	HCV E1/E2
710	34	46.6	271	4	AAE00446	Aae00446	HCV E2-63	783	34	46.6	614	9	ADW71305	Adw71305	Hepatitis
711	34	46.6	271	4	AAE00445	Aae00445	HCV E2-63	784	34	46.6	615	8	ADL04953	Adl04953	M. catarr
712	34	46.6	271	7	ADB70324	Abd70324	Calretini	785	34	46.6	617	4	ABG15495	Abg15495	Novel hum
713	34	46.6	271	7	ADJ37103	Adj37103	Human mal	786	34	46.6	620	9	ADL72978	Adl72978	Hepatitis
714	34	46.6	271	7	ADJ37103	Adj37103	Human mal	787	34	46.6	620	9	ADL72978	Adl72978	Hepatitis
715	34	46.6	271	8	ADX89468	Adx89468	Plant ful	788	34	46.6	645	8	ADJ10454	Adj10454	HCV E2 TB
716	34	46.6	271	8	ADX89468	Adx89468	Plant ful	789	34	46.6	645	9	ADW71303	Adw71303	Hepatitis
717	34	46.6	279	5	ABP53576	Abp53576	Human NOV	790	34	46.6	645	9	ADW71303	Adw71303	Hepatitis
718	34	46.6	280	4	ABG17374	Abg17374	Novel hum	791	34	46.6	645	9	ADW71303	Adw71303	Hepatitis
719	34	46.6	280	6	ABO00771	Ab000771	Polypepti	792	34	46.6	645	9	ADW71303	Adw71303	Hepatitis
720	34	46.6	294	7	ABO80718	Ab080718	Pseudomon	793	34	46.6	645	9	ADW71303	Adw71303	Hepatitis
721	34	46.6	301	8	ADR08563	Adr08563	Human pro	794	34	46.6	682	4	ABB62980	Abb62980	Drosophil
722	34	46.6	301	8	AAW00929	Aaw00929	Recombina	795	34	46.6	682	4	ABB62980	Abb62980	Drosophil
723	34	46.6	319	2	AAW00929	Aaw00929	Recombina	796	34	46.6	682	4	ABB62980	Abb62980	Drosophil
724	34	46.6	325	6	ABM67429	Abm67429	Photorhab	797	34	46.6	754	8	ADJ10458	Adj10458	HCV E1/E2
725	34	46.6	332	6	AAW00929	Aaw00929	Recombina	798	34	46.6	754	8	ADJ10458	Adj10458	HCV E1/E2
726	34	46.6	332	6	AAW00929	Aaw00929	Recombina	799	34	46.6	838	9	ADW71307	Adw71307	Hepatitis
727	34	46.6	337	2	AAR79217	Aar79217	Novel hum	800	34	46.6	838	9	ADW71307	Adw71307	Hepatitis
728	34	46.6	342	6	ABO00448	Ab000448	Novel hum	801	34	46.6	838	9	ADW71307	Adw71307	Hepatitis
729	34	46.6	342	7	ADD71112	Ad71112	Human int	802	34	46.6	881	2	AAW72002	Aaw72002	HSV-2 str
730	34	46.6	349	6	ABU33151	Abu33151	Protein e	803	34	46.6	881	2	AAW72002	Aaw72002	HSV-2 str
731	34	46.6	350	5	AAE19891	Aae19891	Hepatitis	804	34	46.6	881	2	AAW72002	Aaw72002	HSV-2 str
732	34	46.6	350	7	ABW00342	Abw00342	Hepatitis	805	34	46.6	882	8	ADJ5407	Adj5407	Human nov
733	34	46.6	355	6	ABU23392	Abu23392	Protein e	806	34	46.6	882	8	ADJ5407	Adj5407	Human nov
734	34	46.6	356	6	ABM68241	Abm68241	Photorhab	807	34	46.6	943	7	ADF55474	Adf55474	Human veg
735	34	46.6	363	6	ABP55567	Abp55567	Hepatitis	808	34	46.6	943	7	ADF55474	Adf55474	Human veg
736	34	46.6	363	6	ABP55567	Abp55567	Hepatitis	809	34	46.6	967	2	AAR79222	Aar79222	Breast ap
737	34	46.6	367	2	AAW00115	Aaw00115	APP-HCV-E	810	34	46.6	975	6	AAE32037	Aae32037	Human veg
738	34	46.6	367	2	AAW00115	Aaw00115	APP-HCV-E	811	34	46.6	975	6	AAE32037	Aae32037	Human veg
739	34	46.6	367	2	AAW00115	Aaw00115	APP-HCV-E	812	34	46.6	990	5	ABG1010	Abg1010	Novel hum
740	34	46.6	377	7	ADF07756	Adf07756	Bacterial	813	34	46.6	990	5	ABG1010	Abg1010	Novel hum
741	34	46.6	377	7	ADF07756	Adf07756	Bacterial	814	34	46.6	990	5	ABG1010	Abg1010	Novel hum
742	34	46.6	383	9	ABE54574	Ab54574	Vibrio vu	815	34	46.6	990	6	ABOL14700	Abol14700	Angiogene
743	34	46.6	388	6	ABU23061	Abu23061	Photorhab	816	34	46.6	990	6	ABOL14700	Abol14700	Angiogene
744	34	46.6	391	6	ABU23061	Abu23061	Photorhab	817	34	46.6	1006	2	AAW12715	Aaw12715	HCV genom
745	34	46.6	397	2	AAW00117	Aaw00117	Protein e	818	34	46.6	1114	5	ABG69798	Abg69798	Human RBM
746	34	46.6	401	2	AAW21970	Aaw21970	Protein e	819	34	46.6	1114	5	ABG69798	Abg69798	Human RBM
747	34	46.6	401	2	AAW55033	Aaw55033	Actinobac	820	34	46.6	1157	2	AAW25997	Aar25997	Toxin 50C
748	34	46.6	402	2	AAW55033	Aaw55033	Actinobac	821	34	46.6	1157	2	AAW25997	Aar25997	Toxin 50C
749	34	46.6	402	2	AAW55033	Aaw55033	Actinobac	822	34	46.6	1157	2	AAW25997	Aar25997	Toxin 50C
750	34	46.6	402	2	AAW55033	Aaw55033	Actinobac	823	34	46.6	1157	2	AAW25997	Aar25997	Toxin 50C
751	34	46.6	409	2	AAW34439	Aar34439	Sequence	824	34	46.6	1157	2	AAW25997	Aar25997	Toxin 50C
752	34	46.6	409	2	AAW34439	Aar34439	Sequence	825	34	46.6	1157	2	AAW25997	Aar25997	Toxin 50C
753	34	46.6	410	2	AAW34439	Aar34439	Sequence	826	34	46.6	1157	2	AAW25997	Aar25997	Toxin 50C
754	34	46.6	417	2	AAW34439	Aar34439	Sequence	827	34	46.6	1157	2	AAW25997	Aar25997	Toxin 50C
	34	46.6	421	8	ADJ10452	Adj10452	HCV E2 pr		34	46.6	1360	4	ABW59858	Abw59858	Drosophil

828	34	46.6	1997	5	AAU84802	Aau84802	HCV HepC	901	33	45.2	176	4	AAU20983	Aau20983	Human nov
829	34	46.6	2984	4	AAE00449	Aae00449	Hepatitis	902	33	45.2	183	3	AAU44884	Aay44884	Corn tran
830	34	46.6	2984	4	AAE00447	Aae00447	Hepatitis	903	33	45.2	187	3	ABO71281	AbO71281	Pseudomon
831	34	46.6	2984	4	AAE00442	Aae00442	Hepatitis	904	33	45.2	198	8	ADY04356	AdY04356	Plant ful
832	34	46.6	3002	7	AAE00442	Aae00442	Hepatitis	905	33	45.2	199	3	AAG24245	Aag24245	Arabidops
833	34	46.6	3011	2	ADM22154	Adm22154	NANBV Hut	906	33	45.2	204	8	ADY13976	AdY13976	Plant ful
834	34	46.6	3011	2	AAAR40119	Aar40119	HCV genom	907	33	45.2	208	7	ABM74197	Abm74197	DNA clone
835	34	46.6	3011	2	AAAR66995	Aar66995	Hepatitis	908	33	45.2	223	7	ABM89886	Abm89886	Rice abio
836	34	46.6	3011	2	AAAR79232	Aar79232	HCV sequ	909	33	45.2	235	7	AD121207	Ad121207	Novel hum
837	34	46.6	3011	2	AAW77397	Aaw77397	Hepatitis	910	33	45.2	236	7	ADC33168	Adc33168	Human nov
838	34	46.6	3011	2	AAW77398	Aaw77398	Hepatitis	911	33	45.2	244	2	AAV37743	Aay37743	Amino aci
839	34	46.6	3011	2	AAW98020	Aaw98020	Infectiou	912	33	45.2	245	6	ABU01853	Abu01853	S. pneumo
840	34	46.6	3011	4	AAAB59173	Aab59173	Protein e	913	33	45.2	245	6	ABU46119	Abu46119	Protein e
841	34	46.6	3011	4	AAAB31169	Aab31169	Amino aci	914	33	45.2	245	8	ADK46984	Adk46984	Streptoco
842	34	46.6	3011	5	AAU99290	Aau99290	Hepatitis	915	33	45.2	254	8	ADR94587	Adr94587	Novel S.
843	34	46.6	3011	5	AAU84597	Aau84597	HCV polyp	916	33	45.2	254	9	AEA58457	Aea58457	Streptoco
844	34	46.6	3011	5	AAU79221	Aau79221	Hepatitis	917	33	45.2	261	8	ADX70691	Adx70691	Plant ful
845	34	46.6	3011	5	AAAE19888	Aae19888	Hepatitis	918	33	45.2	268	6	ABU40461	Abu40461	Protein e
846	34	46.6	3011	6	AAO26784	Aao26784	Protein d	919	33	45.2	273	4	ABG09597	Abg09597	Novel hum
847	34	46.6	3011	6	ABP71460	Abp71460	Amino aci	920	33	45.2	273	4	ABG09597	Abg09597	Novel hum
848	34	46.6	3011	6	ABU61849	Abu61849	HCV-H. 8/	921	33	45.2	277	7	ADF07952	Adf07952	Bacterial
849	34	46.6	3011	7	ABW00339	Abw00339	Hepatitis	922	33	45.2	286	8	ADL05360	Adl05360	M. catarr
850	34	46.6	3011	8	ADH79949	Adh79949	E2 HCV en	923	33	45.2	286	6	ABU08215	Abu08215	Human syn
851	34	46.6	3011	8	ADJ56744	Adj56744	Hepatitis	924	33	45.2	287	6	ABU08214	Abu08214	Human Zep
852	34	46.6	3011	8	ADJ64256	Adj64256	Hepatitis	925	33	45.2	287	8	ADO19757	Ado19757	Human PRO
853	34	46.6	3011	8	ADL72983	Adl72983	Hepatitis	926	33	45.2	287	9	ADY16389	Ady16389	PRO polyp
854	34	46.6	3011	9	ADX40785	Adx40785	HCV polym	927	33	45.2	287	9	ADZ77616	Adz77616	Human SNA
855	34	46.6	3011	9	ADX40784	Adx40784	HCV polym	928	33	45.2	288	4	ABG04313	Abg04313	Novel hum
856	34	46.6	3011	9	ADX40802	Adx40802	HCV polym	929	33	45.2	289	3	AAG32624	Aag32624	Arabidops
857	34	46.6	3011	9	AEA06142	Aea06142	Full leng	930	33	45.2	289	3	AAG52306	Aag52306	Arabidops
858	34	46.6	3011	9	AEA62080	Aea62080	Hepatitis	931	33	45.2	292	3	AAG52305	Aag52305	Arabidops
859	34	46.6	3011	9	AEA62088	Aea62088	Hepatitis	932	33	45.2	292	3	AAG32623	Aag32623	Arabidops
860	34	46.6	3011	9	AEA62078	Aea62078	Hepatitis	933	33	45.2	294	7	ABO65908	AbO65908	Klebsiell
861	34	46.6	3011	9	ABE17053	AbE17053	Hepatitis	934	33	45.2	296	7	ABO81296	AbO81296	Pseudomon
862	34	46.6	3012	5	AAU99289	Aau99289	Hepatitis	935	33	45.2	300	4	AAU65033	Aau65033	Propionib
863	34	46.6	3012	5	ABU61848	Abu61848	HCV H77 c	936	33	45.2	300	6	ABM61552	Abm61552	Propionib
864	34	46.6	3180	6	ABG73195	Abg73195	MKO-Z vir	937	33	45.2	309	3	ABM25283	Abm25283	Eucalyptu
865	34	46.6	3194	6	ABU31122	Abu31122	Protein e	938	33	45.2	313	8	ADM42776	Adm42776	Murine ca
866	34	46.6	3194	6	ABU31122	Abu31122	Protein e	938	33	45.2	315	8	ADT60334	Adt60334	Plant pol
867	34	46.6	3208	7	ADD67948	AdD67948	Microbial	939	33	45.2	317	8	ADI53718	Adi53718	Streptomy
868	34	46.6	3261	9	ADV23776	Adv23776	Hepatitis	940	33	45.2	318	8	ADI53717	Adi53717	Streptomy
869	34	46.6	3835	4	AAAB31167	AaB31167	Amino aci	941	33	45.2	346	8	ADS43166	AdS43166	Bacterial
870	34	46.6	5985	5	AAU84799	Aau84799	HCV HepC1	942	33	45.2	350	7	ABO77322	AbO77322	Pseudomon
871	34	46.6	19938	6	ABB98398	AbB98398	Streptomy	943	33	45.2	351	3	AAG32622	Aag32622	Arabidops
872	33.5	45.9	652	4	ABB58621	AbB58621	Drosophil	944	33	45.2	351	3	AAG52304	Aag52304	Arabidops
873	33.5	45.9	652	4	ABB65548	AbB65548	Drosophil	945	33	45.2	351	4	ABAB96657	AbB96657	Putative
874	33.5	45.9	657	4	AAAB94585	AaB94585	Human pro	946	33	45.2	351	5	ABB92959	AbB92959	Herbicida
875	33.5	45.9	1208	4	AAAB95292	AaB95292	Human pro	947	33	45.2	351	8	ABO80171	AbO80171	Pseudomon
876	33.5	45.9	1208	8	ADQ96328	AdQ96328	T cell ac	948	33	45.2	366	7	ABO80171	AbO80171	Pseudomon
877	33.5	45.9	1208	9	ADY15794	AdY15794	PRO polyp	949	33	45.2	373	8	ADU02767	AdU02767	Novel hum
878	33.5	45.9	1208	9	ADY15792	AdY15792	PRO polyp	950	33	45.2	395	8	ADX76039	Adx76039	Plant ful
879	33.5	45.9	1213	5	AAO22597	Aao22597	1213-mer	951	33	45.2	396	4	ABG13640	Abg13640	Novel hum
880	33	45.2	9	9	ADZ37635	Adz37635	Human kin	952	33	45.2	435	3	AAG52270	Aag52270	Arabidops
881	33	45.2	15	3	AAAB15818	AaB15818	Human che	953	33	45.2	436	9	ABE12240	Aeb12240	Thale cre
882	33	45.2	58	4	AAU55086	Aau55086	Propionib	954	33	45.2	437	2	AAV34786	Aay34786	Amino aci
883	33	45.2	58	6	ABM51605	AbM51605	Propionib	955	33	45.2	447	8	ADN99753	Adn99753	Novel hum
884	33	45.2	76	4	AAAG2738	AaM2738	Human imm	956	33	45.2	450	3	AAG52269	Aag52269	Arabidops
885	33	45.2	84	4	ABG25360	Abg25360	Novel hum	957	33	45.2	457	7	ADC31549	Adc31549	Human nov
886	33	45.2	107	3	AAAB41543	AaB41543	Human ORF	958	33	45.2	457	8	ADN19823	Adn19823	Bacterial
887	33	45.2	112	8	ADMA2760	Adm42760	Murine ca	959	33	45.2	458	5	ABB93883	AbB93883	Herbicida
888	33	45.2	119	6	ABM71531	Abm71531	Staphyloc	960	33	45.2	481	3	AAG22093	Aag22093	Arabidops
889	33	45.2	134	7	ABO75832	AbO75832	Pseudomon	961	33	45.2	500	4	AAW93943	Aam93943	Human pol
890	33	45.2	135	7	ABO70109	AbO70109	Pseudomon	962	33	45.2	500	5	ABG95660	Abg95660	Human nuc
891	33	45.2	137	4	AAW91823	Aam91823	Human imm	963	33	45.2	500	8	ADH44816	Adh44816	Human KRZ
892	33	45.2	140	3	AAAY44885	Aay44885	Corn tran	964	33	45.2	500	8	ADL32095	AdL32095	Human pro
893	33	45.2	146	7	ABO76760	AbO76760	Pseudomon	965	33	45.2	501	4	AAU66224	Aau66224	Propionib
894	33	45.2	148	2	AAAR62755	Aar62755	Sefid sequ	966	33	45.2	501	6	ABM62743	Abm62743	Propionib
895	33	45.2	148	2	AAW23574	Aaw23574	Salmonell	967	33	45.2	511	5	ABB84430	AbB84430	Human neu
896	33	45.2	148	7	ABO79792	AbO79792	Pseudomon	968	33	45.2	521	5	AD116762	Ad116762	Human NOV
897	33	45.2	150	8	ADY11798	AdY11798	Plant ful	969	33	45.2	521	8	ADN42416	Adn42416	Human nov
898	33	45.2	151	9	AEA98545	Aea98545	HPV (onco	970	33	45.2	522	9	AEA20030	Aea20030	Novel hum
899	33	45.2	166	4	AAG72587	Aag72587	Human OR-	971	33	45.2	523	3	AAG52268	Aag52268	Arabidops
900	33	45.2	166	4	AAG72308	Aag72308	Human OR-	972	33	45.2	542	3	AAU44905	Aay44905	Human pot
								973	33	45.2	548	5	AD116976	Ad116976	Murine NO

chemokines which can be used to produce derivatives, agonists and antagonists which are then useful in disease treatment. The chemokines include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848. These chemokine derivatives can be used to treat diseases such as autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated diseases, endotoxaemia, myocardial infarction, acute ischaemia and rheumatoid arthritis, and can be used to prevent strokes and as contractives. The coding sequences for the chemokines can be used in gene therapy for the same diseases, as well as in the production of animal models

CC chemokines which can be used to produce derivatives, agonists and
CC antagonists which are then useful in disease treatment. The chemokines
CC include sequences AAB15785-B15794, AAB15803-B15813 and AAB15831-B15848.
CC These chemokine derivatives can be used to treat diseases such as
CC autoimmune diseases, atherosclerosis, osteoporosis, HIV infection and
CC AIDS, psoriasis, inflammatory diseases, hypertension, basophil-mediated
CC diseases, endotoxaemia, myocardial infarction, acute ischaemia and
CC rheumatoid arthritis, and can be used to prevent strokes and as
CC contractives. The coding sequences for the chemokines can be used in
CC gene therapy for the same diseases, as well as in the production of
CC animal models
XX
SQ Sequence 23 AA;

Query Match 100.0%; Score 73; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQLASVYRRITSSK 16
DB 8 ISVQLASVYRRITSSK 23
|||||
RESULT 2
AAV72689
ID AAY72689 standard; peptide; 23 AA.
XX
AC AAY72689;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human monocyte chemoattractant protein-1 (MCP-1) fragment #6.
XX
KW Human; monocyte chemoattractant protein-1; MCP-1; therapy;
KW atherosclerotic plaque; autoimmune disease; asthma; inhibitor;
KW ligand-protein binding; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
FN WO200114886-A2.
XX
PD 01-MAR-2001.
XX
PF 23-AUG-2000; 2000WO-US023346.
XX
PR 23-AUG-1999; 99US-0150230P.
PR 23-AUG-1999; 99US-0150318P.
PR 03-SEP-1999; 99US-0152421P.
XX
PA (POLA-) POLARIS PHARM INC.
XX
PI Jenson JC, Sworin M;
XX
DR WPI; 2001-211321/21.
XX
PT Identifying inhibitors of binding between a protein and a ligand,
PT comprises preparing analogs of a lead compound which inhibit binding,
PT combining analog, ligand, protein and assaying inhibition of ligand-
PT protein binding.
XX
PS Disclosure; Fig 3; 45pp; English.
XX
CC The invention relates to identification of compounds which inhibit the
CC binding between a target protein and a macromolecular ligand. These
CC compounds comprise a targeting group, an attaching group and optionally a
CC linker group. They are capable of covalently binding to the surface of a
CC target protein in sufficient proximity to the target protein/ligand
CC binding site in order to inhibit binding of ligand with the target
CC protein. The compounds of the invention serve as potent inhibitors and
CC are useful as drugs which can inhibit protein/macromolecular ligand
CC binding or can serve as leads to optimise biological activity or some
CC other pharmacologically relevant property. The compounds are also useful
CC for detecting target protein in a sample or assessing the quantity of

AAB15074 Protein e
Abp73260 Candida a
Aag22092 Arabidops
Aag22091 Arabidops
Adn24288 Bacterial
Adg22363 Cyanophag
Adt05651 Haemophil
Aau15107 Protein e
Abp73232 Candida e
Aau39123 Propionib
Abm35642 Propionib
Aab50093 GB1 prote
Abm8922 Rice abio
Abb71266 Drosophil
Adn24287 Bacterial
Abu35225 Protein e
Adl04690 M. catarr
Abb71505 Drosophil
Adz10462 P. gingiv
Aeb42540 L. pneumo
Abu50517 Protein e
Aay34576 Porphyrom

974 33 45.2 552 4 AAU15074
975 33 45.2 552 5 ABP73260
976 33 45.2 554 3 AAG22092
977 33 45.2 574 3 AAG22091
978 33 45.2 624 8 ADN24288
979 33 45.2 656 8 ADG22363
980 33 45.2 657 8 ADT05651
981 33 45.2 714 4 AAU15107
982 33 45.2 714 5 ABP73232
983 33 45.2 718 4 AAU39123
984 33 45.2 718 6 ABM35642
985 33 45.2 753 4 AAB50093
986 33 45.2 783 7 ABM8922
987 33 45.2 819 4 ABB71266
988 33 45.2 843 8 ADS23575
989 33 45.2 844 9 ADY93057
990 33 45.2 878 5 ABG93380
991 33 45.2 878 5 ABP73678
992 33 45.2 886 4 ABG15346
993 33 45.2 965 8 ADN24287
994 33 45.2 1033 6 ABU35225
995 33 45.2 1046 8 ADL04690
996 33 45.2 1114 4 ABB71505
997 33 45.2 1123 9 ADZ10462
998 33 45.2 1130 9 AEB42540
999 33 45.2 1148 6 ABU50517
1000 33 45.2 1158 2 AAY34576

ALIGNMENTS

RESULT 1
AAB15851
ID AAB15851 standard; peptide; 23 AA.
XX
AC AAB15851;
XX
DT 17-JAN-2001 (first entry)
XX
DE Chemokine derived peptide SEQ ID NO: 103.
XX
KW Macrophage recruitment; chemokine derivative; MCP-1; osteoporosis;
KW monocyte chemoattractant protein-1; inflammation; atherosclerosis; HIV;
KW AIDS; stroke; psoriasis; autoimmune disease; hypertension; endotoxaemia;
KW basophil-mediated disease; myocardial infarction; acute ischaemia;
KW rheumatoid arthritis; contraception.
XX
OS Unidentified.
XX
FN WO200042071-A2.
XX
PD 20-JUL-2000.
XX
PF 12-JAN-2000; 2000WO-US000821.
XX
PR 12-JAN-1999; 99US-00229071.
PR 17-MAR-1999; 99US-00271192.
PR 01-DEC-1999; 99US-00452406.
XX
PA (NEOR-) NEORX CORP.
XX
PI Grainger DJ, Tatalick LM;
XX
DR WPI; 2000-499101/44.
XX
PT New peptide 3, amide and heterocyclic compounds and saccharide conjugates
PT used for inhibiting chemokine induced activity and for treating e.g.
PT stroke, vascular diseases, autoimmune diseases and tumor growth.
XX
PS Disclosure; Page 387; 387pp; English.
XX
CC The present invention concerns the identification of a number of

CC target protein in a sample which is useful for diagnosing a disease
 CC characterised by over or under abundance of target protein in a tissue or
 CC blood sample. They are also used to assess whether the individual
 CC expresses target protein or its polymorphic form, where the compound has
 CC greater affinity for target protein than its polymorphic form or vice
 CC versa. The present sequence is a fragment of human monocyte
 CC chemoattractant protein-1 (MCP-1). This sequence functions as a
 CC degradable targeting group and inhibits the binding between MCP-1 and its
 CC receptor. Hence this peptide can be useful as drugs in the treatment of
 CC atherosclerotic plaque and autoimmune diseases such as asthma and
 CC rheumatoid arthritis
 XX
 SQ Sequence 23 AA;

Query Match 100.0%; Score 73; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 4.3e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQLASRYRITSSK 16
 |||||
 DB 8 ISVQLASRYRITSSK 23

RESULT 3
 AAY72682
 ID AAY72682 standard; peptide; 24 AA.
 XX
 AC AAY72682;

XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human monocyte chemoattractant protein-1 (MCP-1) fragment #3.
 XX

KW Human; monocyte chemoattractant protein-1; MCP-1; therapy;
 KW atherosclerotic plaque; autoimmune disease; asthma; inhibitor;
 KW ligand-protein binding; rheumatoid arthritis.

XX
 OS Homo sapiens.
 XX
 PN WO200114886-A2.

XX
 PD 01-MAR-2001.

XX
 PF 23-AUG-2000; 2000WO-US023346.

XX
 PR 23-AUG-1999; 99US-0150230P.

XX
 PR 23-AUG-1999; 99US-0150318P.

XX
 PR 03-SEP-1999; 99US-0152421P.

XX
 PA (POLA-) POLARIS PHARM INC.

XX
 PI Jenson JC, Sworin M;

XX
 DR WPI; 2001-211321/21.

XX
 PT Identifying inhibitors of binding between a protein and a ligand,
 PT comprises preparing analogs of a lead compound which inhibit binding,
 PT combining analog, ligand, protein and assaying inhibition of ligand-
 PT protein binding.

XX
 PS Disclosure; Page 12; 45pp; English.

XX The invention relates to identification of compounds which inhibit the
 CC binding between a target protein and a macromolecular ligand. These
 CC compounds comprise a targeting group, an attaching group and optionally a
 CC linker group. They are capable of covalently binding to the surface of a
 CC target protein in sufficient proximity to the target protein/ligand
 CC binding site in order to inhibit binding of ligand with the target
 CC protein. The compounds of the invention serve as potent inhibitors and
 CC are useful as drugs which can inhibit protein/macromolecular ligand
 CC binding or can serve as leads to optimise biological activity or some
 CC other pharmacologically relevant property. The compounds are also useful
 CC for detecting target protein in a sample or assessing the quantity of

CC target protein in a sample which is useful for diagnosing a disease
 CC characterised by over or under abundance of target protein in a tissue or
 CC blood sample. They are also used to assess whether the individual
 CC expresses target protein or its polymorphic form, where the compound has
 CC greater affinity for target protein than its polymorphic form or vice
 CC versa. The present sequence is a fragment of human monocyte
 CC chemoattractant protein-1 (MCP-1). This sequence functions as a
 CC degradable targeting group and inhibits the binding between MCP-1 and its
 CC receptor. Hence this peptide can be useful as drugs in the treatment of
 CC atherosclerotic plaque and autoimmune diseases such as asthma and
 CC rheumatoid arthritis
 XX
 SQ Sequence 24 AA;

Query Match 100.0%; Score 73; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 4.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQLASRYRITSSK 16
 |||||
 DB 9 ISVQLASRYRITSSK 24

RESULT 4
 AAY72683
 ID AAY72683 standard; peptide; 26 AA.
 XX
 AC AAY72683;

XX
 DT 31-MAY-2001 (first entry)
 XX
 DE Human monocyte chemoattractant protein-1 (MCP-1) fragment #4.

KW Human; monocyte chemoattractant protein-1; MCP-1; therapy;
 KW atherosclerotic plaque; autoimmune disease; asthma; inhibitor;
 KW ligand-protein binding; rheumatoid arthritis; cyclic.

XX
 OS Homo sapiens.

XX
 PN Key Location/Qualifiers

XX
 FH Disulfide-bond 2..26
 XX
 FT /note= "Forms a cyclic structure"

XX
 PN WO200114886-A2.

XX
 PD 01-MAR-2001.

XX
 PF 23-AUG-2000; 2000WO-US023346.

XX
 PR 23-AUG-1999; 99US-0150230P.

XX
 PR 23-AUG-1999; 99US-0150318P.

XX
 PR 03-SEP-1999; 99US-0152421P.

XX
 PA (POLA-) POLARIS PHARM INC.

XX
 PI Jenson JC, Sworin M;

XX
 DR WPI; 2001-211321/21.

XX
 PT Identifying inhibitors of binding between a protein and a ligand,
 PT comprises preparing analogs of a lead compound which inhibit binding,
 PT combining analog, ligand, protein and assaying inhibition of ligand-
 PT protein binding.

XX
 PS Disclosure; Page 12; 45pp; English.

XX The invention relates to identification of compounds which inhibit the
 CC binding between a target protein and a macromolecular ligand. These
 CC compounds comprise a targeting group, an attaching group and optionally a
 CC linker group. They are capable of covalently binding to the surface of a
 CC target protein in sufficient proximity to the target protein/ligand
 CC binding site in order to inhibit binding of ligand with the target
 CC protein. The compounds of the invention serve as potent inhibitors and

are useful as drugs which can inhibit protein/macromolecular ligand binding or can serve as leads to optimise biological activity or some other pharmacologically relevant property. The compounds are also useful for detecting target protein in a sample or assessing the quantity of target protein in a sample which is useful for diagnosing a disease characterised by over or under abundance of target protein in a tissue or blood sample. They are also used to assess whether the individual expresses target protein or its polymorphic form, where the compound has greater affinity for target protein than its polymorphic form or vice versa. The present sequence is a disulphide cyclised fragment of human monocyte chemoattractant protein-1 (MCP-1). This sequence functions as a degradable targeting group and inhibits the binding between MCP-1 and its receptor. Hence this peptide can be useful as drugs in the treatment of atherosclerotic plaque and autoimmune diseases such as asthma and rheumatoid arthritis

Sequence 26 AA;

Query Match 100.0%; Score 73; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | |
Db 10 ISVQRLASYRRITSSK 25

RESULT 5
ADM71779
ID ADM71779 standard; peptide; 26 AA.
AC ADM71779;
XX
XX
DT 17-JUN-2004 (first entry)
XX
DE Chemokine analog, 963, SEQ ID 1412.
XX
KW Chemokine analog; Chemokine; interleukin-8; IL-8;
KW Interferon Inducible Protein-10; IP-10; CXCL 10;
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
KW infectious disease; inflammatory condition; graft rejection;
KW bacterial infection; viral infection; vascular condition;
KW atherosclerosis; restenosis; systemic lupus erythematosus;
KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
KW Immunosuppressive; Dermatological; Antiinflammatory; cyclic.
XX
OS Synthetic.

Key Location/Qualifiers
FH Modified-site 1 /note= "RNH-Ala"
FT
FT Misc-difference 3
FT
FT Modified-site 9 /note= "Any amino acid"
FT
FT /note= "The residue at this position forms a bond with Glu26 to form a cyclic peptide"
FT
FT Modified-site 26 /note= "Glu-(OH)-NH2. The residue at this position forms a bond with Lys9 to form a cyclic peptide"
FT
FT
XX WO2004024088-A2.
XX
XX 25-MAR-2004.
XX
XX 11-SEP-2003; 2003WO-US028745.
XX
XX 13-SEP-2002; 2002US-00243795.
XX
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.

PI Merzouk A, Wong D, Salari H;
XX WPI; 2004-329387/30.
DR
XX Compound useful for treating cancer and cardiovascular disease, comprises
PT structure of chemokine analogs such as interleukin-8 and interferon
PT inducible protein-10.
XX
PS Claim 1; SEQ ID NO 1412; 271pp; English.
XX
XX The present invention relates to chemokine analogs (I, ADM70378-
CC ADM72006), including interleukin (IL)-8 analogs, Interferon Inducible
CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
CC analogs. (I) are useful for treating a disease or disorder by
CC administering (I) to a patient. The disease or disorder is chosen from
CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
CC or infectious disease. The administration increases the hemocrit, assist
CC in mobilizing stem cells, in vaccine production or in gene therapy, which
CC are also useful for modulating the activity of chemokine receptor, which
CC involves contacting the chemokine receptor with (I), for mobilizing
CC intracellular calcium in a patient, which involves administering (I) to a
CC patient in need of such treatment. (I) are also useful for protecting
CC haematopoietic cells in a patient undergoing treatment with cytotoxic
CC agent, by administering (I) to the patient, where the survival of white
CC blood cells or leukocytes is increased. (I) are also useful for
CC maintaining cells capable of divisions in a quiescent state cells in a
CC patient undergoing treatment with a cytotoxic agent, by administering (I)
CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
CC patient by administering (I) to the patient. (I) are also useful for
CC treating or preventing inflammatory conditions, graft rejection,
CC bacterial infection, viral infection, vascular conditions (e.g.
CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell
CC mobilization, vaccine production and blood cell recovery following
CC chemotherapy. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 26 AA;
Query Match 100.0%; Score 73; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 4.9e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | |
Db 10 ISVQRLASYRRITSSK 25
RESULT 6
ADM71742
ID ADM71742 standard; peptide; 26 AA.
XX
XX ADM71742;
DT
DT 17-JUN-2004 (first entry)
XX
DE Chemokine analog, 926, SEQ ID 1375.
XX
XX Chemokine analog; Chemokine; interleukin-8; IL-8;
KW Interferon Inducible Protein-10; IP-10; CXCL 10;
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
KW infectious disease; inflammatory condition; graft rejection;
KW bacterial infection; viral infection; vascular condition;
KW atherosclerosis; restenosis; systemic lupus erythematosus;
KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
KW Immunosuppressive; Dermatological; Antiinflammatory.

```

XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "RNH-Ala"
XX FT Misc-difference 3 /note= "Any amino acid"
XX FT Modified-site 26 /note= "Glu- (OH) -NH2"
XX FT
XX PN WO2004024088-A2.
XX XX
XX PD 25-MAR-2004.
XX XX
XX PF 11-SEP-2003; 2003WO-US028745.
XX XX
XX PR 13-SEP-2002; 2002US-00243795.
XX XX
XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX PI Merzouk A, Wong D, Salari H;
XX DR WPI; 2004-329387/30.
XX XX
XX PT Compound useful for treating cancer and cardiovascular disease, comprises
XX PT structure of chemokine analogs such as interleukin-8 and interferon
XX PT inducible protein-10.
XX PS Claim 1; SEQ ID NO 1375; 271pp; English.
XX XX
XX CC The present invention relates to chemokine analogs (I, ADM70378-
XX CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
XX CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
XX CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
XX CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
XX CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
XX CC analogs. (I) are useful for treating a disease or disorder by
XX CC administering (I) to a patient. The disease or disorder is chosen from
XX CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
XX CC or infectious diseases. The administration increases the hemocrit, assist
XX CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
XX CC are also useful for modulating the activity of chemokine receptor, which
XX CC involves contacting the chemokine receptor with (I), for mobilizing
XX CC intracellular calcium in a patient, which involves administering (I) to a
XX CC patient in need of such treatment. (I) are also useful for protecting
XX CC haematopoietic cells in a patient undergoing treatment with cytotoxic
XX CC agent, by administering (I) to the patient, where the survival of white
XX CC blood cells or leukocytes is increased. (I) are also useful for
XX CC maintaining cells capable of divisions in a quiescent state cells in a
XX CC patient undergoing treatment with a cytotoxic agent, by administering (I)
XX CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
XX CC patient by administering (I) to the patient. (I) are also useful for
XX CC treating or preventing inflammatory conditions, graft rejection,
XX CC bacterial infection, viral infection, vascular conditions (e.g.
XX CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
XX CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell
XX CC mobilization, vaccine production and blood cell recovery following
XX CC chemotherapy. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 26 AA;
XX
XX Query Match 100.0%; Score 73; DB 8; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 4.9e-06;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 ISVQLASYYRRTTSK 16
XX | |||||
XX Db 10 ISVQLASYYRRTTSK 25

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RESULT 7
ADM71778
ID ADM71778 standard; peptide; 26 AA.
XX AC ADM71778;
XX DT 17-JUN-2004 (first entry)
XX XX Chemokine analog, g62, SEQ ID 1411.
XX DE
XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;
XX KW Interferon inducible Protein-10; IP-10; CXCL 10;
XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
XX KW infectious disease; inflammatory condition; graft rejection;
XX KW bacterial infection; viral infection; vascular condition;
XX KW atherosclerosis; restenosis; systemic lupus erythematosus;
XX KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;
XX KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
XX KW Immunosuppressive; Dermatological; Antiinflammatory; cyclic.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "RNH-Ala"
XX FT Modified-site 2 /note= "The residue at this position forms a bond with
XX FT Glu26 to form a cyclic peptide"
XX FT Misc-difference 3 /note= "Any amino acid"
XX FT Modified-site 26 /note= "Glu- (OH) -NH2. The residue at this position forms
XX FT a bond with Lys2 to form a cyclic peptide"
XX PN WO2004024088-A2.
XX XX
XX PD 25-MAR-2004.
XX XX
XX PF 11-SEP-2003; 2003WO-US028745.
XX XX
XX PR 13-SEP-2002; 2002US-00243795.
XX XX
XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX PI Merzouk A, Wong D, Salari H;
XX XX WPI; 2004-329387/30.
XX DR
XX PT Compound useful for treating cancer and cardiovascular disease, comprises
XX PT structure of chemokine analogs such as interleukin-8 and interferon
XX PT inducible protein-10.
XX PS Claim 1; SEQ ID NO 1411; 271pp; English.
XX XX
XX CC The present invention relates to chemokine analogs (I, ADM70378-
XX CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
XX CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
XX CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
XX CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
XX CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
XX CC analogs. (I) are useful for treating a disease or disorder by
XX CC administering (I) to a patient. The disease or disorder is chosen from
XX CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
XX CC or infectious diseases. The administration increases the hemocrit, assist
XX CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
XX CC are also useful for modulating the activity of chemokine receptor, which
XX CC involves contacting the chemokine receptor with (I), for mobilizing
XX CC intracellular calcium in a patient, which involves administering (I) to a
XX CC patient in need of such treatment. (I) are also useful for protecting
XX CC haematopoietic cells in a patient undergoing treatment with cytotoxic
XX CC agent, by administering (I) to the patient, where the survival of white
XX CC blood cells or leukocytes is increased. (I) are also useful for
XX CC maintaining cells capable of divisions in a quiescent state cells in a
XX CC patient undergoing treatment with a cytotoxic agent, by administering (I)
XX CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
XX CC patient by administering (I) to the patient. (I) are also useful for
XX CC treating or preventing inflammatory conditions, graft rejection,
XX CC bacterial infection, viral infection, vascular conditions (e.g.
XX CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
XX CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell
XX CC mobilization, vaccine production and blood cell recovery following
XX CC chemotherapy. Note: The sequence data for this patent did not form part
XX CC of the printed specification, but was obtained in electronic format
XX CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 26 AA;

```

CC blood cells or leukocytes is increased. (I) are also useful for
 CC maintaining cells capable of divisions in a quiescent state cells in a
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
 CC patient by administering (I) to the patient. (I) are also useful for
 CC treating or preventing inflammatory conditions, graft rejection,
 CC bacterial infection, viral infection, vascular conditions (e.g.
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell
 CC mobilization, vaccine production and blood cell recovery following
 CC chemotherapy. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 26 AA;
 Query Match 100.0%; Score 73; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 4.9e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ISVQLASVYRRITSSK 16
 |||||
 DB 10 ISVQLASVYRRITSSK 25
 |||||
 RESULT 8
 ADM71727
 ID ADM71727 standard; peptide; 35 AA.
 AC ADM71727;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Chemokine analog, g11, SEQ ID 1360.
 XX
 KW Chemokine analog; Chemokine; interleukin-8; IL-8;
 KW Interferon inducible Protein-10; IP-10; CXCL 10;
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
 KW infectious disease; inflammatory condition; graft rejection;
 KW bacterial infection; viral infection; vascular condition;
 KW atherosclerosis; restenosis; systemic lupus erythematosus;
 KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 KW Immunosuppressive; Dermatological; Antiinflammatory.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "RNH-Gln"
 FT
 FT Misc-difference 8
 FT /note= "Any amino acid"
 FT
 FT Misc-difference 11
 FT /note= "Any amino acid"
 FT
 FT Misc-difference 12
 FT /note= "Any amino acid"
 FT
 FT Modified-site 35
 FT /note= "Lys- (OH)-NH2"
 FT
 XX WO2004024088-A2.
 XX
 XX 25-MAR-2004.
 XX
 XX 11-SEP-2003; 2003WO-US028745.
 XX
 XX 13-SEP-2002; 2002US-00243795.
 XX
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 XX Merzouk A, Wong D, Salari H;
 XX

DR WPI; 2004-329387/30.

XX Compound useful for treating cancer and cardiovascular disease, comprises
 PT structure of chemokine analogs such as interleukin-8 and interferon
 PT inducible protein-10.

XX Claim 1; SEQ ID NO 1360; 271pp; English.

PS The present invention relates to chemokine analogs (I, ADM70378-
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
 CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
 CC analogs. (I) are useful for treating a disease or disorder by
 CC administering (I) to a patient. The disease or disorder is chosen from
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
 CC or infectious disease. The administration increases the hemocrit, assist
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
 CC are also useful for modulating the activity of chemokine receptor, which
 CC involves contacting the chemokine receptor with (I), for mobilizing
 CC intracellular calcium in a patient, which involves administering (I) to a
 CC patient in need of such treatment. (I) are also useful for protecting
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic
 CC agent, by administering (I) to the patient, where the survival of white
 CC blood cells or leukocytes is increased. (I) are also useful for
 CC maintaining cells capable of divisions in a quiescent state cells in a
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
 CC patient by administering (I) to the patient. (I) are also useful for
 CC treating or preventing inflammatory conditions, graft rejection,
 CC bacterial infection, viral infection, vascular conditions (e.g.
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell
 CC mobilization, vaccine production and blood cell recovery following
 CC chemotherapy. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQLASVYRRITSSK 16

|||||
 DB 20 ISVQLASVYRRITSSK 35

RESULT 9

ADM71718

ID ADM71718 standard; peptide; 35 AA.

XX ADM71718;

DT 17-JUN-2004 (first entry)

DE Chemokine analog, g2, SEQ ID 1351.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;

KW Interferon inducible Protein-10; IP-10; CXCL 10;

KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;

KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

KW infectious disease; inflammatory condition; graft rejection;

KW bacterial infection; viral infection; vascular condition;

KW atherosclerosis; restenosis; systemic lupus erythematosus;

KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;

KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

KW Immunosuppressive; Dermatological; Antiinflammatory.

XX Synthetic.

OS

XX Key Location/Qualifiers
 FH Modified-site 1 /note= "RNH-Gln"
 FT Misc-difference 11 /note= "Any amino acid"
 FT Misc-difference 12 /note= "Any amino acid"
 FT Modified-site 35 /note= "Lys- (OH)-NH2"
 FT
 XX WO2004024088-A2.
 XX
 XX 25-MAR-2004.
 XX
 XX 11-SEP-2003; 2003WO-US028745.
 XX
 XX 13-SEP-2002; 2002US-00243795.
 XX
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 XX Merzouk A, Wong D, Salari H;
 XX WPI; 2004-329387/30.
 XX
 XX Compound useful for treating cancer and cardiovascular disease, comprises
 XX structure of chemokine analogs such as interleukin-8 and interferon
 XX inducible protein-10.
 XX
 XX Claim 1; SEQ ID NO 1351; 271pp; English.
 XX
 XX The present invention relates to chemokine analogs (I, ADM70378-
 XX ADM72006), including interleukin (IL)-8 analogs, interferon inducible
 XX Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-
 XX alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
 XX Normal T-cell Expressed, and Presumably Secreted or CCL5) analogs, I-309
 XX analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
 XX analogs. (I) are useful for treating a disease or disorder by
 XX administering (I) to a patient. The disease or disorder is chosen from
 XX autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
 XX or infectious disease. The administration increases the hemocrit, assist
 XX in mobilizing stem cells, in vaccine production or in gene therapy. (I)
 XX are also useful for modulating the activity of chemokine receptor, which
 XX involves contacting the chemokine receptor with (I), for mobilizing
 XX intracellular calcium in a patient, which involves administering (I) to a
 XX patient in need of such treatment. (I) are also useful for protecting
 XX haematopoietic cells in a patient undergoing treatment with cytotoxic
 XX agent, by administering (I) to the patient, where the survival of white
 XX blood cells or leukocytes is increased. (I) are also useful for
 XX maintaining cells capable of divisions in a quiescent state cells in a
 XX
 XX Query Match 100.0%; Score 73; DB 8; Length 35;
 XX Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 ISVQRLASYRRTSSK 16
 XX |||||||
 XX 20 ISVQRLASYRRTSSK 35

RESULT 10
 ADM71720
 ID ADM71720 standard; peptide; 35 AA.
 XX
 XX AC
 XX ADM71720;
 XX
 XX DT 17-JUN-2004 (first entry)
 XX
 XX DE Chemokine analog, g4, SEQ ID 1353.
 XX
 XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;
 XX KW Interferon inducible Protein-10; IP-10; CXCL10;
 XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
 XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
 XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
 XX KW infectious disease; inflammatory condition; graft rejection;
 XX KW bacterial infection; viral infection; vascular condition;
 XX KW atherosclerosis; restenosis; systemic lupus erythematosus;
 XX KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
 XX KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 XX KW Immunosuppressive; Dermatological; Antiinflammatory.
 XX
 XX OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "RNH-Xaa, where Xaa is any amino acid"
 FT Misc-difference 11 /note= "Any amino acid"
 FT Misc-difference 12 /note= "Any amino acid"
 FT Modified-site 35 /note= "Lys- (OH)-NH2"
 FT
 XX WO2004024088-A2.
 XX
 XX 25-MAR-2004.
 XX
 XX 11-SEP-2003; 2003WO-US028745.
 XX
 XX 13-SEP-2002; 2002US-00243795.
 XX
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 XX Merzouk A, Wong D, Salari H;
 XX WPI; 2004-329387/30.
 XX
 XX Compound useful for treating cancer and cardiovascular disease, comprises
 XX structure of chemokine analogs such as interleukin-8 and interferon
 XX inducible protein-10.
 XX
 XX Claim 1; SEQ ID NO 1353; 271pp; English.
 XX
 XX The present invention relates to chemokine analogs (I, ADM70378-
 XX ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
 XX Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-
 XX alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
 XX Normal T-cell Expressed, and Presumably Secreted or CCL5) analogs, I-309
 XX analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
 XX analogs. (I) are useful for treating a disease or disorder by
 XX administering (I) to a patient. The disease or disorder is chosen from
 XX autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
 XX or infectious disease. The administration increases the hemocrit, assist
 XX in mobilizing stem cells, in vaccine production or in gene therapy. (I)
 XX are also useful for modulating the activity of chemokine receptor, which
 XX involves contacting the chemokine receptor with (I), for mobilizing
 XX intracellular calcium in a patient, which involves administering (I) to a
 XX patient in need of such treatment. (I) are also useful for protecting
 XX haematopoietic cells in a patient undergoing treatment with cytotoxic
 XX agent, by administering (I) to the patient, where the survival of white
 XX blood cells or leukocytes is increased. (I) are also useful for
 XX maintaining cells capable of divisions in a quiescent state cells in a
 XX patient undergoing treatment with a cytotoxic agent, by administering (I)
 XX to the patient, and for mobilizing leukocytes e.g. neutrophils in a
 XX patient by administering (I) to the patient. (I) are also useful for
 XX treating or preventing inflammatory conditions, graft rejection,
 XX bacterial infection, viral infection, vascular conditions (e.g.
 XX atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
 XX reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
 XX mobilization, vaccine production and blood cell recovery following
 XX chemotherapy. Note: The sequence data for this patent did not form part
 XX of the printed specification, but was obtained in electronic format
 XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 35 AA;

CC patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Dy 20 ISVQRLASYRRITSSK 35

RESULT 11

ADM71736
ID ADM71736 standard; peptide; 35 AA.

XX AC ADM71736;

XX DT 17-JUN-2004 (first entry)

XX DE Chemokine analog, g20, SEQ ID 1369.

XX DE Chemokine analog; Chemokine; interleukin-8; IL-8;

XX KW Interferon inducible Protein-10; IP-10; CXCL 10;

XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;

XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

XX KW infectious disease; inflammatory condition; graft rejection;

XX KW bacterial infection; viral infection; vascular condition;

XX KW atherosclerosis; restenosis; systemic lupus erythematosus;

XX KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;

XX KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

XX KW Immunosuppressive; Dermatological; Antiinflammatory.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "RNH-Gln"

FT Misc-difference 5 /note= "Any amino acid"

FT Misc-difference 11 /note= "Any amino acid"

FT Misc-difference 12 /note= "Any amino acid"

FT Modified-site 35 /note= "Lys- (OH) -NH2"

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

PT Compound useful for treating cancer and cardiovascular disease, comprises PT structure of chemokine analogs such as interleukin-8 and interferon PT inducible protein-10.

PS Claim 1; SEQ ID NO 1369; 271pp; English.

XX The present invention relates to chemokine analogs (I, ADM70378- CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1- CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, CC Normal T-cell expressed, and presumably Secreted or CCU5) analogs, I-309 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 CC analogs. (I) are useful for treating a disease or disorder by CC administering (I) to a patient. The disease or disorder is chosen from CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease CC or infectious disease. The administration increases the hemocrit, assist CC in mobilizing stem cells, in vaccine production or in gene therapy. (I) CC are also useful for modulating the activity of chemokine receptor, which CC involves contacting the chemokine receptor with (I), for mobilizing CC intracellular calcium in a patient, which involves administering (I) to a CC patient in need of such treatment. (I) are also useful for protecting CC haematopoietic cells in a patient undergoing treatment with cytotoxic CC agent, by administering (I) to the patient, where the survival of white CC blood cells or leukocytes is increased. (I) are also useful for CC maintaining cells capable of divisions in a quiescent state cells in a CC patient undergoing treatment with a cytotoxic agent, by administering (I) CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a CC patient by administering (I) to the patient. (I) are also useful for CC treating or preventing inflammatory conditions, graft rejection, CC bacterial infection, viral infection, systemic lupus erythematosus, and ischaemia- CC atherosclerosis, restenosis, tumourigenesis, and angiogenesis, stem cell CC mobilization, vaccine production and blood cell recovery following CC chemotherapy. Note: The sequence data for this patent did not form part CC of the printed specification, but was obtained in electronic format CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Dy 20 ISVQRLASYRRITSSK 35

RESULT 12

ADM71741
ID ADM71741 standard; peptide; 35 AA.

XX AC ADM71741;

XX DT 17-JUN-2004 (first entry)

XX DE Chemokine analog, g25, SEQ ID 1374.

XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;

XX KW Interferon inducible Protein-10; IP-10; CXCL 10;

XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;

XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

XX KW infectious disease; inflammatory condition; graft rejection;

XX KW bacterial infection; viral infection; vascular condition;

XX KW atherosclerosis; restenosis; systemic lupus erythematosus;

XX KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;

XX KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

XX KW Immunosuppressive; Dermatological; Antiinflammatory.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "RNH-Gln"

FT Misc-difference 5 /note= "Any amino acid"

FT Misc-difference 11 /note= "Any amino acid"

FT Misc-difference 12 /note= "Any amino acid"

FT Modified-site 35 /note= "Lys- (OH) -NH2"

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT FT

FT Modified-site 1 /note= "RNH-Gln"
FT Misc-difference 10 /note= "Any amino acid"
FT Misc-difference 11 /note= "Any amino acid"
FT Misc-difference 12 /note= "Any amino acid"
FT Modified-site 35 /note= "Lys- (OH) -NH2"
XX WO2004024088-A2.
XX 25-MAR-2004.
XX 11-SEP-2003; 2003WO-US028745.
XX 13-SEP-2002; 2002US-00243795.
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX Merzouk A, Wong D, Salari H;
XX WPI; 2004-329387/30.
XX
XX Compound useful for treating cancer and cardiovascular disease, comprises
XX structure of chemokine analogs such as interleukin-8 and interferon
XX inducible protein-10.
XX
XX Claim 1; SEQ ID NO 1374; 271pp; English.
XX
XX The present invention relates to chemokine analogs (I, ADM70378-
XX ADM72006), including interleukin (IL)-8 analogs, interferon inducible
XX Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
XX alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
XX Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
XX analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
XX analogs. (I) are useful for treating a disease or disorder by
XX administering (I) to a patient. The disease or disorder is chosen from
XX autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
XX or infectious disease. The administration increases the hemocrit, assist
XX in mobilizing stem cells, in vaccine production or in gene therapy. (I)
XX are also useful for modulating the activity of chemokine receptor, which
XX involves contacting the chemokine receptor with (I), for mobilizing
XX intracellular calcium in a patient, which involves administering (I) to a
XX patient in need of such treatment. (I) are also useful for protecting
XX haematopoietic cells in a patient undergoing treatment with cytotoxic
XX agent, by administering (I) to the patient, where the survival of white
XX blood cells or leukocytes is increased. (I) are also useful for
XX maintaining cells capable of divisions in a quiescent state cells in a
XX patient undergoing treatment with a cytotoxic agent, by administering (I)
XX to the patient, and for mobilizing leukocytes e.g. neutrophils in a
XX patient by administering (I) to the patient. (I) are also useful for
XX treating or preventing inflammatory conditions, graft rejection,
XX bacterial infection, viral infection, vascular conditions (e.g.
XX atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
XX reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
XX mobilization, vaccine production and blood cell recovery following
XX chemotherapy. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 35 AA;
XX
XX Query Match 100.0%; Score 73; DB 8; Length 35;
XX Best Local Similarity 100.0%; Pred. No. 6.7e-06;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ISVQRLASYYRITSSK 16
XX |||||
XX 20 ISVQRLASYYRITSSK 35

RESULT 13
ADM71725
ID ADM71725 standard; peptide; 35 AA.
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XX ADM71725;
XX
XX 17-JUN-2004 (first entry)
XX
XX Chemokine analog, g9, SEQ ID 1358.
XX
XX Chemokine analog; Chemokine; interleukin-8; IL-8;
XX Interferon inducible Protein-10; IP-10; CXCL 10;
XX Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
XX I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
XX autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
XX infectious disease; inflammatory condition; graft rejection;
XX bacterial infection; viral infection; vascular condition;
XX atherosclerosis; restenosis; systemic lupus erythematosus;
XX ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
XX Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
XX Immunosuppressive; Dermatological; Antiinflammatory.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "RNH-Gln"
XX Misc-difference 6 /note= "Any amino acid"
XX Misc-difference 11 /note= "Any amino acid"
XX Misc-difference 12 /note= "Any amino acid"
XX Modified-site 35 /note= "Lys- (OH) -NH2"
XX
XX WO2004024088-A2.
XX 25-MAR-2004.
XX 11-SEP-2003; 2003WO-US028745.
XX 13-SEP-2002; 2002US-00243795.
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX Merzouk A, Wong D, Salari H;
XX WPI; 2004-329387/30.
XX
XX Compound useful for treating cancer and cardiovascular disease, comprises
XX structure of chemokine analogs such as interleukin-8 and interferon
XX inducible protein-10.
XX
XX Claim 1; SEQ ID NO 1358; 271pp; English.
XX
XX The present invention relates to chemokine analogs (I, ADM70378-
XX ADM72006), including interleukin (IL)-8 analogs, interferon inducible
XX Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
XX alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
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XX patient in need of such treatment. (I) are also useful for protecting
XX haematopoietic cells in a patient undergoing treatment with cytotoxic
XX agent, by administering (I) to the patient, where the survival of white
XX blood cells or leukocytes is increased. (I) are also useful for
XX maintaining cells capable of divisions in a quiescent state cells in a
XX patient undergoing treatment with a cytotoxic agent, by administering (I)
XX to the patient, and for mobilizing leukocytes e.g. neutrophils in a
XX patient by administering (I) to the patient. (I) are also useful for
XX treating or preventing inflammatory conditions, graft rejection,
XX bacterial infection, viral infection, vascular conditions (e.g.
XX atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
XX reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
XX mobilization, vaccine production and blood cell recovery following
XX chemotherapy. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 35 AA;
XX
XX Query Match 100.0%; Score 73; DB 8; Length 35;
XX Best Local Similarity 100.0%; Pred. No. 6.7e-06;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 ISVQRLASYYRITSSK 16
XX |||||
XX 20 ISVQRLASYYRITSSK 35

CC blood cells or leukocytes is increased. (I) are also useful for
CC maintaining cells capable of divisions in a quiescent state cells in a
CC patient undergoing treatment with a cytotoxic agent, by administering (I)
CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
CC patient by administering (I) to the patient. (I) are also useful for
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CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell
CC mobilization, vaccine production and blood cell recovery following
CC chemotherapy. Note: The sequence data for this patent did not form part
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XX
XX
XX Sequence 35 AA;
Query Match 100.0%; Score 73; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ISVQRLASYRRITSSK 16
Db 20 ISVQRLASYRRITSSK 35
RESULT 14
ADM71726
ID ADM71726 standard; peptide; 35 AA.
XX AC ADM71726;
XX DT 17-JUN-2004 (first entry)
XX DE Chemokine analog, g10, SEQ ID 1359.
XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;
XX KW Interferon inducible Protein-10; IP-10; CXCL 10;
XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
XX KW infectious disease; inflammatory condition; graft rejection;
XX KW bacterial infection; viral infection; vascular condition;
XX KW atherosclerosis; restenosis; systemic lupus erythematosus;
XX KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;
XX KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
XX KW Immunosuppressive; Dermatological; Antiinflammatory.
XX OS Synthetic.
FH Key Location/Qualifiers
FT Modified-site 1 /note= "RNH-Gln"
FT FT
FT Misc-difference 7 /note= "Any amino acid"
FT FT
FT Misc-difference 11 /note= "Any amino acid"
FT FT
FT Misc-difference 12 /note= "Any amino acid"
FT FT
FT Modified-site 35 /note= "Lys- (OH) -NH2"
FT FT
XX WO2004024088-A2.
PN
XX 25-MAR-2004.
PD
XX 11-SEP-2003; 2003WO-US028745.
PP
XX 13-SEP-2002; 2002US-00243795.
PR
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
PA
XX Merzouk A, Wong D, Salari H;
PI
XX

DR WPI; 2004-329387/30.
XX Compound useful for treating cancer and cardiovascular disease, comprises
PT structure of chemokine analogs such as interleukin-8 and interferon
PT inducible protein-10.
XX Claim 1; SEQ ID NO 1359; 271pp; English.
XX The present invention relates to chemokine analogs (I, ADM70378-
CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (regulated upon Activation,
CC Normal T-cell Expressed, and presumably Secreted or CCU5) analogs, I-309
CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
CC analogs. (I) are useful for treating a disease or disorder by
CC administering (I) to a patient. The disease or disorder is chosen from
CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
CC or infectious disease. The administration increases the hemocrit, assist
CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
CC are also useful for modulating the activity of chemokine receptor, which
CC involves contacting the chemokine receptor with (I), for mobilizing
CC intracellular calcium in a patient, which involves administering (I) to a
CC patient in need of such treatment. (I) are also useful for protecting
CC haematopoietic cells in a patient undergoing treatment with cytotoxic
CC agent, by administering (I) to the patient, where the survival of white
CC blood cells or leukocytes is increased. (I) are also useful for
CC maintaining cells capable of divisions in a quiescent state cells in a
CC patient undergoing treatment with a cytotoxic agent, by administering (I)
CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
CC patient by administering (I) to the patient. (I) are also useful for
CC treating or preventing inflammatory conditions, graft rejection,
CC bacterial infection, viral infection, vascular conditions (e.g.
CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell
CC mobilization, vaccine production and blood cell recovery following
CC chemotherapy. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 35 AA;
Query Match 100.0%; Score 73; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ISVQRLASYRRITSSK 16
Db 20 ISVQRLASYRRITSSK 35
RESULT 15
ADM71719
ID ADM71719 standard; peptide; 35 AA.
XX AC ADM71719;
XX DT 17-JUN-2004 (first entry)
XX DE Chemokine analog, g3, SEQ ID 1352.
XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;
XX KW Interferon inducible Protein-10; IP-10; CXCL 10;
XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
XX KW infectious disease; inflammatory condition; graft rejection;
XX KW bacterial infection; viral infection; vascular condition;
XX KW atherosclerosis; restenosis; systemic lupus erythematosus;
XX KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;
XX KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
XX KW Immunosuppressive; Dermatological; Antiinflammatory.
XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "RNH-Gln"
 FT Misc-difference 11
 FT Misc-difference 12 /note= "Any amino acid"
 FT Misc-difference 12 /note= "Any amino acid"
 FT Modified-site 35
 FT /note= "Lys- (OH)-NH2"
 XX
 PN WO2004024088-A2.
 XX
 XX 25-MAR-2004.
 XX
 XX 11-SEP-2003; 2003WO-US028745.
 XX
 XX 13-SEP-2002; 2002US-00243795.
 XX
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 XX Merzouk A, Wong D, Salari H;
 XX WPI; 2004-329387/30.
 XX
 XX Compound useful for treating cancer and cardiovascular disease, comprises
 FT structure of chemokine analogs such as interleukin-8 and interferon
 FT inducible protein-10.
 XX
 XX Claim 1; SEQ ID NO 1352; 271pp; English.
 XX
 XX The present invention relates to chemokine analogs (I, ADM70378-
 CC ADM72006), including interleukin (IL)-8 analogs, interferon inducible
 CC protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
 CC analogs. (I) are useful for treating a disease or disorder by
 CC administering (I) to a patient. The disease or disorder is chosen from
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
 CC or infectious diseases. The administration increases the hemocrit, assist
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
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 CC involves contacting the chemokine receptor with (I), for mobilizing
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 CC haematopoietic cells in a patient undergoing treatment with cytotoxic
 CC agent, by administering (I) to the patient, where the survival of white
 CC blood cells or leukocytes is increased. (I) are also useful for
 CC maintaining cells capable of divisions in a quiescent state cells in a
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
 CC patient by administering (I) to the patient. (I) are also useful for
 CC treating or preventing inflammatory conditions, graft rejection,
 CC bacterial infection, viral infection, vascular conditions (e.g.
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
 CC mobilization, vaccine production and blood cell recovery following
 CC chemotherapy. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 35 AA;
 SQ
 Query Match 100.0%; Score 73; DB 8; Length 35;
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ISVQRLASYRRITSSK 16
 |||||
 Db 20 ISVQRLASYRRITSSK 35

RESULT 16
 ADM71723
 ID ADM71723 standard; peptide; 35 AA.
 XX
 AC ADM71723;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Chemokine analog, g7, SEQ ID 1356.
 XX
 KW Chemokine analog; Chemokine; interleukin-8; IL-8;
 KW Interferon inducible Protein-10; IP-10; CXCL 10;
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
 KW infectious disease; inflammatory condition; graft rejection;
 KW bacterial infection; viral infection; vascular condition;
 KW atherosclerosis; restenosis; systemic lupus erythematosus;
 KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 KW Immunosuppressive; Dermatological; Antiinflammatory.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "RNH-Gln"
 FT Misc-difference 4 /note= "Any amino acid"
 FT Misc-difference 11 /note= "Any amino acid"
 FT Misc-difference 12 /note= "Any amino acid"
 FT Misc-difference 12 /note= "Any amino acid"
 FT Modified-site 35
 FT /note= "Lys- (OH)-NH2"
 PN WO2004024088-A2.
 XX
 XX 25-MAR-2004.
 XX
 XX 11-SEP-2003; 2003WO-US028745.
 XX
 XX 13-SEP-2002; 2002US-00243795.
 XX
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 XX Merzouk A, Wong D, Salari H;
 XX WPI; 2004-329387/30.
 XX
 XX Compound useful for treating cancer and cardiovascular disease, comprises
 FT structure of chemokine analogs such as interleukin-8 and interferon
 FT inducible protein-10.
 XX
 XX Claim 1; SEQ ID NO 1356; 271pp; English.
 XX
 XX The present invention relates to chemokine analogs (I, ADM70378-
 CC ADM72006), including interleukin (IL)-8 analogs, interferon inducible
 CC protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
 CC analogs. (I) are useful for treating a disease or disorder by
 CC administering (I) to a patient. The disease or disorder is chosen from
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 CC or infectious diseases. The administration increases the hemocrit, assist
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 CC involves contacting the chemokine receptor with (I), for mobilizing
 CC intracellular calcium in a patient, which involves administering (I) to a
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 CC haematopoietic cells in a patient undergoing treatment with cytotoxic
 CC agent, by administering (I) to the patient, where the survival of white
 CC blood cells or leukocytes is increased. (I) are also useful for
 CC maintaining cells capable of divisions in a quiescent state cells in a
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
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 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
 CC mobilization, vaccine production and blood cell recovery following
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 CC of the printed specification, but was obtained in electronic format
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 XX
 XX Sequence 35 AA;
 SQ
 Query Match 100.0%; Score 73; DB 8; Length 35;
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ISVQRLASYRRITSSK 16
 |||||
 Db 20 ISVQRLASYRRITSSK 35

CC blood cells or leukocytes is increased. (I) are also useful for
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 XX Sequence 35 AA;
 CC
 CC Query Match 100.0%; Score 73; DB 8; Length 35;
 CC Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Qy 1 ISVQRLASYRRITSSK 16
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 CC Db 20 ISVQRLASYRRITSSK 35
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 CC RESULT 17
 CC ADM71730
 CC ID ADM71730 standard; peptide; 35 AA.
 CC AC
 CC AD71730;
 CC
 CC DT 17-JUN-2004 (first entry)
 CC
 CC DE Chemokine analog, g14, SEQ ID 1363.
 CC
 CC KW Chemokine analog; Chemokine; interleukin-8; IL-8;
 CC KW Interferon inducible Protein-10; IP-10; CXCL 10;
 CC KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
 CC KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
 CC KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
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 CC KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 CC KW Immunosuppressive; Dermatological; Antiinflammatory.
 CC
 CC OS Synthetic.
 CC
 CC FH Key Location/Qualifiers
 CC FT Modified-site 1 /note= "RNH-Gln"
 CC FT Misc-difference 11 /note= "Any amino acid"
 CC FT Misc-difference 12 /note= "Any amino acid"
 CC FT Modified-site 35 /note= "Lys-(OH)-NH2"
 CC FT
 CC FN WO2004024088-A2.
 CC
 CC PD 25-MAR-2004.
 CC
 CC XX 11-SEP-2003; 2003WO-US028745.
 CC XX 13-SEP-2002; 2002US-00243795.
 CC XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 CC XX Merzouk A, Wong D, Salari H;
 CC WPI; 2004-329387/30.
 CC
 CC XX

PT Compound useful for treating cancer and cardiovascular disease, comprises
 PT structure of chemokine analogs such as interleukin-8 and interferon
 XX inducible protein-10.
 PS Claim 1; SEQ ID NO 1363; 271pp; English.
 XX
 CC The present invention relates to chemokine analogs (I, ADM70378-
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
 CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
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 CC agent, by administering (I) to the patient, where the survival of white
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 CC maintaining cells capable of divisions in a quiescent state cells in a
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 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
 CC mobilization, vaccine production and blood cell recovery following
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 XX
 XX Sequence 35 AA;
 CC
 CC Query Match 100.0%; Score 73; DB 8; Length 35;
 CC Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC Qy 1 ISVQRLASYRRITSSK 16
 CC | | | | | | | | | | | | | | | |
 CC Db 20 ISVQRLASYRRITSSK 35
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 CC RESULT 18
 CC ADM71722
 CC ID ADM71722 standard; peptide; 35 AA.
 CC AC
 CC AD71722;
 CC
 CC DT 17-JUN-2004 (first entry)
 CC
 CC DE Chemokine analog, g6, SEQ ID 1355.
 CC
 CC KW Chemokine analog; Chemokine; interleukin-8; IL-8;
 CC KW Interferon inducible Protein-10; IP-10; CXCL 10;
 CC KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
 CC KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
 CC KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
 CC KW infectious disease; inflammation; graft rejection;
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 CC KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 CC KW Immunosuppressive; Dermatological; Antiinflammatory.
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 CC
 CC FH Key Location/Qualifiers

FT Modified-site 1 /note= "RNH-Gln"
 FT Misc-difference 3 /note= "Any amino acid"
 FT Misc-difference 11 /note= "Any amino acid"
 FT Misc-difference 12 /note= "Any amino acid"
 FT Modified-site 35 /note= "Lys-(OH)-NH2"
 XX WO2004024088-A2.
 XX 25-MAR-2004.
 XX 11-SEP-2003; 2003WO-US028745.
 XX 13-SEP-2002; 2002US-00243795.
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX Merzouk A, Wong D, Salari H;
 XX WPI; 2004-329387/30.
 XX Compound useful for treating cancer and cardiovascular disease, comprises
 FT structure of chemokine analogs such as interleukin-8 and interferon
 FT inducible protein-10.
 XX Claim 1; SEQ ID NO 1355; 271pp; English.
 PS The present invention relates to chemokine analogs (I, ADM70378-
 CC ADM72006), including interleukin (IL)-8 analogs, interferon inducible
 CC Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
 CC analogs. (I) are useful for treating a disease or disorder by
 CC administering (I) to a patient. The disease or disorder is chosen from
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
 CC or infectious diseases. The administration increases the hemocrit, assist
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
 CC are also useful for modulating the activity of chemokine receptor, which
 CC involves contacting the chemokine receptor with (I), for mobilizing
 CC intracellular calcium in a patient, which involves administering (I) to a
 CC patient in need of such treatment. (I) are also useful for protecting
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic
 CC agent, by administering (I) to the patient, where the survival of white
 CC blood cells or leukocytes is increased. (I) are also useful for
 CC maintaining cells capable of divisions in a quiescent state cells in a
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
 CC patient by administering (I) to the patient. (I) are also useful for
 CC treating or preventing inflammatory conditions, graft rejection,
 CC bacterial infection, viral infection, vascular conditions (e.g.
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
 CC mobilization, vaccine production and blood cell recovery following
 CC chemotherapy. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYYRRTSSK 16
 |||||
 Db 20 ISVQRLASYYRRTSSK 35

RESULT 19
 ADM71728
 ID ADM71728 standard; peptide; 35 AA.
 XX AC ADM71728;
 XX 17-JUN-2004 (first entry)
 XX Chemokine analog, g12, SEQ ID 1361.
 XX Chemokine analog; Chemokine; Interleukin-8; IL-8;
 KW Interferon inducible Protein-10; IP-10; CXCL 10;
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
 KW infectious disease; inflammatory condition; graft rejection;
 KW bacterial infection; viral infection; vascular condition;
 KW atherosclerosis; restenosis; systemic lupus erythematosus;
 KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 KW Immunosuppressive; Dermatological; Antiinflammatory.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "RNH-Gln"
 FT Misc-difference 9 /note= "Any amino acid"
 FT Misc-difference 11 /note= "Any amino acid"
 FT Misc-difference 12 /note= "Any amino acid"
 FT Modified-site 35 /note= "Lys-(OH)-NH2"
 XX WO2004024088-A2.
 XX 25-MAR-2004.
 XX 11-SEP-2003; 2003WO-US028745.
 XX 13-SEP-2002; 2002US-00243795.
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX Merzouk A, Wong D, Salari H;
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 CC ADM72006), including interleukin (IL)-8 analogs, interferon inducible
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 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
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 CC bacterial infection, viral infection, vascular conditions (e.g.
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 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
 CC mobilization, vaccine production and blood cell recovery following
 CC chemotherapy. Note: The sequence data for this patent did not form part
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 CC mobilization, vaccine production and blood cell recovery following
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 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 35 AA;
 Query Match 100.0%; Score 73; DB 8; Length 35;
 Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ISVQRLASYRRITSSK 16
 |||||
 Db 20 ISVQRLASYRRITSSK 35
 RESULT 20
 ADM71734
 ID ADM71734 standard; peptide; 35 AA.
 AC ADM71734;
 XX
 DT 17-JUN-2004 (first entry)
 DE Chemokine analog, g18, SEQ ID 1367.
 XX
 KW Chemokine analog; Chemokine; interleukin-8; IL-8;
 KW Interferon inducible Protein-10; IP-10; CXCL 10;
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
 KW infectious disease; inflammatory condition; graft rejection;
 KW bacterial infection; viral infection; vascular condition;
 KW atherosclerosis; restenosis; systemic lupus erythematosus;
 KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 KW Immunosuppressive; Dermatological; Antiinflammatory.
 XX
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "RNH-Gln"
 FT Misc-difference 3
 FT /note= "Any amino acid"
 FT Misc-difference 11
 FT /note= "Any amino acid"
 FT Misc-difference 12
 FT /note= "Any amino acid"
 FT Modified-site 35
 FT /note= "Lys- (OH)-NH2"
 XX
 PN WO2004024088-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 11-SEP-2003; 2003WO-US028745.
 XX
 PR 13-SEP-2002; 2002US-00243795.
 XX
 PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 XX
 PI Merzouk A, Wong D, Salari H;
 XX

DR WPI; 2004-329387/30.

XX Compound useful for treating cancer and cardiovascular disease, comprises
 PT structure of chemokine analogs such as interleukin-8 and interferon
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XX Claim 1; SEQ ID NO 1367; 271pp; English.

XX The present invention relates to chemokine analogs (I, ADM70378-
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
 CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
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 CC agent, by administering (I) to the patient, where the survival of white
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 CC patient undergoing treatment with a cytotoxic agent, by administering (I)
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 CC mobilization, vaccine production and blood cell recovery following
 CC chemotherapy. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16

|||||

Db 20 ISVQRLASYRRITSSK 35

RESULT 21

ADM71735

ID ADM71735 standard; peptide; 35 AA.

XX ADM71735;

DT 17-JUN-2004 (first entry)

DE Chemokine analog, g19, SEQ ID 1368.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;

KW Interferon inducible Protein-10; IP-10; CXCL 10;

KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;

KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

KW infectious disease; inflammatory condition; graft rejection;

KW bacterial infection; viral infection; vascular condition;

KW atherosclerosis; restenosis; systemic lupus erythematosus;

KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;

KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

KW Immunosuppressive; Dermatological; Antiinflammatory.

XX Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "RNH-Gln"
 FT Misc-difference 4 /note= "Any amino acid"
 FT Misc-difference 11 /note= "Any amino acid"
 FT Misc-difference 12 /note= "Any amino acid"
 FT Modified-site 35 /note= "Lys-(OH)-NH2"
 XX WO2004024088-A2.
 XX PD 25-MAR-2004.
 XX PF 11-SEP-2003; 2003WO-US028745.
 XX PR 13-SEP-2002; 2002US-00243795.
 XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.
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 XX WPI; 2004-329387/30.
 XX Compound useful for treating cancer and cardiovascular disease, comprises
 FT structure of chemokine analogs such as interleukin-8 and interferon
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 PS Claim 1; SEQ ID NO 1368; 271pp; English.
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 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
 CC Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-
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 CC agent, by administering (I) to the patient, where the survival of white
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 CC directly from WIPO at ftp.wipo.int/pub/published_pt_sequences.
 XX Sequence 35 AA;
 XX Query Match 100.0%; Score 73; DB 8; Length 35;
 XX Best Local Similarity 100.0%; Pred. No. 6,7e-06;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ISVQRLASRYRITSSK 16
 |||||
 DB 20 ISVQRLASRYRITSSK 35

RESULT 22
 ADM71740
 ID ADM71740 standard; peptide; 35 AA.
 XX AC ADM71740;
 XX DT 17-JUN-2004 (first entry)
 XX DE Chemokine analog, g24, SEQ ID 1373.
 XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;
 KW Interferon inducible Protein-10; IP-10; CXCL 10;
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
 KW infectious disease; inflammatory condition; graft rejection;
 KW bacterial infection; viral infection; vascular condition;
 KW atherosclerosis; restenosis; systemic lupus erythematosus;
 KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 KW Immunosuppressive; Dermatological; Antiinflammatory.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "RNH-Gln"
 FT Misc-difference 9 /note= "Any amino acid"
 FT Misc-difference 11 /note= "Any amino acid"
 FT Misc-difference 12 /note= "Any amino acid"
 FT Modified-site 35 /note= "Lys-(OH)-NH2"
 XX WO2004024088-A2.
 XX PD 25-MAR-2004.
 XX PF 11-SEP-2003; 2003WO-US028745.
 XX PR 13-SEP-2002; 2002US-00243795.
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 XX PI Merzouk A, Wong D, Salari H;
 XX WPI; 2004-329387/30.
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 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
 CC mobilization, vaccine production and blood cell recovery following
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 XX Sequence 35 AA;
 XX Query Match 100.0%; Score 73; DB 8; Length 35;
 XX Best Local Similarity 100.0%; Pred. No. 6,7e-06;
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ISVQRLASRYRITSSK 16
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 23
ADM71733
ID ADM71733 standard; peptide; 35 AA.
XX
AC ADM71733;
XX
DT 17-JUN-2004 (first entry)
XX
DE Chemokine analog, g17, SEQ ID 1366.
XX
KW Chemokine analog; Chemokine; interleukin-8; IL-8;
KW Interferon inducible Protein-10; IP-10; CXCL 10;
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
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KW Immunosuppressive; Dermatological; Antiinflammatory.
XX
OS Synthetic.
XX
Key Location/Qualifiers
FH Modified-site 1 /note= "RNH-Gln"
FT
FT Misc-difference 2 /note= "Any amino acid"
FT
FT Misc-difference 11 /note= "Any amino acid"
FT
FT Misc-difference 12 /note= "Any amino acid"
FT
FT Modified-site 35 /note= "Lys- (OH)-NH2"
FT
XX
XX WO2004024088-A2.
XX
XX 25-MAR-2004.
XX
XX 11-SEP-2003; 2003WO-US028745.
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XX 13-SEP-2002; 2002US-00243795.
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PI Merzouk A, Wong D, Salari H;
XX WPI; 2004-329387/30.
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XX
PS Claim 1; SEQ ID NO 1366; 271pp; English.
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 24
ADM71780
ID ADM71780 standard; peptide; 35 AA.
XX
AC ADM71780;
XX
DT 17-JUN-2004 (first entry)
XX
DE Chemokine analog, g64, SEQ ID 1413.
XX
XX Chemokine analog; Chemokine; interleukin-8; IL-8;
KW Interferon inducible Protein-10; IP-10; CXCL 10;
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
KW infectious disease; inflammatory condition; graft rejection;
KW bacterial infection; viral infection; vascular condition;
KW atherosclerosis; restenosis; systemic lupus erythematosus;
KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
KW Immunosuppressive; Dermatological; Antiinflammatory; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "RNH-Gln"

XX FT Misc-difference 11 /note= "Any amino acid"

XX FT Misc-difference 12 /note= "Any amino acid"

XX FT Modified-site 13 /note= "Any amino acid"

XX FT FT /note= "The residue at this position forms a bond with Lys19 to form a cyclic peptide"

XX FT FT /note= "The residue at this position forms a bond with Glu3 to form a cyclic peptide"

XX FT FT /note= "Lys-(OH)-NH2"

XX PN WO2004024088-A2.

XX XX 25-MAR-2004.

XX PD 11-SEP-2003; 2003WO-US028745.

XX PF 13-SEP-2002; 2002US-00243795.

XX PR (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX PA Merzouk A, Wong D, Salari H;

XX PI WPI; 2004-329387/30.

XX DR Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

XX FT Claim 1; SEQ ID NO 1413; 271pp; English.

XX PS The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, Interferon inducible Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
|||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 25

ADM71721

ID ADM71721 standard; peptide; 35 AA.

XX AC ADM71721;

XX DT 17-JUN-2004 (first entry)

XX DE Chemokine analog, G5, SEQ ID 1354.

XX XX Chemokine analog; Chemokine; interleukin-8; IL-8; Interferon inducible Protein-10; IP-10; CXCL10; Macrophage inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5; I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28; autoimmune disease; cancer; chronic inflammation; cardiovascular disease; infectious disease; inflammatory condition; graft rejection; bacterial infection; viral infection; vascular condition; atherosclerosis; restenosis; systemic lupus erythematosus; ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic; Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic; Immunosuppressive; Dermatological; Antiinflammatory.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "RNH-Gln"

XX FT Misc-difference 2 /note= "Any amino acid"

XX FT Misc-difference 11 /note= "Any amino acid"

XX FT Misc-difference 12 /note= "Any amino acid"

XX FT Modified-site 35 /note= "Lys-(OH)-NH2"

XX PN WO2004024088-A2.

XX XX 25-MAR-2004.

XX PD 11-SEP-2003; 2003WO-US028745.

XX PR 13-SEP-2002; 2002US-00243795.

XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX PI Merzouk A, Wong D, Salari H;

XX WPI; 2004-329387/30.

XX XX Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

XX FT Claim 1; SEQ ID NO 1354; 271pp; English.

XX PS The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, Interferon inducible Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease

or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7e-06; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 0;

QY 1 ISVQRLASYRRITSSK 16
|||||
DB 20 ISVQRLASYRRITSSK 35

RESULT 26

ADM71724
ID ADM71724 standard; peptide; 35 AA.

AC ADM71724;

XX 17-JUN-2004 (first entry)

XX Chemokine analog, g9, SEQ ID 1357.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;
KW Interferon inducible Protein-10; IP-10; CXCL 10;
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
KW infectious disease; inflammatory condition; graft rejection;
KW bacterial infection; viral infection; vascular condition;
KW atherosclerosis; restenosis; systemic lupus erythematosus;
KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis; Cytostatic;
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
KW Immunosuppressive; Dermatological; Antiinflammatory.
XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "RNH-Gln"

XX Misc-difference 5 /note= "Any amino acid"

XX Misc-difference 11 /note= "Any amino acid"

XX Misc-difference 12 /note= "Any amino acid"

XX Modified-site 35 /note= "Lys- (OH) -NH2"

XX WO2004024088-A2.

XX 25-MAR-2004.

PF 11-SEP-2003; 2003WO-US028745.

XX 13-SEP-2002; 2002US-00243795.

PR (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX Merzouk A, Wong D, Salari H;

XX WPI; 2004-329387/30.

DR Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

XX Claim 1; SEQ ID NO 1357; 271pp; English.

XX The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, interferon inducible Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0;

QY 1 ISVQRLASYRRITSSK 16
|||||
DB 20 ISVQRLASYRRITSSK 35

RESULT 27

ADM71731
ID ADM71731 standard; peptide; 35 AA.

XX ADM71731;

XX 17-JUN-2004 (first entry)

XX Chemokine analog, g15, SEQ ID 1364.

XX Chemokine analog; Chemokine; interleukin-8; IL-8;

KW Interferon inducible Protein-10; IP-10; CXCL 10;

KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;

KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

infectious disease; inflammatory condition; graft rejection;
bacterial infection; viral infection; vascular condition;
atherosclerosis; restenosis; systemic lupus erythematosus;
ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis;
Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
Immunosuppressive; Dermatological; Antiinflammatory.
Synthetic.

Key Location/Qualifiers
Modified-site 1 /note= "RNH-Gln"
Misc-difference 11 /note= "Any amino acid"
Misc-difference 12 /note= "Any amino acid"
Modified-site 35 /note= "Lys- (OH) -NH2"

WO2004024088-A2.
25-MAR-2004.
11-SEP-2003; 2003WO-US028745.
13-SEP-2002; 2002US-00243795.
(CHEM-) CHEMOKINE THERAPEUTICS CORP.
Merzouk A, Wong D, Salari H;
WPI; 2004-329387/30.

Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

Claim 1; SEQ ID NO 1364; 271pp; English.

The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, Interferon inducible Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
|||||
DB 20 ISVQRLASYRRITSSK 35

RESULT 28
ADM71739
ID ADM71739 standard; peptide; 35 AA.
XX
AC ADM71739;
XX
DI 17-JUN-2004 (first entry)
XX
DE Chemokine analog, g23, SEQ ID 1372.
XX
KW Chemokine analog; Chemokine; interleukin-8; IL-8;
KW Interferon inducible Protein-10; IP-10; CXCL10;
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; CCL3; RANTES; CCL5;
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
KW infectious disease; inflammatory condition; graft rejection;
KW bacterial infection; viral infection; vascular condition;
KW atherosclerosis; restenosis; systemic lupus erythematosus;
KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
KW Immunosuppressive; Dermatological; Antiinflammatory.
OS Synthetic.

Key Location/Qualifiers
Modified-site 1 /note= "RNH-Gln"
Misc-difference 8 /note= "Any amino acid"
Misc-difference 11 /note= "Any amino acid"
Misc-difference 12 /note= "Any amino acid"
Modified-site 35 /note= "Lys- (OH) -NH2"

WO2004024088-A2.
25-MAR-2004.
11-SEP-2003; 2003WO-US028745.
13-SEP-2002; 2002US-00243795.
(CHEM-) CHEMOKINE THERAPEUTICS CORP.
Merzouk A, Wong D, Salari H;
WPI; 2004-329387/30.

Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

Claim 1; SEQ ID NO 1372; 271pp; English.

The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, Interferon inducible Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease

or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | |
Db 20 ISVQRLASYRRITSSK 35

RESULT 29
ADM71729
ID ADM71729 standard; peptide; 35 AA.
XX AC ADM71729;
XX DT 17-JUN-2004 (first entry)
XX DE Chemokine analog, g13, SEQ ID 1362.
XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;
KW Interferon inducible Protein-10; IP-10; CXCL 10;
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
KW infectious disease; inflammatory condition; graft rejection;
KW bacterial infection; viral infection; vascular condition;
KW atherosclerosis; restenosis; systemic lupus erythematosus;
KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis;
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
KW Immunosuppressive; Dermatological; Antiinflammatory.
XX OS Synthetic.
XX Key Location/Qualifiers
XX Modified-site 1
FT FT /note= "RNH-Gln"
FT FT Misc-difference 10
FT FT /note= "Any amino acid"
FT FT Misc-difference 11
FT FT /note= "Any amino acid"
FT FT Misc-difference 12
FT FT /note= "Any amino acid"
FT FT Modified-site 35
FT FT /note= "Lys-(OH)-NH2"
XX XX
XX WO2004024088-A2.
XX XX
XX PD 25-MAR-2004.
XX XX

PF 11-SEP-2003; 2003WO-US028745.
XX 13-SEP-2002; 2002US-00243795.
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX Merzouk A, Wong D, Salari H;
XX WPI; 2004-329387/30.
XX Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.
XX Claim 1; SEQ ID NO 1362; 271pp; English.
XX The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, interferon inducible Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | |
Db 20 ISVQRLASYRRITSSK 35

RESULT 30
ADM71732
ID ADM71732 standard; peptide; 35 AA.
XX AC ADM71732;
XX DT 17-JUN-2004 (first entry)
XX DE Chemokine analog, g16, SEQ ID 1365.
XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;
KW Interferon inducible Protein-10; IP-10; CXCL 10;
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
KW infectious disease; inflammatory condition; graft rejection;
KW bacterial infection; viral infection; vascular condition;
KW atherosclerosis; restenosis; systemic lupus erythematosus;
KW ischaemia-reperfusion; sepsis; tumourigenesis; angiogenesis;
KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
KW Immunosuppressive; Dermatological; Antiinflammatory.
XX OS Synthetic.

KW infectious disease; inflammatory condition; graft rejection;
 KW bacterial infection; viral infection; vascular condition;
 KW atherosclerosis; restenosis; systemic lupus erythematosus;
 KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 KW Immunosuppressive; Dermatological; Antiinflammatory.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "RNH-Xaa, where Xaa is any amino acid"
 FT Misc-difference 11
 FT /note= "Any amino acid"
 FT Misc-difference 12
 FT /note= "Any amino acid"
 FT Modified-site 35
 FT /note= "Lys-(OH)-NH2"
 FT
 FT
 PN WO2004024088-A2.
 XX
 XX 25-MAR-2004.
 XX
 XX 11-SEP-2003; 2003WO-US028745.
 XX
 XX 13-SEP-2002; 2002US-00243795.
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 PA
 XX Merzouk A, Wong D, Salari H;
 PI
 XX WPI; 2004-329387/30.
 DR
 XX Compound useful for treating cancer and cardiovascular disease, comprises
 PT structure of chemokine analogs such as interleukin-8 and interferon
 PT inducible protein-10.
 XX
 XX Claim 1; SEQ ID NO 1365; 271pp; English.
 PS
 XX The present invention relates to chemokine analogs (I, ADM70378-
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
 CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
 CC alpha (MIP-1-alpha or CXCL3) analogs, RANTES (Regulated upon Activation,
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
 CC analogs. (I) are useful for treating a disease or disorder by
 CC administering (I) to a patient. The disease or disorder is chosen from
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
 CC or infectious disease. The administration increases the hemocrit, assist
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
 CC are also useful for modulating the activity of chemokine receptor, which
 CC involves contacting the chemokine receptor with (I), for mobilizing
 CC intracellular calcium in a patient, which involves administering (I) to a
 CC patient in need of such treatment. (I) are also useful for protecting
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic
 CC agent, by administering (I) to the patient, where the survival of white
 CC blood cells or leukocytes is increased. (I) are also useful for
 CC maintaining cells capable of divisions in a quiescent state cells in a
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
 CC patient by administering (I) to the patient. (I) are also useful for
 CC treating or preventing inflammatory conditions, graft rejection,
 CC bacterial infection, viral infection, vascular conditions (e.g.
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
 CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell
 CC mobilization, vaccine production and blood cell recovery following
 CC chemotherapy. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;

Best Local Similarity 100.0%; Pred. No. 6.7e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ISVQRLASYRRITSSK 16
 |||||
 Db 20 ISVQRLASYRRITSSK 35
 |||||
 RESULT 31
 ADM71737
 ID ADM71737 standard; peptide; 35 AA.
 XX
 AC ADM71737;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Chemokine analog, g21, SEQ ID 1370.
 XX
 KW Chemokine analog; Chemokine; interleukin-8; IL-8;
 KW Interferon inducible Protein-10; IP-10; CXCL 10;
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
 KW infectious disease; inflammatory condition; graft rejection;
 KW bacterial infection; viral infection; vascular condition;
 KW atherosclerosis; restenosis; systemic lupus erythematosus;
 KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 KW Immunosuppressive; Dermatological; Antiinflammatory.
 XX
 OS Synthetic.

FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "RNH-Gln"
 FT Misc-difference 6
 FT /note= "Any amino acid"
 FT Misc-difference 11
 FT /note= "Any amino acid"
 FT Misc-difference 12
 FT /note= "Any amino acid"
 FT Modified-site 35
 FT /note= "Lys-(OH)-NH2"
 XX
 PN WO2004024088-A2.
 XX
 XX 25-MAR-2004.
 XX
 XX 11-SEP-2003; 2003WO-US028745.
 XX
 XX 13-SEP-2002; 2002US-00243795.
 XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 PA
 XX Merzouk A, Wong D, Salari H;
 PI
 XX WPI; 2004-329387/30.

DR Compound useful for treating cancer and cardiovascular disease, comprises
 XX structure of chemokine analogs such as interleukin-8 and interferon
 XX inducible protein-10.
 XX
 PS Claim 1; SEQ ID NO 1370; 271pp; English.
 XX
 XX The present invention relates to chemokine analogs (I, ADM70378-
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
 CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
 CC alpha (MIP-1-alpha or CXCL3) analogs, RANTES (Regulated upon Activation,
 CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
 CC analogs. (I) are useful for treating a disease or disorder by
 CC administering (I) to a patient. The disease or disorder is chosen from
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease

or infectious disease. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16
|||||
Db 20 ISVORLASVRRITSSK 35

RESULT 32
ADM71738

ID ADM71738 standard; peptide; 35 AA.

XX AC ADM71738;

XX DT 17-JUN-2004 (first entry)

XX DE Chemokine analog, g22, SEQ ID 1371.

XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;

XX KW Interferon inducible Protein-10; IP-10; CXCL 10;

XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;

XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

XX KW infectious disease; inflammatory condition; graft rejection;

XX KW bacterial infection; viral infection; vascular condition;

XX KW atherosclerosis; restenosis; systemic lupus erythematosus;

XX KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis;

XX KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;

XX KW Immunosuppressive; Dermatological; Antiinflammatory.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT FT Modified-site 1

FT FT /note= "RNH-Gln"

FT FT Misc-difference 7

FT FT /note= "Any amino acid"

FT FT Misc-difference 11

FT FT /note= "Any amino acid"

FT FT Misc-difference 12

FT FT /note= "Any amino acid"

FT FT Modified-site 35

FT FT /note= "Lys-(OH)-NH2"

XX WO2004024088-A2.

XX PD 25-MAR-2004.

XX XX

PF 11-SEP-2003; 2003WO-US028745.

XX PR 13-SEP-2002; 2002US-00243795.

XX PA (CHEM-) CHEMOKINE THERAPEUTICS CORP.

XX PI Merzouk A, Wong D, Salari H;

XX PI WPI; 2004-329387/30.

DR PF1; SEQ ID NO 1371; 271pp; English.

XX The present invention relates to chemokine analogs (I, ADM70378-

CC ADM72006), including interleukin (IL)-8 analogs, interferon inducible

CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-

CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,

CC Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309

CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28

CC analogs. (I) are useful for treating a disease or disorder by

CC administering (I) to a patient. The disease or disorder is chosen from

CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease

CC or infectious disease. The administration increases the hemocrit, assist

CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)

CC are also useful for modulating the activity of chemokine receptor, which

CC involves contacting the chemokine receptor with (I), for mobilizing

CC intracellular calcium in a patient, which involves administering (I) to a

CC patient in need of such treatment. (I) are also useful for protecting

CC haematopoietic cells in a patient undergoing treatment with cytotoxic

CC agent, by administering (I) to the patient, where the survival of white

CC blood cells or leukocytes is increased. (I) are also useful for

CC maintaining cells capable of divisions in a quiescent state cells in a

CC patient undergoing treatment with a cytotoxic agent, by administering (I)

CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a

CC patient by administering (I) to the patient. (I) are also useful for

CC treating or preventing inflammatory conditions, graft rejection,

CC bacterial infection, viral infection, vascular conditions (e.g.

CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-

CC reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell

CC mobilization, vaccine production and blood cell recovery following

CC chemotherapy. Note: The sequence data for this patent did not form part

CC of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 35 AA;

Query Match 100.0%; Score 73; DB 8; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16
|||||
Db 20 ISVORLASVRRITSSK 35

RESULT 33

ADM71745

ID ADM71745 standard; peptide; 41 AA.

XX AC ADM71745;

XX DT 17-JUN-2004 (first entry)

XX DE Chemokine analog, g29, SEQ ID 1378.

XX KW Chemokine analog; Chemokine; interleukin-8; IL-8;

XX KW Interferon inducible Protein-10; IP-10; CXCL 10;

XX KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;

XX KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;

XX KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;

infectious disease; inflammatory condition; graft rejection;
 bacterial infection; viral infection; vascular condition;
 atherosclerosis; restenosis; systemic lupus erythematosus;
 ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis;
 antiarteriosclerotic; virucide; antibacterial; vasotropic;
 immunosuppressive; dermatological; antiinflammatory.
 Synthetic.

Key Location/Qualifiers
 Modified-site 1
 Modified-site 23..28
 Modified-site /note= "RNH-Tyr"
 /note= "Lys-[linker]-Lys, where linker is a bifunctional group covalently attached to the N-terminal and C-terminal portions of the analog having the structure: H2N -ZA-COOH, wherein Za is selected from the group consisting of: (1) alkyl, alkenyl, aralkyl, alkynyl, (2) -(CH2)n- wherein n is an integer n=19 to 14, (3) any combination of four natural amino acids or non-natural amino acids and (4) -(Gly)4- (SEQ ID 1640)."
 Modified-site 41
 /note= "Thr-(OH)-NH2"

WO2004024088-A2.
 25-MAR-2004.
 11-SEP-2003; 2003WO-US028745.
 13-SEP-2002; 2002US-00243795.
 (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 Merzouk A, Wong D, Salari H;
 WPI; 2004-329387/30.

Compound useful for treating cancer and cardiovascular disease, comprises structure of chemokine analogs such as interleukin-8 and interferon inducible protein-10.

Claim 1; SEQ ID NO 1378; 271pp; English.

The present invention relates to chemokine analogs (I, ADM70378-ADM72006), including interleukin (IL)-8 analogs, interferon inducible Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-alpha (MIP-1-alpha or CXCL3) analogs, RANTES (Regulated upon Activation, Normal T-cell Expressed, and presumably Secreted or CCL5) analogs, I-309 analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28 analogs. (I) are useful for treating a disease or disorder by administering (I) to a patient. The disease or disorder is chosen from autoimmune diseases, cancer, chronic inflammation, cardiovascular disease or infectious diseases. The administration increases the hemocrit, assist in mobilizing stem cells, in vaccine production or in gene therapy. (I) are also useful for modulating the activity of chemokine receptor, which involves contacting the chemokine receptor with (I), for mobilizing intracellular calcium in a patient, which involves administering (I) to a patient in need of such treatment. (I) are also useful for protecting haematopoietic cells in a patient undergoing treatment with cytotoxic agent, by administering (I) to the patient, where the survival of white blood cells or leukocytes is increased. (I) are also useful for maintaining cells capable of divisions in a quiescent state cells in a patient undergoing treatment with a cytotoxic agent, by administering (I) to the patient, and for mobilizing leukocytes e.g. neutrophils in a patient by administering (I) to the patient. (I) are also useful for treating or preventing inflammatory conditions, graft rejection, bacterial infection, viral infection, vascular conditions (e.g. atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-reperfusion), sepsis, tumorigenesis, and angiogenesis, stem cell mobilization, vaccine production and blood cell recovery following chemotherapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX Sequence 41 AA;
 SQ

Query Match 100.0%; Score 73; DB 8; Length 41;
 Best Local Similarity 100.0%; Pred. No. 7.9e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRITSSK 16
 Db 8 ISVORLASYYRRITSSK 23
 |||||
 |||||

RESULT 34
 ADM71783
 ID ADM71783 standard; peptide; 41 AA.
 XX
 AC ADM71783;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Chemokine analog, 967, SEQ ID 1416.
 XX
 KW Chemokine analog; Chemokine; interleukin-8; IL-8;
 KW Interferon inducible Protein-10; IP-10; CXCL10;
 KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;
 KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
 KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
 KW infectious disease; inflammatory condition; graft rejection;
 KW bacterial infection; viral infection; vascular condition;
 KW atherosclerosis; restenosis; systemic lupus erythematosus;
 KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
 KW Antiarteriosclerotic; Virucide; Antibacterial; Vasotropic;
 KW Immunosuppressive; Dermatological; Antiinflammatory; cyclic.
 XX
 OS Synthetic.
 XX

Key Location/Qualifiers
 Modified-site 1
 Modified-site /note= "RNH-Tyr"
 Modified-site 23..28
 /note= "Lys-[linker]-Lys, where linker is a bifunctional group covalently attached to the N-terminal and C-terminal portions of the analog having the structure: H2N -ZA-COOH, wherein Za is selected from the group consisting of: (1) alkyl, alkenyl, aralkyl, alkynyl, (2) -(CH2)n- wherein n is an integer n=19 to 14, (3) any combination of four natural amino acids or non-natural amino acids and (4) -(Gly)4- (SEQ ID 1640)."
 Modified-site 35
 /note= "The residue at this position forms a bond with Lys39 to form a cyclic peptide"
 Modified-site 39
 /note= "The residue at this position forms a bond with Asp35 to form a cyclic peptide"
 Modified-site 41
 /note= "Thr-(OH)-NH2"

WO2004024088-A2.
 25-MAR-2004.
 11-SEP-2003; 2003WO-US028745.
 13-SEP-2002; 2002US-00243795.
 (CHEM-) CHEMOKINE THERAPEUTICS CORP.
 Merzouk A, Wong D, Salari H;
 WPI; 2004-329387/30.
 Compound useful for treating cancer and cardiovascular disease, comprises

PT structure of chemokine analogs such as interleukin-8 and interferon
 PT inducible protein-10.
 XX
 PS Claim 1; SEQ ID NO 1416; 271pp; English.
 XX
 CC The present invention relates to chemokine analogs (I, ADM70378-
 CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
 CC Protein-10 (IP-10 or CXCL10) analogs, Macrophage Inflammatory Protein-1-
 CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
 CC Normal T-cell Expressed, and presumably Secreted or CCU5) analogs, I-309
 CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
 CC analogs. (I) are useful for treating a disease or disorder by
 CC administering (I) to a patient. The disease or disorder is chosen from
 CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
 CC or infectious disease. The administration increases the hemocrit, assist
 CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
 CC are also useful for modulating the activity of chemokine receptor, which
 CC involves contacting the chemokine receptor with (I), for mobilizing
 CC intracellular calcium in a patient, which involves administering (I) to a
 CC patient in need of such treatment. (I) are also useful for protecting
 CC haematopoietic cells in a patient undergoing treatment with cytotoxic
 CC agent, by administering (I) to the patient, where the survival of white
 CC blood cells or leukocytes is increased. (I) are also useful for
 CC maintaining cells capable of divisions in a quiescent state cells in a
 CC patient undergoing treatment with a cytotoxic agent, by administering (I)
 CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
 CC patient by administering (I) to the patient. (I) are also useful for
 CC treating or preventing inflammatory conditions, graft rejection,
 CC bacterial infection, viral infection, systemic lupus erythematosus, and ischaemia-
 CC atherosclerosis, restenosis, systemic lupus erythematosus, and ischaemia-
 CC reperfusion), sepsis, tumourigenesis, and angiogenesis, stem cell
 CC mobilization, vaccine production and blood cell recovery following
 CC chemotherapy. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 41 AA;

Query Match 100.0%; Score 73; DB 8; Length 41;
 Best Local Similarity 100.0%; Pred. No. 7.9e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
 |||||
 Db 8 ISVQRLASYRRITSSK 23

RESULT 35
 AEB70238
 ID AEB70238 standard; protein; 65 AA.
 XX
 AC AEB70238;
 XX

20-OCT-2005 (first entry)

Small inducible cytokine A2 precursor variant S71513_P2.

gynecological; gene therapy; diagnosis; selectable marker; endometriosis;
 KW gynecological; genitourinary disease; gynecology and obstetrics;
 KW S71513_P2; small inducible cytokine A2 precursor.

OS Homo sapiens.

XX WO2005072049-A2.

XX 11-AUG-2005.

XX 27-JAN-2005; 2005WO-IB001188.

XX 27-JAN-2004; 2004US-0539128P.

PR 27-JAN-2004; 2004US-0539129P.

PR 22-OCT-2004; 2004US-0621004P.

PR 17-NOV-2004; 2004US-0628145P.

PR 17-NOV-2004; 2004US-0628178P.
 PR 17-NOV-2004; 2004US-0628230P.
 PR 27-JAN-2005; 55US-00621004.
 XX
 PA (COMP-) COMPUGEN USA INC.

XX Cohen Y, Pollock S, Novik A, Diber A;

XX WPI; 2005-555591/56.

DR N-PSDB; AEB70230.

XX New mammalian nucleic acid and polypeptide sequences useful for

PT screening, diagnosing or treating endometriosis, or in monitoring disease

PT progression or efficacy of treatment for endometriosis.

XX Claim 3; SEQ ID NO 9; 804pp; English.

XX The invention describes a nucleic acid sequence comprising any of the 7
 CC nucleotide sequences having 29-1404 bp fully defined in the specification
 CC (SEQ ID NOS: 1-7). Also described are: an amino acid sequence comprising
 CC 65 amino acids fully defined in the specification (SEQ ID NO: 9); an
 CC isolated chimeric polypeptide encoding for S71513_P2, comprising a first
 CC amino acid sequence being at least 90% homologous to Met-Lys-Val-Ser-Ala-
 CC Ala-Leu-Leu-Cys-Leu-Leu-Ile-Ala-Ala-Thr-Phe-Ile-Pro-Gln-Gly-Leu-Ala-
 CC Gln-Pro-Asp-Ala-Ile-Ala-Pro-Val-Thr-Cys-Tyr-Asn-Phe-Thr-Arg-Arg-
 CC Lys-Ile-Ser-Val-Gln-Arg-Leu-Ala-Ser-Tyr-Arg-Arg-Ile-Thr-Ser-Lys-Cys-
 CC Pro-Lys-Glu-Ala-Val corresponding to amino acids 1-64 of SY02 HUMAN,
 CC which also corresponds to amino acids 1-64 of S71513_P2, and a second
 CC amino acid sequence comprising a polypeptide having the sequence M
 CC corresponding to amino acid 65 of S71513_P2, where the first amino acid
 CC sequence and second amino acid sequence are contiguous and in a
 CC sequential order; an antibody capable of specifically binding to an
 CC epitope of the amino acid sequence mentioned above; a kit for detecting
 CC endometriosis, comprising a kit detecting overexpression of the splice
 CC variant or a kit comprising the above antibody; methods for detecting,
 CC diagnosing or screening for endometriosis; a biomarker capable of
 CC detecting endometriosis, comprising the above nucleic acid or amino acid
 CC sequences, or their fragments; a method for monitoring disease
 CC progression and/or treatment efficacy and/or relapse of endometriosis;
 CC and a method of selecting a therapy for endometriosis. The composition
 CC and methods are useful for screening, diagnosing or treating
 CC endometriosis. These may also be used in monitoring disease progression
 CC and the efficacy of treatment for endometriosis. This is the amino acid
 CC sequence of S71513_P2, a variant of the protein small inducible cytokine
 CC A2 precursor (also known as SY02 HUMAN, CCL2, MCP-1, monocyte
 CC chemoattractant protein-1, MCA, monocyte secretory protein JE or HC11), a
 CC candidate marker for endometriosis.

XX Sequence 65 AA;

Query Match 100.0%; Score 73; DB 9; Length 65;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16

|||||

Db 43 ISVQRLASYRRITSSK 58

RESULT 36

AAW13598

ID AAW13598 standard; peptide; 66 AA.

XX AAW13598;

XX 07-NOV-1997 (first entry)

XX Monocyte chemoattractant protein analogue MCP-1 (10-76) .

XX Truncated monocyte chemoattractant protein-1; inhibitor;
 KW receptor binding; anti inflammatory; basophil; lymphocyte; allergy;
 KW chronic inflammatory disease; arthritis; arteriosclerosis; lung disease.
 XX

OS Homo sapiens.
 PN CA2152141-A.
 XX
 PD 20-DEC-1996.
 XX
 XX 19-JUN-1995; 95CA-02152141.
 PP
 XX 19-JUN-1995; 95CA-02152141.
 PR
 XX (LEWIS I.
 PA Lewis I, Gong J;
 XX WPI; 1997-165844/16.
 XX
 XX N-terminally truncated monocyte chemoattractant protein-1 (MCP-1) -
 PT lacks MCP-1 activity and inhibits receptor binding, useful as anti-
 PT inflammatory agent.
 PT
 XX Disclosure; Page 5; 27pp; English.
 PS
 XX The present sequence represents an analogue, MCP-1 (11-76), of monocyte
 CC chemoattractant protein-1 (MCP-1). The analogue, which lacks the N-
 CC terminal amino acids 1-9 of MCP-1, acts as an antagonist of MCP-1 as it
 CC lacks MCP-1 biological activity and inhibits binding to a MCP-1 receptor.
 CC The analogue is useful as an anti-inflammatory agent to block the effects
 CC of MCP-1 which is an inflammatory mediator causing migration of monocytes
 CC and other cells e.g. basophils and lymphocytes into inflammation sites.
 CC MCP-1 has been implicated in allergic and chronic inflammatory diseases
 CC e.g. arthritis, arteriosclerosis and several lung diseases. The analogue
 CC competes more effectively with MCP-1 for binding MCP-1 receptors than
 CC prior art mutant versions of MCP-1 e.g. preferably providing 50%
 CC inhibition of binding at a 25:1 ratio or less, compared with 75:1 for
 CC prior art mutant 7ND
 CC
 XX Sequence 66 AA;
 SQ
 Query Match 100.0%; Score 73; DB 2; Length 66;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ISVQRLASYRRITSSK 16
 DB 10 ISVQRLASYRRITSSK 25
 RESULT 37
 AAW13599
 ID AAW13599 standard; peptide; 67 AA.
 XX
 AC AAW13599;
 XX
 XX 07-NOV-1997 (first entry)
 DT Monocyte chemoattractant protein analogue MCP-1 (11-76).
 XX
 DE Truncated monocyte chemoattractant protein-1; inhibitor;
 XX receptor binding; anti inflammatory; basophil; lymphocyte; allergy;
 KW chronic inflammatory disease; arthritis; arteriosclerosis; lung disease.
 KW
 XX Homo sapiens.
 OS
 XX CA2152141-A.
 PN
 XX 20-DEC-1996.
 PD
 XX 19-JUN-1995; 95CA-02152141.
 PP
 XX 19-JUN-1995; 95CA-02152141.
 PR
 XX (LEWIS I.
 PA Lewis I, Gong J;
 XX WPI; 1997-165844/16.
 XX
 XX N-terminally truncated monocyte chemoattractant protein-1 (MCP-1) -
 PT lacks MCP-1 activity and inhibits receptor binding, useful as anti-
 PT inflammatory agent.
 PT
 XX Disclosure; Page 5; 27pp; English.
 PS
 XX The present sequence represents an analogue, MCP-1 (11-76), of monocyte
 CC chemoattractant protein-1 (MCP-1). The analogue, which lacks the N-
 CC terminal amino acids 1-10 of MCP-1, acts as an antagonist of MCP-1 as it
 CC lacks MCP-1 biological activity and inhibits binding to a MCP-1 receptor.
 CC The analogue is useful as an anti-inflammatory agent to block the effects
 CC of MCP-1 which is an inflammatory mediator causing migration of monocytes
 CC and other cells e.g. basophils and lymphocytes into inflammation sites.
 CC MCP-1 has been implicated in allergic and chronic inflammatory diseases
 CC e.g. arthritis, arteriosclerosis and several lung diseases. The analogue
 CC competes more effectively with MCP-1 for binding MCP-1 receptors than
 CC prior art mutant versions of MCP-1 e.g. preferably providing 50%
 CC inhibition of binding at a 25:1 ratio or less, compared with 75:1 for
 CC prior art mutant 7ND
 CC
 XX Sequence 67 AA;
 SQ
 Query Match 100.0%; Score 73; DB 2; Length 67;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ISVQRLASYRRITSSK 16
 DB 11 ISVQRLASYRRITSSK 26
 RESULT 38
 AAW13597
 ID AAW13597 standard; peptide; 68 AA.
 XX
 AC AAW13597;
 XX
 XX 07-NOV-1997 (first entry)
 DT Monocyte chemoattractant protein analogue MCP-1 (9-76).
 XX
 DE Truncated monocyte chemoattractant protein-1; inhibitor;
 XX receptor binding; anti inflammatory; basophil; lymphocyte; allergy;
 KW chronic inflammatory disease; arthritis; arteriosclerosis; lung disease.
 KW
 XX Homo sapiens.
 OS
 XX CA2152141-A.
 PN
 XX 20-DEC-1996.
 PD
 XX 19-JUN-1995; 95CA-02152141.
 PP
 XX 19-JUN-1995; 95CA-02152141.
 PR
 XX (LEWIS I.
 PA Lewis I, Gong J;
 XX WPI; 1997-165844/16.
 XX
 XX N-terminally truncated monocyte chemoattractant protein-1 (MCP-1) -
 PT lacks MCP-1 activity and inhibits receptor binding, useful as anti-
 PT inflammatory agent.
 PT
 XX Claim 7; Page 5; 27pp; English.
 PS
 XX The present sequence represents an analogue, MCP-1 (9-76), of monocyte
 CC chemoattractant protein-1 (MCP-1). The analogue, which lacks the N-

CC terminal amino acids 1-8 of MCP-1, acts as an antagonist of MCP-1 as it
 CC lacks MCP-1 biological activity and inhibits binding to a MCP-1 receptor.
 CC The analogue is useful as an anti-inflammatory agent to block the effects
 CC of MCP-1 which is an inflammatory mediator causing migration of monocytes
 CC and other cells e.g. basophils and lymphocytes into inflammation sites.
 CC MCP-1 has been implicated in allergic and chronic inflammatory diseases
 CC e.g. arthritis, arteriosclerosis and several lung diseases. The analogue
 CC competes more effectively with MCP-1 for binding MCP-1 receptors than
 CC prior art mutant versions of MCP-1 e.g. preferably providing 50%
 CC inhibition of binding at a 25:1 ratio or less, compared with 75:1 for
 CC prior art mutant 7ND
 CC
 SQ Sequence 68 AA;

Query Match 100.0%; Score 73; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
 |||||
 DB 12 ISVQRLASYRRITSSK 27

RESULT 39
 AAW95037
 ID AAW95037 standard; protein; 68 AA.

AC AAW95037;

XX 13-MAY-1999 (first entry)

DE MCP-1 analogue [V9T]MCP1(9-76) (residues 9-76).

XX Monocyte chemoattractant protein-1; MCP-1; analogue; inflammatory;
 KW rheumatoid arthritis; glomerular nephritides; lung fibrosis; restenosis;
 KW alveolitis; asthma; atherosclerosis; psoriasis; hypersensitivity; skin;
 KW inflammatory bowel disease; multiple sclerosis; brain tumour; stroke;
 KW reperfusion injury; ischemia; myocardial infarction; medicament.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /label= V9T
 FT /note= "wild-type Val is replaced with Thr"

XX WO9905279-A1.

XX 04-FEB-1999.

XX 21-JUL-1998; 98WO-GB002179.

XX 25-JUL-1997; 97GB-00015659.

XX 25-JUL-1997; 97GB-00015661.

XX 25-JUL-1997; 97GB-00015663.

XX (ZENE) ZENECA LTD.

XX Barratt DG, Needham MRC;

XX WPI; 1999-142934/12.

XX N-PSDB; AAX21543.

XX New analogues of Monocyte Chemoattractant Protein-1 (MCP-1) - useful to
 FT treat inflammatory diseases.

XX Claim 1; Page 42-43; 49pp; English.

XX The invention relates to novel analogues ([V9A]MCP1(9-76), [V9G]MCP1 (9-
 CC 76) and [V9T]MCP1(9-76)) of monocyte chemoattractant protein-1 (MCP-1)
 CC having substitution of an Ala, Gly or Thr for the natural Val at position
 CC 9 of full-length MCP-1. Host cells containing a vector comprising the

CC nucleic acids encoding the analogues are used for recombinant expression
 CC of the proteins. MCP-1 is implicated in inflammatory diseases including
 CC rheumatoid arthritis, glomerular nephritides, lung fibrosis, restenosis,
 CC alveolitis, and asthma and in atherosclerosis, psoriasis, delayed-type
 CC hypersensitivity reactions of the skin, inflammatory bowel disease, ful to
 CC multiple sclerosis, and brain tumour. An MCP-1 inhibitor may be useful to
 CC treat stroke, reperfusion injury, ischemia, myocardial infarction, and
 CC transplant rejection. The analogues can be used as medicaments. The
 CC present sequence represents a MCP-1 analogue [V9T]MCP1(9-76) where the
 CC wild-type valine is replaced with threonine

XX
 SQ Sequence 68 AA;

Query Match 100.0%; Score 73; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
 |||||
 DB 12 ISVQRLASYRRITSSK 27

RESULT 40

AAW95035

ID AAW95035 standard; protein; 68 AA.

AC AAW95035;

XX 13-MAY-1999 (first entry)

DE MCP-1 analogue [V9A]MCP1(9-76) (residues 9-76).

XX Monocyte chemoattractant protein-1; MCP-1; analogue; inflammatory;
 KW rheumatoid arthritis; glomerular nephritides; lung fibrosis; restenosis;
 KW alveolitis; asthma; atherosclerosis; psoriasis; hypersensitivity; skin;
 KW inflammatory bowel disease; multiple sclerosis; brain tumour; stroke;
 KW reperfusion injury; ischemia; myocardial infarction; medicament.

OS Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /label= V9A
 FT /note= "wild-type Val is replaced with Ala"

XX WO9905279-A1.

XX 04-FEB-1999.

XX 21-JUL-1998; 98WO-GB002179.

XX 25-JUL-1997; 97GB-00015659.

XX 25-JUL-1997; 97GB-00015661.

XX 25-JUL-1997; 97GB-00015663.

XX (ZENE) ZENECA LTD.

XX Barratt DG, Needham MRC;

XX WPI; 1999-142934/12.

XX N-PSDB; AAX21525.

XX New analogues of Monocyte Chemoattractant Protein-1 (MCP-1) - useful to
 FT treat inflammatory diseases.

XX Claim 1; Page 37; 49pp; English.

XX The invention relates to novel analogues ([V9A]MCP1(9-76), [V9G]MCP1 (9-
 CC 76) and [V9T]MCP1(9-76)) of monocyte chemoattractant protein-1 (MCP-1)
 CC having substitution of an Ala, Gly or Thr for the natural Val at position
 CC 9 of full-length MCP-1. Host cells containing a vector comprising the
 CC nucleic acids encoding the analogues are used for recombinant expression

CC of the proteins. MCP-1 is implicated in inflammatory diseases including
 CC rheumatoid arthritis, glomerular nephritides, lung fibrosis, restenosis,
 CC alveolitis, and asthma, and in atherosclerosis, psoriasis, delayed-type
 CC hypersensitivity reactions of the skin, inflammatory bowel disease,
 CC multiple sclerosis, and brain tumour. An MCP-1 inhibitor may be useful to
 CC treat stroke, reperfusion injury, ischemia, myocardial infarction, and
 CC transplant rejection. The analogues can be used as medicaments. The
 CC present sequence represents a MCP-1 analogue [V9A]MCP1(9-76) where the
 CC wild-type valine is substituted with alanine
 XX
 SQ Sequence 68 AA;

Query Match 100.0%; Score 73; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
 |||||
 Db 12 ISVQRLASYRRITSSK 27
 |||||

RESULT 41
 AAW95036
 ID AAW95036 standard; protein; 68 AA.
 XX
 AC AAW95036;
 XX
 DT 13-MAY-1999 (first entry)
 XX
 DE MCP-1 analogue [V9G]MCP1(9-76) (residues 9-76).
 XX
 KW Monocyte chemoattractant protein-1; MCP-1; analogue; inflammatory;
 KW rheumatoid arthritis; glomerular nephritides; lung fibrosis; restenosis;
 KW alveolitis; asthma; atherosclerosis; psoriasis; hypersensitivity; skin;
 KW inflammatory bowel disease; multiple sclerosis; brain tumour; stroke;
 KW reperfusion injury; ischemia; myocardial infarction; medicament.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /label= V9G
 FT /note= "wild-type Val is replaced with Gly"
 XX
 XX WO9905279-A1.
 XX
 XX 04-FEB-1999.
 XX
 XX 21-JUL-1998; 98WO-GB002179.
 XX
 XX 25-JUL-1997; 97GB-00015659.
 PR 25-JUL-1997; 97GB-00015661.
 PR 25-JUL-1997; 97GB-00015663.
 XX
 XX (ZENE) ZENECA LTD.
 XX
 XX Barratt DG, Needham MRC;
 PI
 XX
 XX WPI; 1999-142934/12.
 DR N-PSDB; AAX21541.
 XX
 XX New analogues of Monocyte Chemoattractant Protein-1 (MCP-1) - useful to
 PT treat inflammatory diseases.
 PT
 XX Claim 1; Page 41-42; 49pp; English.
 PS
 XX The invention relates to novel analogues ([V9A]MCP1(9-76), [V9G]MCP1 (9-
 CC 76) and [V9T]MCP1(9-76)) of monocyte chemoattractant protein-1 (MCP-1)
 CC having substitution of an Ala, Gly or Thr for the natural Val at position
 CC 9 of full-length MCP-1. Host cells containing a vector comprising the
 CC nucleic acids encoding the analogues are used for recombinant expression
 CC of the proteins. MCP-1 is implicated in inflammatory diseases including

CC rheumatoid arthritis, glomerular nephritides, lung fibrosis, restenosis,
 CC alveolitis, and asthma, and in atherosclerosis, psoriasis, delayed-type
 CC hypersensitivity reactions of the skin, inflammatory bowel disease,
 CC multiple sclerosis, and brain tumour. An MCP-1 inhibitor may be useful to
 CC treat stroke, reperfusion injury, ischemia, myocardial infarction, and
 CC transplant rejection. The analogues can be used as medicaments. The
 CC present sequence represents a MCP-1 analogue [V9G]MCP1(9-76) where the
 CC wild-type valine is substituted with glycine
 XX
 SQ Sequence 68 AA;

Query Match 100.0%; Score 73; DB 2; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
 |||||
 Db 12 ISVQRLASYRRITSSK 27
 |||||

RESULT 42
 ADN36565
 ID ADN36565 standard; protein; 68 AA.
 XX
 AC ADN36565;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Chemokine receptor inhibitor-related protein R2 (MCP-1 (9-76)) #12.2.
 XX
 KW Chemokine receptor inhibitor; chimeric protein; HIV infection;
 KW tumour metastasis; organ transplant rejection; autoimmune disease;
 KW anti-HIV; cytostatic; immunosuppressive; R2; MCP-1.
 XX
 OS Unidentified.
 XX
 XX CN1435433-A.
 XX
 XX 13-AUG-2003.
 XX
 XX 30-AUG-2002; 2002CN-00129301.
 XX
 XX 30-AUG-2002; 2002CN-00129301.
 XX
 XX (GONG/) GONG X.
 XX
 XX Gong J;
 PI
 XX WPI; 2004-000227/01.
 DR N-PSDB; ADN36586.
 XX
 XX Long-acting broad-spectrum chemotactic factor receptor inhibiting matter.
 PT
 XX Claim 16; Page 27; 43pp; Chinese.
 PS
 XX The invention relates to chimeric proteins for inhibition of chemokine
 CC receptors. The invention also relates to nucleic acids encoding the
 CC chimeric proteins, and a process for preparing and testing the chimeric
 CC proteins. The chimeric proteins provide long-acting, broad spectrum
 CC inhibition of chemokine receptors with high selectivity. They can be used
 CC to prevent or treat HIV infection, tumour metastasis, organ transplant
 CC rejection and autoimmune diseases. The present sequence represents a
 CC protein sequence which may be incorporated into a chimeric protein of the
 CC invention.
 XX
 SQ Sequence 68 AA;

Query Match 100.0%; Score 73; DB 8; Length 68;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
 |||||

```

Db      12 ISVORLASVRRITSSK 27

RESULT 43
AD575933
ID      ADS75933 standard; protein; 68 AA.
XX
AC      ADS75933;
XX
DT      16-DEC-2004 (first entry)
XX
DE      Monocyte chemoattractant protein 1 protein fragment.
XX
KW      cytosstatic; prostate cancer; monocyte chemoattractant protein-1; MCP-1.
XX
OS      Homo sapiens.
XX
PN      WO2004080273-A2.
XX
PD      23-SEP-2004.
XX
PF      14-MAR-2004; 2004WO-IL000240.
XX
PR      12-MAR-2003; 2003US-0453514P.
XX
PR      12-MAR-2003; 2003US-0453515P.
XX
PR      28-NOV-2003; 2003US-0525135P.
XX
PR      05-JAN-2004; 2004US-0534111P.
XX
PA      (RAPP-) RAPPAPORT FAMILY INST RES IN MEDICAL SCI.
XX
PI      Karin N;
XX
DR      WPI; 2004-690440/67.
XX
DR      N-PSDB; ADS75932.
XX
PT      Treating prostate cancer, involves administering agent capable of
PT      reducing activity and/or expression of monocyte chemoattractant protein-1
PT      or its effector to subject, thus treating prostate cancer in subject.
XX
PS      Disclosure; SEQ ID NO 12; 78pp; English.
XX
SQ      Sequence 68 AA;

XX      The invention relates to a method of treating (M1) prostate cancer, by
XX      administering an agent capable of reducing activity and/or expression of
XX      monocyte chemoattractant protein-1 (MCP-1) or its effector to a subject,
XX      thus treating the prostate cancer in the subject. (M1) is useful for
XX      treating prostate cancer. An antibody (I) to MCP-1 is useful for
XX      manufacturing a medicament for the treatment of prostate cancer. This
XX      sequence corresponds to a fragment of the MCP-1 protein.

Query Match      100.0%; Score 73; DB 8; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVORLASVRRITSSK 16
        |||||
Db      12 ISVORLASVRRITSSK 27

RESULT 44
AAR87678
ID      AAR87678 standard; protein; 69 AA.
XX
AC      AAR87678;
XX
DT      21-FEB-1996 (first entry)
XX
DE      des (2-8) MCP-1.
XX
KW      monocyte chemoattractant protein; MCP-1; mutant; restenosis; angioplasty.
XX
OS      Homo sapiens.

XX      Key      Location/Qualifiers
XX      Modified-site 2..3
XX      /note= "amino acids 2-8 of the native protein have been
XX      deleted between these residues"
XX      Disulfide-bond 4..29
XX      Disulfide-bond 5..45
XX      WO9513295-A1.
XX      18-MAY-1995.
XX      07-NOV-1994; 94WO-US012874.
XX      12-NOV-1993; 93US-00152301.
XX      (DAND ) DANA FARBER CANCER INST INC.
XX      Rollins B, Zhang YJ;
XX      WPI; 1995-215051/28.
XX      Human monocyte chemo-attractant protein-1 (MCP-1) derive. - are capable
XX      of inhibiting the monocyte chemo-attractant activity of endogenous MCP-1
XX      and can be used to treat restenosis.
XX      Claim 4; Page 11; 22pp; English.
XX      Monocyte chemoattractant protein-1 (MCP-1) derivatives are mutated such
XX      that they inhibit the monocyte chemoattractant activity of endogenous MCP
XX      -1, provided that the derivative has not been modified by the
XX      substitution of 28-Tyr by Leu and/or 30-Arg by Val. Preferred mutations
XX      are: (1) substitution of 28 Tyr by aspartate; (2) substitution of 24 Arg
XX      by Phe; (3) substitution of 3-Asp by Ala; and/or (4) deletion of amino
XX      acids 2-8. The present sequence is a specifically claimed human MCP-1
XX      derivative based on the parent protein disclosed in Rollins, Molecular
XX      and Cellular Biology, Vol. 9, No. 11, pp. 4687-4695, Nov. 1989. The
XX      peptides can be used to prevent restenosis, e.g. in patients undergoing
XX      coronary artery angioplasty
XX      Sequence 69 AA;

Query Match      100.0%; Score 73; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVORLASVRRITSSK 16
        |||||
Db      13 ISVORLASVRRITSSK 28

RESULT 45
AAW13596
ID      AAW13596 standard; peptide; 69 AA.
XX
AC      AAW13596;
XX
DT      07-NOV-1997 (first entry)
XX
DE      Monocyte chemoattractant protein analogue MCP-1 (8-76).
XX
KW      Truncated monocyte chemoattractant protein-1; inhibitor;
KW      receptor binding; anti inflammatory; basophil; lymphocyte; allergy;
KW      chronic inflammatory disease; arthritis; arteriosclerosis; lung disease.
XX
OS      Homo sapiens.
XX
PN      CA2152141-A.
XX
PD      20-DEC-1996.
XX
PF      19-JUN-1995; 95CA-02152141.
XX

```

PR 19-JUN-1995; 95CA-02152141.
XX (LEWIS) LEWIS I.
XX Lewis I, Gong J;
PI WPI; 1997-165844/16.
XX N-terminally truncated monocyte chemoattractant protein-1 (MCP-1) -
PT lacks MCP-1 activity and inhibits receptor binding, useful as anti-
PT inflammatory agent.
XX Claim 5; Page 5; 27pp; English.
XX The present sequence represents an analogue, MCP-1 (8-76), of monocyte
CC chemoattractant protein-1 (MCP-1). The analogue, which lacks the N-
CC terminal amino acids 1-7 of MCP-1, acts as an antagonist of MCP-1 as it
CC lacks MCP-1 biological activity and inhibits binding to a MCP-1 receptor.
CC The analogue is useful as an anti-inflammatory agent to block the effects
CC of MCP-1 which is an inflammatory mediator causing migration of monocytes
CC and other cells e.g. basophils and lymphocytes into inflammation sites.
CC MCP-1 has been implicated in allergic and chronic inflammatory diseases
CC e.g. arthritis, arteriosclerosis and several lung diseases. The analogue
CC competes more effectively with MCP-1 for binding MCP-1 receptors than
CC prior art mutant versions of MCP-1 e.g. preferably providing 50%
CC inhibition of binding at a 25:1 ratio or less, compared with 75:1 for
CC prior art mutant 7ND
XX Sequence 69 AA;
SQ

Query Match 100.0%; Score 73; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | |
Db 13 ISVQRLASYRRITSSK 28

RESULT 46
AAMS3049
ID AAMS3049 standard; protein; 69 AA.
XX AAMS3049;
AC
XX 26-MAR-2002 (first entry)
DT Human mutant monocyte chemoattractant protein-1, 7ND-MCP-1.
DE Human; monocyte chemoattractant protein-1; MCP-1; C-C chemokine family;
KW pulmonary hypertension; primary; hypotensive; mutant; mutein.
XX Homo sapiens.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 2.3
FT /note= "There is an insertion of the sequence PDAINAP
FT between these two residues in the wild-type human MCP-1
FT (AAMS3048)"
XX WO200189582-A1.
FN
XX 29-NOV-2001.
PD
XX 25-MAY-2001; 2001WO-JP004391.
PF
XX 26-MAY-2000; 2000JP-00161145.
PR (TAKE) TAKEDA CHEM IND LTD.
XX (EGAS/) EGASHIRA K.
PA Egashira K, Yonemitsu Y, Sueishi K, Ikeda Y, Inada Y;
XX

XX WPI; 2002-083059/11.
DR N-PSDB; ABA02498.
XX Preventives and remedies for pulmonary hypertension containing mutant of
PT MCP-1 antagonistic inhibitory type or its salt, encoded DNA or
PT neutralization antibody.
XX Claim 2; Page 32; 39pp; Japanese.
XX The invention relates to preventives and remedies for pulmonary
CC hypertension, comprising an antagonistic inhibitory mutant of monocyte
CC chemoattractant protein-1 (MCP-1). DNA encoding the mutant MCP-1, or a
CC neutralising antibody against MCP-1. MCP-1 is a member of the C-C
CC chemokine family. The preventives and remedies have hypotensive activity
CC and can be used in the prevention and treatment of pulmonary hypertension
CC particularly pulmonary primary hypertension. The present sequence
CC represents a specifically claimed MCP-1 mutant, 7ND-MCP-1
XX Sequence 69 AA;
SQ

Query Match 100.0%; Score 73; DB 5; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | |
Db 13 ISVQRLASYRRITSSK 28

RESULT 47
ADD14999
ID ADD14999 standard; protein; 69 AA.
XX ADD14999;
AC
XX 15-JAN-2004 (first entry)
DT Truncated monocyte chemoattractant protein-1 (MCP-1) seq id 4.
DE
XX antiinflammatory; MCP-1 Antagonist; biocompatibility; medical device;
KW monocyte chemoattractant protein 1; MCP-1; MCP-1 antagonist;
KW chronic inflammation; fibrous encapsulation; human.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Misc-difference 1
FT /note= "Encoded by CCA"
XX US2003129214-A1.
FN
XX 10-JUL-2003.
PD
XX 09-JAN-2003; 2003US-00339778.
PF
XX 10-JAN-2002; 2002US-0347560P.
PR (UNIW) UNIV WASHINGTON.
XX Bornstein P, Kyriakides T;
PI
XX WPI; 2003-787133/74.
DR N-PSDB; ADD14996.
XX Enhancing biocompatibility of a medical device implanted in a portion of
PT a living body by contacting the portion of the body that is in contact
PT with the implanted device with monocyte chemoattractant protein 1 (MCP-1)
PT antagonist.
XX Claim 19; SEQ ID NO 4; 18pp; English.
PS The invention describes a method of enhancing (M1) the biocompatibility
CC

CC of a medical device implanted within a portion of a living body
CC comprising contacting a portion of the living body in contact with the
CC device with a monocyte chemoattractant protein 1 (MCP-1) antagonist to
CC inhibit chronic inflammation induced by the presence of the medical
CC device or fibrous encapsulation of the medical device. The method is
CC useful for enhancing the biocompatibility of a medical device implanted
CC in a portion of a living body by inhibiting chronic inflammation or
CC formation of fibrous capsules around the device. This is the amino acid
CC sequence of a truncated version of human monocyte chemoattractant protein
CC -1 (MCP-1).
XX
SQ Sequence 69 AA;

Query Match 100.0%; Score 73; DB 7; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 13 ISVQRLASYRRITSSK 28
|||||

RESULT 48
ADN36567
ID ADN36567 standard; protein; 69 AA.
XX
AC ADN36567;

DT 17-JUN-2004 (first entry)

XX Chemokine receptor inhibitor-related protein R2-4 (MCP-1 (8-76)) #13.2.

XX Chemokine receptor inhibitor; chimeric protein; HIV infection;
KW tumour metastasis; organ transplant rejection; autoimmune disease;
KW anti-HIV; cytostatic; immunosuppressive; R2; MCP-1.

XX Unidentified.

XX CN1435433-A.

XX 13-AUG-2003.

XX 30-AUG-2002; 2002CN-00129301.

XX 30-AUG-2002; 2002CN-00129301.

XX (GONG/) GONG X.

XX Gong J;

XX WPI: 2004-000227/01.

XX N-PSDB; ADN36585.

XX Long-acting broad-spectrum chemotactic factor receptor inhibiting matter.

XX Claim 16; Page 27; 43pp; Chinese.

XX The invention relates to chimeric proteins for inhibition of chemokine
CC receptors. The invention also relates to nucleic acids encoding the
CC chimeric proteins, and a process for preparing and testing the chimeric
CC proteins. The chimeric proteins provide long-acting, broad spectrum
CC inhibition of chemokine receptors with high selectivity. They can be used
CC to prevent or treat HIV infection, tumour metastasis, organ transplant
CC rejection and autoimmune diseases. The present sequence represents a
CC protein sequence which may be incorporated into a chimeric protein of the
XX invention.

SQ Sequence 69 AA;

Query Match 100.0%; Score 73; DB 8; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 13 ISVQRLASYRRITSSK 28
|||||

RESULT 49

ADT99562
ID ADT99562 standard; protein; 69 AA.

XX
AC ADT99562;

XX 27-JAN-2005 (first entry)

XX Monocyte chemotactic factor-1 antagonist protein sequence - SEQ ID 2.

XX kidney ischaemia reperfusion injury;

XX monocyte chemotactic factor-1 inhibition; MCP-1 inhibition;

XX ischaemia reperfusion trauma; kidney transplantation; kidney surgery;

XX renal injury; renal infarction; renal-artery constriction;

XX renal arteriosclerosis; nephrosclerosis; renal haemorrhage; burn;

XX thermal burn; shock.

XX Homo sapiens.

XX JP2004307427-A.

XX 04-NOV-2004.

XX 10-APR-2003; 2003JP-00106080.

XX 10-APR-2003; 2003JP-00106080.

XX (EGAS/) EGASHIRA K.

XX (ANJE-) ANJESU MG KK.

XX WPI: 2004-778670/77.

XX N-PSDB; ADT99561.

XX Treatment, improvement and preventive agent of kidney ischemia
PT reperfusion trauma, useful for treating kidney ischemia reperfusion
PT trauma, comprises monocyte chemotactic factor-1 functional inhibitor as
PT active ingredient.

XX Claim 9; SEQ ID NO 2; 15pp; Japanese.

XX The invention comprises an agent for the treatment or prevention of
CC kidney ischaemia reperfusion injury, the agent of the invention comprises
CC a monocyte chemotactic factor-1 (MCP-1) functional inhibitor (MCP-1
CC antagonist) as an active ingredient. The agent of the invention is useful
CC for treating or preventing kidney ischaemia reperfusion trauma, caused
CC by: kidney transplantation, kidney surgery, renal injury, renal
CC infarction, renal-artery constriction, renal arteriosclerosis,
CC nephrosclerosis, renal haemorrhage, burn, thermal burn, or a shock. The
CC present amino acid sequence represents the MCP-1 antagonist of the
XX invention.

SQ Sequence 69 AA;

Query Match 100.0%; Score 73; DB 8; Length 69;

Best Local Similarity 100.0%; Pred. No. 1.4e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16

Db 13 ISVQRLASYRRITSSK 28
|||||

RESULT 50

ADR90677

ID ADR90677 standard; protein; 74 AA.

XX
AC ADR90677;

XX 02-DEC-2004 (first entry)
DT Human monocyte chemotactic protein 1 partial protein.
DE
DE dipeptidyl peptidase cleavage; antidiabetic; anorectic; antiinflammatory;
XX antiarteriosclerotic; tranquiliser; anticonvulsant; hypnotic;
KW gene therapy; metabolic disease; diabetes; obesity; inflammation;
KW atherosclerosis; nervous system disorder; anxiety; seizures;
KW sleep disorder; monocyte chemotactic protein 1; MCP-1; human.
XX
OS Homo sapiens.
XX
XX WO2004078777-A2.
FN
XX 16-SEP-2004.
PD
XX 04-MAR-2004; 2004WO-US006462.
PF
XX 04-MAR-2003; 2003US-00378094.
PR
XX 28-AUG-2003; 2003WO-US026818.
PR
XX (BIOR-) BIOREXIS PHARM CORP.
PA
XX Sadeghi H, Prior CP, Ballance DJ;
PI
XX WPI; 2004-653689/63.
DR
XX New modified polypeptides that are resistant to dipeptidyl peptidase
PT cleavage, useful for treating metabolic diseases (e.g. diabetes or
PT obesity), inflammation, atherosclerosis or nervous system disorders (e.g.
PT anxiety).
XX
XX Disclosure; SEQ ID NO 58; 125pp; English.
PS
XX This invention relates to a novel polypeptide molecule modified to
CC contain at least one additional amino acid at the N-terminal end that
CC substantially protects the polypeptide molecule from dipeptidyl peptidase
CC cleavage, where the modified polypeptide substantially retains
CC polypeptide activity. The invention may be useful for the production of
CC compounds with an antidiabetic, anorectic, antiinflammatory,
CC antiarteriosclerotic, tranquiliser, anticonvulsant or hypnotic activity.
CC In addition, the invention may be useful for gene therapy. The compounds
CC may be useful for treating metabolic diseases (for example diabetes or
CC obesity), inflammation, atherosclerosis and nervous system disorders,
CC such as anxiety, seizures and sleep disorders. The present sequence is
CC that of a polypeptide derived from a human protein which is related to
CC the invention.
XX
SQ Sequence 74 AA;
Query Match 100.0%; Score 73; DB 8; Length 74;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ISVQRLASYRRITSSK 16
Db 20 ISVQRLASYRRITSSK 35
|||||
|||||

Search completed: February 6, 2006, 14:25:10
Job time : 229 secs

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OM protein - protein search, using sw model

Run on: February 6, 2006, 14:25:28 ; Search time 42 Seconds

(without alignments)
36.654 Million cell updates/sec

Title: US-10-644-277-149_COPY_20_35

Perfect score: 73

Sequence: 1 ISVQRLASYRRITSSK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

1: PIR_80.*

2: Pirl.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	99	2 A60299	monocyte chemoattr
2	64	87.7	72	2 A55984	monocyte chemoattr
3	64	87.7	99	2 JC2136	monocyte chemoattr
4	61	83.6	99	1 A39296	monocyte chemoattr
5	61	83.6	99	2 JC2336	monocyte chemoattr
6	56	76.7	97	2 JC4912	eotaxin precursor
7	56	76.7	125	2 I46857	monocyte chemoattr
8	52	71.2	96	2 JC2478	eotaxin precursor
9	52	71.2	96	2 I48099	eotaxin precursor
10	49	67.1	148	1 A30209	PDGF-inducible JE
11	47	64.4	109	2 A54678	monocyte chemoattr
12	46	63.0	148	1 S07723	immediate-early se
13	45	61.6	97	2 A48093	monocytic cytokine
14	44	60.3	99	2 JC5295	monocyte chemoattr
15	42	57.5	60	2 S62188	hypothetical prote
16	41	56.2	120	2 I48147	monocyte chemoattr
17	41	56.2	339	2 F83066	conserved hypothe
18	41	56.2	1199	1 S76549	transcription-repa
19	39	53.4	398	2 T38233	probable cystathio
20	39	53.4	893	2 F72253	hypothetical prote
21	38	52.1	99	2 JC2417	monocyte chemoattr
22	38	52.1	242	2 A82754	lipoprotein XF0855
23	38	52.1	311	2 JC5200	chemoreceptor Tb33
24	37.5	51.4	59	2 D37314	regulatory protein
25	37.5	51.4	146	2 A37774	lcrR protein - Yer
26	37.5	51.4	146	2 T43592	low calcium respon
27	37	50.7	194	2 T19339	hypothetical prote
28	37	50.7	374	2 T02021	hypothetical prote
29	37	50.7	378	2 C62112	flagellin FlaE VC2

30	37	50.7	379	2	G82107	flagellin core pro
31	37	50.7	474	2	S52444	flagellin - legion
32	37	50.7	498	1	FLEC	flagellin - Escher
33	37	50.7	550	2	S44980	flagellin - Shigel
34	37	50.7	565	2	I41061	flagellin - Escher
35	37	50.7	579	2	S61131	probable membrane
36	37	50.7	584	2	C48658	flagellin - Escher
37	37	50.7	585	2	F85809	hypothetical prote
38	37	50.7	585	2	F90961	flagellin [import
39	37	50.7	595	2	B48658	flagellin - Escher
40	37	50.7	595	2	A48658	probable large ATP
41	37	50.7	840	2	T36175	hypothetical prote
42	37	50.7	1175	2	D85089	hypothetical prote
43	37	50.7	1198	2	H86402	hypothetical prote
44	37	50.7	1285	2	H85041	hypothetical prote
45	37	50.7	1305	2	H96559	hypothetical prote
46	37	50.7	1312	2	D85066	hypothetical prote
47	37	50.7	1314	2	T47331	hypothetical prote
48	37	50.7	1472	2	A84470	hypothetical prote
49	37	50.7	1756	2	T02599	hypothetical prote
50	36	49.3	113	2	B41657	probable immunity
51	36	49.3	113	2	S52207	meso protein - Leu
52	36	49.3	156	2	T07174	tuberculosis-relat
53	36	49.3	217	2	H84852	probable RING zinc
54	36	49.3	223	2	C86233	Golgi SNARE 11 pro
55	36	49.3	269	1	A27067	careinin - chick
56	36	49.3	290	2	C71416	probable ABC trans
57	36	49.3	345	2	F71261	probable lipase -
58	36	49.3	394	2	A37853	flagellin, 40K - P
59	36	49.3	455	2	B83260	conserved hypothe
60	36	49.3	530	2	D87255	apolipoprotein N-a
61	36	49.3	815	2	A71700	phenylalanine-tRNA
62	36	49.3	818	2	F97772	hypothetical prote
63	36	49.3	844	2	C86339	protein F2D10.12 [
64	36	49.3	1113	2	T47381	hypothetical prote
65	36	49.3	1148	1	G64855	transcription/rep
66	36	49.3	1148	2	A10644	transcription-repa
67	36	49.3	1148	2	H85674	hypothetical prote
68	36	49.3	1148	2	D90815	transcription-repa
69	36	49.3	1413	2	G84790	probable ABC trans
70	36	49.3	1742	2	T17120	cellulase (EC 3.2.
71	36	49.3	4302	2	A38971	polycystic kidney
72	35	48.6	319	2	B82381	transcription regu
73	35	47.9	137	2	B83659	hypothetical prote
74	35	47.9	163	2	F85046	hypothetical prote
75	35	47.9	205	2	S34833	stylar protein (al
76	35	47.9	209	2	AF2354	imidazoleglycerol-
77	35	47.9	256	2	G84061	ferrichrome ABC tr
78	35	47.9	281	2	C83802	nicotinate-nucleot
79	35	47.9	287	2	S28040	flagellin - lister
80	35	47.9	287	2	AB1161	flagellin protein
81	35	47.9	287	2	AB1520	flagellin protein
82	35	47.9	300	2	F83621	hypothetical prote
83	35	47.9	311	2	AH0867	transcription acti
84	35	47.9	347	1	A44245	alcohol dehydrogen
85	35	47.9	367	2	JC2560	flagellin flic-2 -
86	35	47.9	438	2	B82077	outer membrane pro
87	35	47.9	463	1	DMCH	desmin - chicken
88	35	47.9	469	1	DMHU	desmin - human
89	35	47.9	469	2	A24783	desmin - golden ha
90	35	47.9	469	2	A54104	desmin - mouse
91	35	47.9	469	2	S52469	desmin - rat
92	35	47.9	473	2	T39028	citrate synthase p
93	35	47.9	548	2	H97820	60K chaperonin (im
94	35	47.9	598	2	T42070	protein serine/thr
95	35	47.9	682	2	E83782	alpha-glucuronidas
96	35	47.9	736	2	JC7518	subtilisin-like se
97	35	47.9	808	2	A96791	hypothetical prote
98	35	47.9	846	2	S54518	hypothetical trp-a
99	35	47.9	846	2	T38840	hypothetical trp-a
100	35	47.9	1490	2	T47840	multi resistance p
101	34.5	47.3	431	2	E69211	UDP-N-acetyl-D-man
102	34.5	47.3	470	2	T32137	hypothetical prote

103	34	46.6	68	2	AF0976	hypothetical prote	176	33	45.2	98	2	S14883	hypothetical prote
104	34	46.6	105	2	E69058	hypothetical prote	177	33	45.2	103	2	T23242	hypothetical prote
105	34	46.6	132	2	S70014	transcription repr	178	33	45.2	128	2	C53380	polyribonucleotide
106	34	46.6	208	2	I64209	ribosomal protein	179	33	45.2	155	2	B72503	hypothetical prote
107	34	46.6	246	2	H82419	conserved hypothet	180	33	45.2	216	2	T47329	hypothetical prote
108	34	46.6	271	1	A60253	calretinin - huma	181	33	45.2	235	2	AB1975	hypothetical prote
109	34	46.6	279	2	JH0655	macrotetrolide res	182	33	45.2	236	2	H84612	hypothetical prote
110	34	46.6	284	2	E83557	probable transcrip	183	33	45.2	245	2	A95164	acyl-ACP thioester
111	34	46.6	296	1	QRECPD	ferrichrome-iron t	184	33	45.2	247	2	H98029	hypothetical prote
112	34	46.6	296	2	D90648	ferrichrome-iron t	185	33	45.2	247	2	D83671	amino acid ABC tra
113	34	46.6	296	2	D85499	ferrichrome-iron t	186	33	45.2	283	2	T31275	2-hydroxyymuconate-
114	34	46.6	313	2	JC5754	flagellin - Xenorh	187	33	45.2	283	2	S34851	hypothetical 31.9K
115	34	46.6	320	2	AE2598	mutT/nudix family	188	33	45.2	283	2	T36996	probable noncompos
116	34	46.6	320	2	B97370	NADH pyrophosphata	189	33	45.2	286	1	JC5419	2-hydroxyymuconate-
117	34	46.6	351	2	JU0036	flagellin - Serrat	190	33	45.2	287	2	JB0094	syntxin 11 - huma
118	34	46.6	358	2	S78460	flagellin fleA, 36	191	33	45.2	291	2	T21475	hypothetical prote
119	34	46.6	364	2	J78461	flagellin fleB, 37	192	33	45.2	305	2	AC1513	oxidoreductase hom
120	34	46.6	365	2	JC2559	flagellin fleC-1 -	193	33	45.2	317	2	T30232	methyltransferase
121	34	46.6	369	2	AG0224	thermoregulated mo	194	33	45.2	338	2	T34364	hypothetical prote
122	34	46.6	378	2	S69767	flagellin fleC, 39	195	33	45.2	346	2	B75111	glycerol 1-phospha
123	34	46.6	379	2	JG0621	flagellin A - Vibr	196	33	45.2	351	2	H71432	probable glucosylt
124	34	46.6	391	2	A40594	major flagellin pr	197	33	45.2	362	2	A70547	probable menE - My
125	34	46.6	401	2	T50548	GTP cyclonhydrolase	198	33	45.2	364	2	T05401	hypothetical prote
126	34	46.6	403	2	T38078	hypothetical prote	199	33	45.2	372	2	T08273	conserved hypothet
127	34	46.6	406	2	S76451	hypothetical prote	200	33	45.2	378	2	T20236	hypothetical prote
128	34	46.6	467	2	T41053	triglyceride lipas	201	33	45.2	387	2	F85066	hypothetical prote
129	34	46.6	476	2	T35769	probable transmemb	202	33	45.2	399	2	AC1601	platelet glycoprot
130	34	46.6	486	2	E84438	hypothetical prote	203	33	45.2	411	1	I55604	hypothetical prote
131	34	46.6	488	2	E83507	flagellin type B P	204	33	45.2	411	2	T19728	hypothetical prote
132	34	46.6	489	2	S09637	flagellin - Salmon	205	33	45.2	430	2	D86514	Cr132 hypothetical
133	34	46.6	490	2	A24262	phase-1 i flagelli	206	33	45.2	430	2	C72108	ct132 hypothetical
134	34	46.6	493	2	S07373	flagellin H-1 - Sa	207	33	45.2	430	2	G81562	conserved hypothet
135	34	46.6	494	2	S07276	flagellin H-1A - S	208	33	45.2	442	2	B75634	hypothetical prote
136	34	46.6	494	2	S16121	flagellin - Salmon	209	33	45.2	457	2	T50402	probable mitochond
137	34	46.6	504	2	S33193	phase-1 flagellin	210	33	45.2	471	1	A35867	cytochrome P450 71
138	34	46.6	504	2	S33190	phase-1 flagellin	211	33	45.2	480	2	B71313	probable V-type AT
139	34	46.6	504	2	S33191	phase-1 flagellin	212	33	45.2	502	2	T52256	cytochrome P-4501X
140	34	46.6	504	2	S33194	phase-1 flagellin	213	33	45.2	506	2	T33770	hypothetical prote
141	34	46.6	504	2	S33186	phase-1 flagellin	214	33	45.2	512	2	I80311	sepc protein - Bsc
142	34	46.6	504	2	S33189	phase-1 flagellin	215	33	45.2	550	2	A71668	60 kd chaparonin (
143	34	46.6	504	2	S33188	phase-1 flagellin	216	33	45.2	624	2	T21072	hypothetical prote
144	34	46.6	504	2	S33187	phase-1 flagellin	217	33	45.2	627	2	S48968	hypothetical prote
145	34	46.6	506	2	S09638	flagellin - Salmon	218	33	45.2	743	2	PN0009	PM75 protein - yea
146	34	46.6	506	2	AH0750	flagellin [importe	219	33	45.2	784	2	F80009	neurofilament trip
147	34	46.6	507	2	S33185	phase-1 flagellin	220	33	45.2	823	2	T35280	probable integral
148	34	46.6	507	2	S33192	phase-1 flagellin	221	33	45.2	843	2	H82362	adenylate cyclase
149	34	46.6	508	2	A53465	phase-1 flagellin	222	33	45.2	965	2	T21073	hypothetical prote
150	34	46.6	524	2	S44982	flagellin - Shigel	223	33	45.2	1075	2	T48805	hypothetical prote
151	34	46.6	577	2	A61372	hemolysin, extrac	224	33	45.2	1148	2	AD0198	transcription-repa
152	34	46.6	578	2	S26577	beta-hemolysin - A	225	33	45.2	1171	2	G97174	pyruvate:ferredoxi
153	34	46.6	586	2	G71656	single-stranded-dn	226	33	45.2	1237	2	T46609	calcium-activated
154	34	46.6	618	2	S06446	citrolysin-related	227	33	45.2	1420	2	T02644	ABC-type transport
155	34	46.6	620	2	JH0821	95K golgi antigen	228	33	45.2	1451	2	B86286	F91.15 protein -
156	34	46.6	637	2	T50951	1,4-alpha-glucan b	229	33	45.2	1673	2	T50806	complement compone
157	34	46.6	666	2	B56639	gene Mx protein -	230	33	45.2	2022	2	T48818	Glucan 1,4-alpha-g
158	34	46.6	721	2	S31824	gene Mx protein -	231	32	43.8	57	2	C48977	carbon storage reg
159	34	46.6	721	2	S31820	gene Mx protein -	232	32	43.8	61	1	B40608	glycogen biosynthe
160	34	46.6	721	2	A37472	interferon-inducib	233	32	43.8	61	2	AD0401	carbon storage reg
161	34	46.6	731	2	I60729	ornithine decarbox	234	32	43.8	61	2	AE0843	carbon storage reg
162	34	46.6	783	1	WMBEHQ	UL5 protein - huma	235	32	43.8	61	2	D85917	glycogen biosynthe
163	34	46.6	882	1	WMBEUS	gene UL5 protein -	236	32	43.8	61	2	A91073	carbon storage reg
164	34	46.6	903	2	G82516	hypothetical prote	237	32	43.8	63	1	H64095	carbon storage reg
165	34	46.6	986	2	T10754	cis-Golgi matrix p	238	32	43.8	67	2	T44077	hypothetical prote
166	34	46.6	1290	2	S76853	hypothetical prote	239	32	43.8	75	2	AG2612	hypothetical prote
167	34	46.6	1389	2	T47796	ABC transporter-li	240	32	43.8	92	2	B82603	hypothetical prote
168	34	46.6	3011	1	GNWVCH	genome polyprotein	241	32	43.8	112	2	T17556	hypothetical prote
169	34	46.6	3011	1	S40770	toxin-like outer m	242	32	43.8	126	2	T23246	hypothetical prote
170	34	46.6	3194	2	D71917	probable glycosylt	243	32	43.8	130	2	C69061	hypothetical prote
171	33.5	45.9	383	2	A58871	hypothetical prote	244	32	43.8	136	2	AB2542	transcription repr
172	33.5	45.9	1065	2	G72330	hypothetical prote	245	32	43.8	175	2	T23245	hypothetical prote
173	33.5	45.9	1208	2	T00362	hypothetical prote	246	32	43.8	179	2	A87654	hypothetical prote
174	33	45.2	75	2	S12191	hypothetical prote	247	32	43.8	183	2	F71127	hypothetical prote
175	33	45.2	93	2	S76897	hypothetical prote	248	32	43.8	194	2	G95941	probable small hea

249	32	43.8	196	2	JC4257	beta A4-crystallin
250	32	43.8	200	1	A71127	hypothetical prote
251	32	43.8	202	2	T13124	repressor protein
252	32	43.8	207	2	AC2069	acyl carrier prote
253	32	43.8	213	2	G30176	conserved hypotet
254	32	43.8	233	2	D81398	hypothetical prote
255	32	43.8	238	2	S75534	hydrogenase chain
256	32	43.8	239	2	AC2643	flagellar L-ring p
257	32	43.8	239	2	G97425	flagellar L-ring p
258	32	43.8	240	2	S01299	OX-45 membrane gly
259	32	43.8	245	2	T43174	hypothetical prote
260	32	43.8	248	2	F69198	conserved hypotet
261	32	43.8	249	1	B70693	probable echa16 pr
262	32	43.8	255	1	Q8ECW3	membrane-bound iro
263	32	43.8	256	2	AS2019	hypothetical prote
264	32	43.8	262	2	A70348	hypothetical prote
265	32	43.8	273	2	AH2222	ABC nitrate transp
266	32	43.8	284	2	D70513	probable hlgG atp
267	32	43.8	291	2	T00855	hypothetical prote
268	32	43.8	293	2	C70160	ribosomal protein
269	32	43.8	294	2	B70692	hypothetical prote
270	32	43.8	299	2	E30777	replication protei
271	32	43.8	299	2	S42400	gene O protein - p
272	32	43.8	304	2	B23431	hypothetical prote
273	32	43.8	309	2	D90520	conserved hypotet
274	32	43.8	317	2	S75694	hypothetical prote
275	32	43.8	320	2	S46824	ribose-phosphate d
276	32	43.8	322	2	F80029	protein F46F5.5 [i
277	32	43.8	332	2	D83159	probable transcrip
278	32	43.8	337	2	A85920	ascBF operon repre
279	32	43.8	337	2	B31075	ascBF operon repre
280	32	43.8	343	2	A86241	hypothetical prote
281	32	43.8	361	2	T25196	hypothetical prote
282	32	43.8	370	2	D75503	hypothetical prote
283	32	43.8	371	2	A13558	glycerol trinitrat
284	32	43.8	377	2	F82107	flagellin FlaC VC2
285	32	43.8	400	2	H31163	probable DNA proce
286	32	43.8	402	2	D84840	hypothetical prote
287	32	43.8	403	2	S71356	glucocorticoid-att
288	32	43.8	404	2	T19480	hypothetical prote
289	32	43.8	428	2	A10034	probable transmem
290	32	43.8	431	2	A86010	probable DNA proce
291	32	43.8	444	2	H75544	hypothetical prote
292	32	43.8	452	2	C97382	probable glutamine
293	32	43.8	458	2	A43554	desmin - African c
294	32	43.8	460	2	AB2600	P60 extracellular
295	32	43.8	465	2	AG1506	cannabinoid recept
296	32	43.8	472	2	S17595	cannabinoid recept
297	32	43.8	473	2	A33117	P60 extracellular
298	32	43.8	482	2	AG1147	protein P60 precu
299	32	43.8	484	2	A41487	type II site-speci
300	32	43.8	489	2	AG1166	CDCl protein - yea
301	32	43.8	491	2	S49779	hypothetical prote
302	32	43.8	503	2	T29868	multidrug resistanc
303	32	43.8	519	2	B71726	beta-mannosidase p
304	32	43.8	520	2	G75141	hypothetical prote
305	32	43.8	532	2	T04748	H+-transporting tw
306	32	43.8	545	1	PWBYA	hydrogenase (EC 1.
307	32	43.8	567	1	C55516	probable large sub
308	32	43.8	567	2	G85958	hydrogenase-2 larg
309	32	43.8	567	2	G31113	conserved hypotet
310	32	43.8	572	2	F90564	hypothetical prote
311	32	43.8	602	2	AH2485	hemagglutinin - ph
312	32	43.8	607	1	HNN2PD	hemagglutinin - ph
313	32	43.8	607	1	J01535	segment polarity p
314	32	43.8	623	2	A49840	hypothetical prote
315	32	43.8	645	2	T27186	probable membrane
316	32	43.8	652	2	S22683	hypothetical prote
317	32	43.8	660	2	H87325	maturase-related p
318	32	43.8	673	2	S53604	maturase-related p
319	32	43.8	674	2	T07017	maturase homolog -
320	32	43.8	675	2	JC5898	beta-galactoside a
321	32	43.8	678	2	B38489	maturase-related p

322	32	43.8	685	2	S43562	KOBE5.3 protein -
323	32	43.8	687	2	A34879	maturase-related p
324	32	43.8	688	2	S33605	hypothetical prote
325	32	43.8	722	2	B83228	hypothetical 91.8K
326	32	43.8	752	2	H98161	GGDEF family prote
327	32	43.8	779	2	AH3125	chitinase (EC 3.2.
328	32	43.8	799	2	PC4106	chitinase (EC 3.2.
329	32	43.8	820	2	A40633	DNA-directed DNA p
330	32	43.8	831	2	S26675	protein F33E2.2 [i
331	32	43.8	848	2	B87950	hypothetical prote
332	32	43.8	853	2	T24279	hypothetical prote
333	32	43.8	855	2	T20082	hypothetical prote
334	32	43.8	891	2	T40417	DNA polymerase I (
335	32	43.8	908	2	C70168	hypothetical prote
336	32	43.8	920	2	T40771	methy1-accepting c
337	32	43.8	953	2	S75285	probable membrane
338	32	43.8	957	2	S66755	hypothetical prote
339	32	43.8	990	2	T43445	hypothetical prote
340	32	43.8	1039	2	B90308	hypothetical prote
341	32	43.8	1039	2	T25591	isoleucine-tRNA li
342	32	43.8	1070	2	T42539	glutamate synthase
343	32	43.8	1081	1	A42339	probable potassium
344	32	43.8	1137	2	T02097	transcription/rep
345	32	43.8	1139	2	A10379	transcription/rep
346	32	43.8	1146	1	I64112	probable RNA-direc
347	32	43.8	1185	2	AG2457	ABC transport prot
348	32	43.8	1309	2	T00078	Rhs-family protein
349	32	43.8	1336	2	T18288	hypothetical prote
350	32	43.8	1354	2	AG0538	MRP-like ABC trans
351	32	43.8	1421	2	T34225	ferredoxin-depende
352	32	43.8	1515	2	T52081	1,4-beta-glucanase
353	32	43.8	1629	2	C84839	hypothetical prote
354	32	43.8	1711	2	T31337	hypothetical prote
355	32	43.8	1892	2	C97804	probable non-ribos
356	32	43.8	2124	2	H83357	unconventional myo
357	31.5	43.2	3530	2	A59266	DNA-directed DNA p
358	31.5	43.2	76	2	AD0217	hypothetical prote
359	31.5	43.2	240	2	T19349	hypothetical prote
360	31.5	43.2	302	2	T19348	alcohol dehydrogen
361	31.5	43.2	347	1	S51120	two-component syet
362	31.5	43.2	386	2	F82721	glutamyl-tRNA synt
363	31.5	43.2	502	2	T45422	cyclic beta 1-2 gl
364	31.5	43.2	2831	2	T31419	cellobiose-phospho
365	31.5	43.2	2867	2	AG3481	hypothetical prote
366	31	42.5	36	2	S70806	hypothetical prote
367	31	42.5	41	2	AH1876	hypothetical prote
368	31	42.5	54	2	F82545	hypothetical prote
369	31	42.5	64	2	S01103	hypothetical prote
370	31	42.5	73	2	T31698	probable cell divi
371	31	42.5	75	2	E90974	hypothetical prote
372	31	42.5	76	2	B64660	hypothetical prote
373	31	42.5	77	2	C84332	keratin, type I, c
374	31	42.5	93	2	S08613	keratin, 52K type
375	31	42.5	93	2	A26135	ribosomal protein
376	31	42.5	97	2	C75089	transcription repr
377	31	42.5	113	2	J00810	hypothetical prote
378	31	42.5	132	2	H97806	hypothetical prote
379	31	42.5	135	2	H72471	transcription regu
380	31	42.5	135	2	AG3590	hypothetical prote
381	31	42.5	137	2	B69747	envelope protein -
382	31	42.5	138	2	PC1208	pyruvate (flavodox
383	31	42.5	146	2	B39414	hypothetical prote
384	31	42.5	154	2	S72939	conserved hypotet
385	31	42.5	154	2	F69520	conserved hypotet
386	31	42.5	157	2	C70080	hypothetical prote
387	31	42.5	159	2	D71033	hypothetical prote
388	31	42.5	160	2	D98089	hypothetical prote
389	31	42.5	165	2	T49872	probable membrane
390	31	42.5	167	2	T35320	conserved hypotet
391	31	42.5	170	2	S66125	hypothetical prote
392	31	42.5	170	2	B83664	beta-crystallin A3
393	31	42.5	177	2	S10088	hypothetical prote
394	31	42.5	181	2	A70673	conserved hypotet
394	31	42.5	185	2	D72118	conserved hypotet

KOBE5.3 protein -
maturase-related p
hypothetical prote
hypothetical 91.8K
GGDEF family prote
chitinase (EC 3.2.
chitinase (EC 3.2.
DNA-directed DNA p
protein F33E2.2 [i
hypothetical prote
hypothetical prote
hypothetical prote
DNA polymerase I (
hypothetical prote
methy1-accepting c
probable membrane
hypothetical prote
hypothetical prote
isoleucine-tRNA li
glutamate synthase
probable potassium
transcription/rep
transcription/rep
probable RNA-direc
ABC transport prot
Rhs-family protein
hypothetical prote
MRP-like ABC trans
ferredoxin-depende
1,4-beta-glucanase
hypothetical prote
probable non-ribos
unconventional myo
DNA-directed DNA p
hypothetical prote
hypothetical prote
alcohol dehydrogen
two-component syet
glutamyl-tRNA synt
cyclic beta 1-2 gl
cellobiose-phospho
hypothetical prote
hypothetical prote
hypothetical prote
probable cell divi
hypothetical prote
keratin, type I, c
keratin, 52K type
ribosomal protein
transcription repr
hypothetical prote
hypothetical prote
transcription regu
hypothetical prote
envelope protein -
pyruvate (flavodox
hypothetical prote
conserved hypotet
conserved hypotet
hypothetical prote
hypothetical prote
probable membrane
conserved hypotet
hypothetical prote
beta-crystallin A3
hypothetical prote
conserved hypotet

395	31	42.5	185	2	E86504	hypothetical prote	468	31	42.5	374	2	E64489	hypothetical prote
396	31	42.5	185	2	G96791	probable RING zinc	469	31	42.5	377	2	B82112	flagellin FlaD VC2
397	31	42.5	190	2	S41476	calretinin - mouse	470	31	42.5	379	2	AF2409	mannosyl transfera
398	31	42.5	198	1	CYMSB	beta-crystallin -	471	31	42.5	382	2	E81195	phospholipase A1,
399	31	42.5	198	2	S55512	beta-AI-2 crystall	472	31	42.5	384	2	E69050	GlcNAc-phosphatidy
400	31	42.5	198	2	S55513	beta-AI-1 crystall	473	31	42.5	384	2	S66758	probable membrane
401	31	42.5	198	2	S01608	beta-crystallin A1	474	31	42.5	386	2	AF2687	conserved hypotnet
402	31	42.5	204	2	T44257	thiamine-phosphate	475	31	42.5	387	2	H82176	carboxymorspermid
403	31	42.5	205	2	C26135	keratin, 50K type	476	31	42.5	391	2	B97469	probable membrane
404	31	42.5	205	2	T33826	hypothetical prote	477	31	42.5	395	2	F82852	conserved hypotnet
405	31	42.5	206	2	G85086	hypothetical prote	478	31	42.5	406	2	T03111	hypothetical prote
406	31	42.5	207	2	T02514	hypothetical prote	479	31	42.5	406	2	H71139	hypothetical prote
407	31	42.5	209	2	D96755	hypothetical prote	480	31	42.5	409	2	H81831	probable phospholip
408	31	42.5	212	2	G82103	phosphoribosylglyc	481	31	42.5	411	2	E75381	conserved hypotnet
409	31	42.5	215	2	T45857	beta-crystallin -	482	31	42.5	413	1	S03631	homeotic protein S
410	31	42.5	215	2	S55514	beta-A3-2 crystall	483	31	42.5	415	2	B70981	hypothetical prote
411	31	42.5	215	2	S55515	beta-A3-1 crystall	484	31	42.5	416	2	S52827	hypothetical prote
412	31	42.5	216	2	T38474	olfactory receptor	485	31	42.5	420	2	T41236	conserved hypotnet
413	31	42.5	216	2	T38470	olfactory receptor	486	31	42.5	421	2	E83108	probable type II s
414	31	42.5	218	2	S51751	dihydrodipicolinat	487	31	42.5	423	2	C72376	hypothetical prote
415	31	42.5	218	2	JC2487	GMP-binding protei	488	31	42.5	424	2	S37780	keratin 20, type I
416	31	42.5	218	2	AC0380	probable tetR-fami	489	31	42.5	429	2	A40452	keratin 21, type I
417	31	42.5	218	2	T10353	hypothetical prote	490	31	42.5	432	2	S30433	keratin 17, type I
418	31	42.5	225	2	T38478	olfactory receptor	491	31	42.5	442	2	T20638	hypothetical prote
419	31	42.5	229	2	B70158	conserved hypotnet	492	31	42.5	445	2	E84714	probable protein k
420	31	42.5	235	2	S32747	genome polyprotein	493	31	42.5	454	2	H81828	probable periplasm
421	31	42.5	235	2	F72522	hypothetical prote	494	31	42.5	454	2	A86345	FlaF4.13 protein -
422	31	42.5	243	2	S19148	thioglucoosidase (B	495	31	42.5	457	2	S38296	gamma-aminobutyric
423	31	42.5	244	2	A11414	merr-family transc	496	31	42.5	466	2	T47789	hypothetical prote
424	31	42.5	244	2	AH1790	transcription init	497	31	42.5	468	2	T20475	hypothetical prote
425	31	42.5	255	1	C37165	transcription init	498	31	42.5	472	1	KRHUE	keratin 14, type I
426	31	42.5	255	2	G95260	hypothetical prote	499	31	42.5	473	4	A33652	keratin 16, type I
427	31	42.5	255	2	D98126	conserved hypotnet	500	31	42.5	473	4	A33652	probable keratin 1
428	31	42.5	259	2	S76205	hypothetical prote	501	31	42.5	475	2	B81047	secretion protein,
429	31	42.5	264	2	E95410	probable ABC trans	502	31	42.5	484	2	S73490	glutamate-tRNA lig
430	31	42.5	271	1	S25006	calretinin - rat	503	31	42.5	484	2	AG2889	modulation protein
431	31	42.5	279	2	T51515	syntaxin homolog F	504	31	42.5	494	2	S23315	hypothetical prote
432	31	42.5	282	2	H82394	pirin-related prot	505	31	42.5	496	2	S51668	tyrosine kinase -
433	31	42.5	286	2	F87075	membrane transport	506	31	42.5	502	2	S38139	LAS1 protein - yea
434	31	42.5	291	2	F87676	ATP synthase Fl, g	507	31	42.5	502	2	T22045	hypothetical prote
435	31	42.5	295	2	S50729	sporulation protei	508	31	42.5	506	2	S13720	coat protein - ara
436	31	42.5	296	2	AB0527	ferrichrome-bindin	509	31	42.5	508	2	AF0314	probable aldehyde
437	31	42.5	297	2	G83216	probable transcrip	510	31	42.5	512	2	A53092	reduced folate car
438	31	42.5	297	2	A41898	positive regulator	511	31	42.5	513	2	JC2304	gluconate kinase (
439	31	42.5	310	2	AD0243	hypothetical prote	512	31	42.5	513	2	D97665	nodT protein homol
440	31	42.5	311	2	B64352	hypothetical prote	513	31	42.5	516	2	F71529	probable exodoxvri
441	31	42.5	314	2	S20572	hypothetical prote	514	31	42.5	518	2	A53207	probable folate tr
442	31	42.5	314	2	AF0540	olfactory receptor	515	31	42.5	528	2	T31505	hypothetical prote
443	31	42.5	315	2	A47269	LysR-family transc	516	31	42.5	532	2	A35149	hypothetical prote
444	31	42.5	317	2	S72851	transcription regu	517	31	42.5	533	2	B86325	T29M8.4 protein -
445	31	42.5	318	2	C69192	stomatin-like prot	518	31	42.5	534	2	T24141	hypothetical prote
446	31	42.5	321	2	T41036	ribose-phosphate p	519	31	42.5	544	2	S65231	tRNA-pseudouridine
447	31	42.5	322	2	C70905	hypothetical prote	520	31	42.5	556	1	A55483	transcription init
448	31	42.5	324	2	A69934	thioredoxin reduct	521	31	42.5	564	2	T40883	WD repeat protein
449	31	42.5	324	2	A43835	regulatory protein	522	31	42.5	567	2	A40899	gag polyprotein -
450	31	42.5	324	2	AF0270	cys regulon transc	523	31	42.5	574	2	B35149	ipah protein - Shi
451	31	42.5	324	2	F84719	probable glyoxalas	524	31	42.5	579	2	C97601	hypothetical prote
452	31	42.5	327	2	T32583	hypothetical prote	525	31	42.5	580	2	F84471	hypothetical prote
453	31	42.5	336	2	A47306	cysteine proteinas	526	31	42.5	588	2	AI3543	60K inner membrane
454	31	42.5	337	2	F65051	asc operon repress	527	31	42.5	595	2	T06111	adenosylhomocyste
455	31	42.5	339	2	AF0300	probable oxidoredu	528	31	42.5	597	2	T08681	hypothetical prote
456	31	42.5	339	2	JC7712	transcription coac	529	31	42.5	603	2	T08955	hypothetical prote
457	31	42.5	341	2	A11429	transcription regu	530	31	42.5	619	2	B71559	probable metallopr
458	31	42.5	341	2	AG1803	transcription regu	531	31	42.5	629	2	AD1838	Na+/H+ antiporter
459	31	42.5	345	2	E69484	conserved hypotnet	532	31	42.5	637	2	AH1160	hypothetical prote
460	31	42.5	347	2	S44846	K06H7.6 protein -	533	31	42.5	667	2	AH1519	hypothetical prote
461	31	42.5	350	2	A82798	hypothetical prote	534	31	42.5	667	2	G90883	probable collagena
462	31	42.5	351	2	D71955	hypothetical prote	535	31	42.5	667	2	H85734	hypothetical prote
463	31	42.5	359	2	B26135	keratin, 52K type	536	31	42.5	667	2	F64895	transcription fact
464	31	42.5	360	2	E69086	cell division prot	537	31	42.5	668	2	A42890	hypothetical prote
465	31	42.5	362	2	S27530	sporulation protei	538	31	42.5	671	2	D38490	maturen-related p
466	31	42.5	364	2	G96666	hypothetical prote	539	31	42.5	675	2	D65083	hypothetical prote
467	31	42.5	369	2	S76784	hypothetical prote	540	31	42.5	731	2	A98109	ornithine decarbox

541	31	42.5	731	2	D85954	ornithine decarbox	614	30	41.1	115	2	S45370	nonspecific lipid
542	31	42.5	737	2	P00219	RNA-2 polypeptin	615	30	41.1	121	2	T48832	hypothetical prote
543	31	42.5	784	2	D8564	myosin-like protei	616	30	41.1	122	2	F82812	hypothetical prote
544	31	42.5	787	2	A83207	conserved hypothet	617	30	41.1	125	2	C83691	hypothetical prote
545	31	42.5	791	2	B90566	conserved hypothet	618	30	41.1	130	2	S17961	BLT4 protein - bar
546	31	42.5	800	2	S29344	protein kinase KIN	619	30	41.1	134	2	D81096	hypothetical prote
547	31	42.5	815	2	I57487	Na+/H+-exchanging	620	30	41.1	138	2	T50998	hypothetical prote
548	31	42.5	816	2	S16328	Na+/H+-exchanging	621	30	41.1	142	2	AC1102	polyribonucleotide
549	31	42.5	818	2	A48858	Na+/H+-exchanging	622	30	41.1	142	2	AC1464	polyribonucleotide
550	31	42.5	820	2	T46412	ubiquitin-protein	623	30	41.1	153	2	G85438	hypothetical prote
551	31	42.5	820	2	A40204	Na+/H+-exchanging	624	30	41.1	155	2	T51842	conserved hypothet
552	31	42.5	822	2	S30198	Na+/H+-exchanging	625	30	41.1	156	2	H82354	conserved hypothet
553	31	42.5	831	2	JX0359	DNA-directed DNA p	626	30	41.1	157	2	A81660	probable membrane
554	31	42.5	832	2	A33530	DNA-directed DNA p	627	30	41.1	159	2	S61040	probable membrane
555	31	42.5	899	2	F88391	protein R06B10.4 [628	30	41.1	168	1	C1F682	gamma-crystallin I
556	31	42.5	927	2	B82075	sensor histidine k	629	30	41.1	169	2	T01783	gamma-2-crystallin
557	31	42.5	943	2	E91286	probable ATP-depen	630	30	41.1	174	2	T01980	dnaj protein homol
558	31	42.5	952	2	A86128	probable ATP-depen	631	30	41.1	174	2	T45335	hypothetical prote
559	31	42.5	980	2	A81844	hypothetical prote	632	30	41.1	175	2	JN0681	gamma-2-crystallin
560	31	42.5	988	2	S37078	chloride channel p	633	30	41.1	176	2	G70599	hypothetical prote
561	31	42.5	1063	2	A33830	cation efflux syst	634	30	41.1	176	2	T42179	hypothetical prote
562	31	42.5	1063	2	JC4700	cadmium, zinc, cob	635	30	41.1	188	2	S75574	transposase sl1080
563	31	42.5	1077	2	D71660	hypothetical prote	636	30	41.1	190	2	C86724	hypothetical prote
564	31	42.5	1092	2	S77546	cobN protein - Syn	637	30	41.1	195	2	S38667	ribonuclease (EC 3
565	31	42.5	1112	2	S46313	phytochrome E - Ar	638	30	41.1	196	2	S06613	chorion protein s1
566	31	42.5	1152	2	T31911	hypothetical prote	639	30	41.1	197	2	F83846	spore maturation p
567	31	42.5	1153	2	A97179	ATP-dependent exon	640	30	41.1	197	2	T24133	hypothetical prote
568	31	42.5	1166	2	T31958	syngAP-b1 protein	641	30	41.1	200	2	A84994	hypothetical prote
569	31	42.5	1171	2	T28701	probable polyketid	642	30	41.1	201	2	AB0759	precorrin-6Y C5,15
570	31	42.5	1177	1	D71416	probable PD85-like	643	30	41.1	205	2	S29308	hypothetical prote
571	31	42.5	1203	2	A39607	DNA-directed RNA p	644	30	41.1	205	2	F83013	probable transcrip
572	31	42.5	1215	2	S50428	probable Cad+-tran	645	30	41.1	206	2	G87251	hypothetical prote
573	31	42.5	1225	2	A49464	chromosome segrega	646	30	41.1	207	2	B27626	hypothetical prote
574	31	42.5	1249	2	T14270	Ras-GTPase activat	647	30	41.1	211	1	JC2368	ribosomal protein
575	31	42.5	1287	2	AF2031	two-component hybr	648	30	41.1	211	2	S23753	glial cell line-de
576	31	42.5	1293	2	T14259	ras GTPase-activat	649	30	41.1	211	2	I49686	glial cell line-de
577	31	42.5	1353	2	JC4279	adenylate cyclase	650	30	41.1	211	2	A37499	hypothetical prote
578	31	42.5	1388	2	T00063	hypothetical prote	651	30	41.1	211	2	H90272	hypothetical prote
579	31	42.5	1408	2	S57049	hypothetical prote	652	30	41.1	215	2	JC1231	beta-crystallin A3
580	31	42.5	1508	2	T27828	hypothetical prote	653	30	41.1	218	2	S35289	competence negativ
581	31	42.5	1519	2	T27829	hypothetical prote	654	30	41.1	225	2	T24226	hypothetical prote
582	31	42.5	1649	2	T39938	hypothetical prote	655	30	41.1	226	2	C82209	hypothetical prote
583	31	42.5	1676	2	E71410	probable centromer	656	30	41.1	230	1	B69876	conserved hypothet
584	31	42.5	1876	2	S50235	1,3-beta-glucan sy	657	30	41.1	230	2	C75552	hypothetical prote
585	31	42.5	1895	2	S50240	1,3-beta-glucan sy	658	30	41.1	232	2	T44456	arginine/ornithine
586	31	42.5	1943	2	B64596	toxin-like outer m	659	30	41.1	232	2	B90318	transporter (proto
587	31	42.5	2039	2	S64540	probable calcium c	660	30	41.1	235	2	A22962	carbonate dehydrat
588	31	42.5	2048	2	C94609	hypothetical prote	661	30	41.1	238	2	T41184	hypothetical prote
589	31	42.5	2562	2	T14266	Xin protein - chic	662	30	41.1	238	2	AD2138	hypothetical prote
590	31	42.5	2588	2	T14342	NSD1 protein - mou	663	30	41.1	243	2	G71507	hypothetical prote
591	31	42.5	4687	1	A39638	plectin - rat	664	30	41.1	253	2	AF0916	uridine phosphoryl
592	30.5	41.8	124	2	A81844	hypothetical prote	665	30	41.1	253	2	T46830	uridine phosphoryl
593	30.5	41.8	159	2	D87585	transcription regu	666	30	41.1	258	2	T08843	14-3-3 protein hom
594	30.5	41.8	251	2	T44757	hypothetical prote	667	30	41.1	258	2	T33409	hypothetical prote
595	30.5	41.8	308	1	Q8EC1H	leucine transport	668	30	41.1	259	2	S57283	14-3-3 brain prote
596	30.5	41.8	308	2	AG0992	high-affinity bran	669	30	41.1	260	1	JH0768	site-specific DNA-
597	30.5	41.8	308	2	H91166	leucine transport	670	30	41.1	260	1	CRH01D	carbonate dehydrat
598	30.5	41.8	308	2	H86012	leucine transport	671	30	41.1	261	2	AB3569	transcription regu
599	30.5	41.8	308	2	JH0668	high-affinity bran	672	30	41.1	266	2	AB0665	conserved hypothet
600	30.5	41.8	308	2	G75137	sun protein (fmu p	673	30	41.1	271	2	AB2898	FHFD protein limpo
601	30.5	41.8	450	2	T00621	hypothetical prote	674	30	41.1	276	2	S39702	transcription anti
602	30.5	41.8	461	2	T00621	probable iron-regu	675	30	41.1	279	2	JC4327	uridine phosphoryl
603	30.5	41.8	714	2	F81962	protamine Y2 - blu	676	30	41.1	280	2	T22357	hypothetical prote
604	30	41.1	34	1	TVTUT2	protamine Y2 - blu	677	30	41.1	281	2	D97673	NAD-dependent form
605	30	41.1	34	1	TVTUT2	protamine Z2 - str	678	30	41.1	283	2	B97167	flagellin family p
606	30	41.1	34	2	JX0204	protamine Z1 - str	679	30	41.1	283	2	C95054	sortase, probable
607	30	41.1	34	2	JX0203	protamine 1 - Japa	680	30	41.1	284	2	E70506	hypothetical prote
608	30	41.1	39	1	S28546	protamine 2 - Japa	681	30	41.1	285	2	A82458	hypothetical prote
609	30	41.1	40	1	S14717	hypothetical prote	682	30	41.1	285	2	A97255	S-adenosylmethioni
610	30	41.1	52	2	G84477	carbon storage reg	683	30	41.1	286	2	G86664	membrane lip
611	30	41.1	65	2	E82308	hypothetical prote	684	30	41.1	287	2	T25064	hypothetical prote
612	30	41.1	90	2	D57418	conserved hypothet	685	30	41.1	289	2	T49154	DNA-binding WRKY-1
613	30	41.1	101	2	AE2636		686	30	41.1	296	2	AC1257	glycyl-tRNA synthet

687	30	41.1	296	2	AG1619	glycyl-tRNA synthetase	760	30	41.1	401	2	G96972	hypothetical protein
688	30	41.1	296	2	T27300	hypothetical protein	761	30	41.1	401	2	AG1238	hypothetical protein
689	30	41.1	300	2	T00274	hypothetical protein	762	30	41.1	403	1	WMLJ92	bel-2 protein - si
690	30	41.1	303	2	G85062	hypothetical protein	763	30	41.1	411	2	D87014	conserved hypothetical protein
691	30	41.1	311	1	RGECK	regulatory protein	764	30	41.1	412	2	B85433	salt-inducible like
692	30	41.1	311	2	C85936	positive regulator	765	30	41.1	418	2	C84565	hypothetical protein
693	30	41.1	311	2	H91090	positive regulator	766	30	41.1	419	2	T23666	hypothetical protein
694	30	41.1	311	2	T40886	hypothetical protein	767	30	41.1	421	2	B69467	hypothetical protein
695	30	41.1	312	2	C71806	hypothetical protein	768	30	41.1	422	2	S18741	bel-2 protein - si
696	30	41.1	312	2	G64712	toxR-activated gene	769	30	41.1	428	2	F85485	flavoprotein, elec
697	30	41.1	313	2	S59448	hypothetical protein	770	30	41.1	428	2	F90634	flavoprotein [impo
698	30	41.1	313	2	F86295	T24D18.18 protein	771	30	41.1	428	2	C64725	fixC protein - Esc
699	30	41.1	314	2	C70579	probable cell divi	772	30	41.1	428	2	T52620	membrane-associate
700	30	41.1	315	2	A99192	nirV precursor (AF	773	30	41.1	433	2	AD0161	serine transporter
701	30	41.1	315	2	A13094	nitrite reductase,	774	30	41.1	433	2	G70345	hypothetical protein
702	30	41.1	316	1	S72959	probable integrase	775	30	41.1	434	2	D86530	N utilization prot
703	30	41.1	316	2	G87079	integrase/recombin	776	30	41.1	434	2	E72093	N utilization subs
704	30	41.1	317	2	T36926	dihydrodipicolinat	777	30	41.1	442	2	H81709	N utilization subs
705	30	41.1	317	2	AD3153	deoxyribose-phosph	778	30	41.1	442	2	AD2113	thiamin-phosphate
706	30	41.1	320	2	B86544	NADH (ubiquinone)	779	30	41.1	442	2	S46117	hypothetical protein
707	30	41.1	320	2	F72078	probable sodium-tr	780	30	41.1	450	2	T23265	hypothetical protein
708	30	41.1	322	2	T21478	hypothetical protein	781	30	41.1	451	2	F88042	protein F56D12.1
709	30	41.1	324	2	F86788	transcription regu	782	30	41.1	453	2	S52206	meas protein - Leu
710	30	41.1	324	2	S50958	hypothetical protein	783	30	41.1	457	2	B83449	conserved hypothetical
711	30	41.1	325	2	S18575	svrM protein - Rhi	784	30	41.1	465	2	I52418	cytochrome P450 -
712	30	41.1	326	2	A44505	svrM protein - Rhi	785	30	41.1	468	2	G87513	beta-glucosidase
713	30	41.1	326	2	F95319	SyrM transcription	786	30	41.1	468	2	F86526	Mg++ transporter
714	30	41.1	327	2	T15534	hypothetical protein	787	30	41.1	470	2	H72097	Mg++ transporter
715	30	41.1	327	2	T38261	hypothetical protein	788	30	41.1	470	2	H22830	hypothetical protein
716	30	41.1	328	2	T39111	chromatin-associat	789	30	41.1	473	2	T22830	serine C-palmitoyl
717	30	41.1	329	2	T47419	hypothetical protein	790	30	41.1	475	2	F85430	probable multidrug
718	30	41.1	333	2	AH0272	conserved hypotet	791	30	41.1	477	2	D82179	hypothetical protein
719	30	41.1	334	2	B89812	hypothetical protein	792	30	41.1	478	2	H90445	hypothetical protein
720	30	41.1	335	2	T22565	hypothetical protein	793	30	41.1	485	2	D91182	probable outer mem
721	30	41.1	336	2	D69074	polyferredoxin 4x2	794	30	41.1	485	2	H86028	probable fimbrial
722	30	41.1	337	2	S29814	glyceraldehyde-3-p	795	30	41.1	487	2	J44248	bsc protein - simi
723	30	41.1	341	2	AB3002	conserved hypotet	796	30	41.1	488	2	JC2241	prostaglandin E re
724	30	41.1	341	2	F98281	hypothetical protein	797	30	41.1	491	2	T25662	interferon-induced
725	30	41.1	343	2	T09239	o-methyltransferas	798	30	41.1	495	1	HHC8BA	chaperonin groEL -
726	30	41.1	345	2	G98134	CGI-26 protein [im	799	30	41.1	495	2	T52168	cytochrome P450 mo
727	30	41.1	345	2	S09858	hypothetical protein	800	30	41.1	497	2	T16900	hypothetical protein
728	30	41.1	345	2	A24587	membrane antigen t	801	30	41.1	499	2	S52422	chitinase (EC 3.2.
729	30	41.1	346	2	D83340	hypothetical protein	802	30	41.1	499	2	S04856	chitinase (EC 3.2.
730	30	41.1	348	2	B64552	conserved hypotet	803	30	41.1	501	2	T31754	hypothetical protein
731	30	41.1	348	2	A83250	O-antigen chain le	804	30	41.1	504	2	I56542	calmodulin-binding
732	30	41.1	349	2	S57453	polyferredoxin 4x2	805	30	41.1	510	2	E71695	hypothetical protein
733	30	41.1	352	2	H86454	CDS protein F9L11.	806	30	41.1	512	2	T00869	probable cytochrom
734	30	41.1	352	2	T09707	isoflavone-O-methy	807	30	41.1	513	2	A46638	conserved hypotet
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736	30	41.1	352	2	T23684	hypothetical protein	809	30	41.1	531	2	B69471	neurofilament trip
737	30	41.1	353	2	H70636	probable ribA prot	810	30	41.1	532	1	OPPGM	protein F3F19.5 [i
738	30	41.1	353	2	A20293	hypothetical protein	811	30	41.1	547	2	C86264	probable triacylg1
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741	30	41.1	363	2	S18765	Sd protein - fruit	814	30	41.1	555	2	S63137	enterobactin synth
742	30	41.1	367	2	E90547	hypothetical protein	815	30	41.1	556	2	B82182	hypothetical protein
743	30	41.1	372	2	H97277	glycoyltransferas	816	30	41.1	575	2	T24681	arginine-tRNA liga
744	30	41.1	372	2	S95974	hypothetical protein	817	30	41.1	585	2	AC3388	hypothetical protein
745	30	41.1	374	2	T00561	nodulin-like prote	818	30	41.1	585	2	T24362	hypothetical protein
746	30	41.1	375	1	H69688	response regulator	819	30	41.1	588	2	B95406	probable oxidoredu
747	30	41.1	378	2	S76183	hypothetical protein	820	30	41.1	588	2	T07616	probable beta-fruc
748	30	41.1	379	2	C75294	zinc metallohydrol	821	30	41.1	592	2	T07616	hypothetical protein
749	30	41.1	380	2	T11299	ubiquinol-cytochro	822	30	41.1	608	2	S09790	abc1 protein homol
750	30	41.1	380	2	B41545	pregnancy-specific	823	30	41.1	610	2	S71110	oligodeoxyribosidase
751	30	41.1	383	2	AG3304	pleiotropic regula	824	30	41.1	611	1	S62811	hypothetical protein
752	30	41.1	386	2	A72313	hypothetical protein	825	30	41.1	611	2	T04510	nifS-like protein
753	30	41.1	387	2	C82336	conserved hypotet	826	30	41.1	611	2	T44909	hypothetical protein
754	30	41.1	391	2	G82320	probable oxygen-in	827	30	41.1	619	2	AC0816	hypothetical protein
755	30	41.1	393	2	A81146	histidyl-tRNA synt	828	30	41.1	620	2	T16657	hypothetical protein
756	30	41.1	394	2	AG0883	D-mannosate hydrol	829	30	41.1	638	2	H83905	neurofilament prot
757	30	41.1	395	2	T09895	hypothetical protein	830	30	41.1	644	2	S55395	neurofilament prot
758	30	41.1	396	2	T18854	hypothetical protein	831	30	41.1	644	2	A72164	A4L protein - vari
759	30	41.1	398	2	A96764	cell division prot	832	30	41.1	644	2	D36848	major core protein

833	30	41.1	644	2	T28545	hypothetical prote	906	30	41.1	1084	2	S23319	hypothetical prote
834	30	41.1	651	2	T95045	transcription regu	907	30	41.1	1085	2	C56797	unknown protein [i
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837	30	41.1	656	2	H69379	chemotaxis histidi	910	30	41.1	1116	2	S41915	DNA-directed RNA p
838	30	41.1	657	1	A64079	2',3'-cyclic-nucle	911	30	41.1	1155	2	G87477	transcription-repa
839	30	41.1	657	2	D71351	probable primosoma	912	30	41.1	1193	2	D82856	transcription-repa
840	30	41.1	658	2	A86828	transketolase (EC	913	30	41.1	1203	2	I55466	N-methyl-D-asparta
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844	30	41.1	667	2	T23010	hypothetical prote	917	30	41.1	1225	2	T09057	probable protein-h
845	30	41.1	668	2	T34317	protein-tyrosine-p	918	30	41.1	1245	2	T42920	hypothetical prote
846	30	41.1	672	2	E70717	hypothetical prote	919	30	41.1	1253	2	F86436	hypothetical prote
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849	30	41.1	692	2	E48376	flagellar biosynth	922	30	41.1	1293	2	S42402	xeroderma pigmento
850	30	41.1	695	2	T40717	orf5 3' to phbc -	923	30	41.1	1327	2	T41647	probable pre-mrna
851	30	41.1	712	2	T12452	hypothetical prote	924	30	41.1	1511	2	S60932	probable membrane
852	30	41.1	719	2	S63392	hypothetical prote	925	30	41.1	1582	2	E70876	probable polyketid
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855	30	41.1	747	1	VPXR4S	hypothetical prote	928	30	41.1	1787	2	F84528	probable retroelem
856	30	41.1	765	2	H84247	outer layer protei	929	30	41.1	2004	2	AC0314	probable membrane
857	30	41.1	775	1	VPXRT2	adaptive-response	930	30	41.1	2115	2	S38480	nonstructural prot
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859	30	41.1	776	1	VPXRB3	outer layer protei	932	30	41.1	2185	1	MMVNRN	nonstructural poly
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862	30	41.1	776	2	S24410	TonB-dependent rec	935	30	41.1	2523	2	T18477	hypothetical prote
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864	30	41.1	779	2	A1094	serine/threonine k	937	30	41.1	3951	1	VP1HB1	F1 protein - avian
865	30	41.1	794	2	T52441	ATP dependent heli	938	30	41.1	4447	2	A96679	polyketide synthas
866	30	41.1	795	2	T07709	hypothetical prote	939	29.5	40.4	4563	1	LNPHUB	apolipoprotein B-1
867	30	41.1	798	2	S40052	hypothetical prote	940	29.5	40.4	99	1	DNBP11	DNA-binding protei
868	30	41.1	800	2	D86712	glycogen phosphory	941	29.5	40.4	167	2	B81951	hypothetical prote
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870	30	41.1	812	2	A81621	conserved hypothet	943	29.5	40.4	186	2	D81154	hypothetical prote
871	30	41.1	817	2	T49642	hypothetical prote	944	29.5	40.4	190	2	D81183	Noak-related prote
872	30	41.1	819	2	T29486	hypothetical prote	945	29.5	40.4	266	2	G84757	hypothetical prote
873	30	41.1	831	2	F72044	ct620 hypothetical	946	29.5	40.4	385	2	A83466	probable RND efflu
874	30	41.1	831	2	C86581	CT620 hypothetical	947	29.5	40.4	713	2	A56268	Fe-regulated prote
875	30	41.1	833	2	H81700	DNA gyrase, chain	948	29.5	40.4	771	2	T21633	hypothetical prote
876	30	41.1	837	2	T00618	hypothetical prote	949	29.5	40.4	1473	2	A20872	ovostatin precursor
877	30	41.1	843	1	JDV1J1	DNA-directed DNA p	950	29	39.7	15	2	G35141	T-cell receptor de
878	30	41.1	843	2	T16906	hypothetical prote	951	29	39.7	57	2	S74994	ribosomal protein
879	30	41.1	845	2	A45669	neurofilament trip	952	29	39.7	57	2	S61291	tyrosyl-tRNA synth
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884	30	41.1	891	2	A46203	mating type A-alpha	957	29	39.7	106	2	S43069	hypothetical prote
885	30	41.1	897	2	G89923	hypothetical prote	958	29	39.7	109	2	S77925	exoskeletal protei
886	30	41.1	898	2	A69092	alanine-tRNA ligas	959	29	39.7	110	2	B64889	ydbL protein precu
887	30	41.1	902	1	S87199	nitrate reductase	960	29	39.7	112	2	T48738	hypothetical prote
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889	30	41.1	924	1	S13913	hexokinase (EC 2.7	962	29	39.7	116	2	T01231	hypothetical prote
890	30	41.1	941	2	F71332	probable chromosom	963	29	39.7	116	2	A83693	transcription regu
891	30	41.1	943	2	E84429	probable receptor-	964	29	39.7	118	2	G70306	ribosomal protein
892	30	41.1	944	2	S26710	spindle pole body	965	29	39.7	119	2	H64341	hypothetical prote
893	30	41.1	969	2	A70912	probable leus prot	966	29	39.7	130	1	WMWG2	14K protein - narc
894	30	41.1	971	2	E36794	hypothetical prote	967	29	39.7	132	2	S40257	hypothetical prote
895	30	41.1	980	2	S71090	peroxisome biogene	968	29	39.7	139	2	S36325	T-cell receptor de
896	30	41.1	984	2	A55137	hyaluronate lyase	969	29	39.7	144	2	E82039	conserved hypothet
897	30	41.1	988	2	T51054	related to alpha-a	970	29	39.7	148	2	T46334	hypothetical prote
898	30	41.1	1028	2	G30022	probable two-compo	971	29	39.7	148	2	T31141	transcription regu
899	30	41.1	1036	2	T16475	hypothetical prote	972	29	39.7	150	2	S36544	E6 protein - human
900	30	41.1	1037	2	G83329	probable RND efflu	973	29	39.7	157	2	H71502	probable (Arpase o
901	30	41.1	1052	2	T00067	ABC transporter-li	974	29	39.7	159	2	Ar1111	B. subtilis fydA p
902	30	41.1	1054	2	T00067	hypothetical prote	975	29	39.7	162	2	D82983	leucine-responsive
903	30	41.1	1054	2	B75384	transcription-repa	976	29	39.7	162	2	T32261	hypothetical prote
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905	30	41.1	1083	1	WZBE6	gene 6 protein - h	978	29	39.7	165	2	S60655	dihydrofolate redu
										178	2	B72556	hypothetical prote

conserved hypothet
gamma-crystallin M
hypothetical prote
hypothetical prote
50S ribosomal prec
somatotropin precu
probable membrane
hypothetical prote
hypothetical prote
hypothetical prote
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conserved hypothet
hypothetical prote
probable V-type AT
oxygen-insensitive
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breast basic conse
ABC transporter in
ABC-type transport

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RESULT 1
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N:Contains: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1993 #sequence revision 20-Feb-1993 #text change 09-Jul-2004
C:Accession: A35474; A33476; S03339; I51841; A60299; A32300; A32396; A34561; I57488; JCI
R:Shyy, Y.J.; Li, Y.S.; Kolattukudy, P.E.
Biochem. Biophys. Res. Commun. 169, 346-351, 1990
A:Title: Structure of human monocyte chemotactic protein gene and its regulation by TPA.
A:Reference number: A35474; MUID:90290466; PMID:2357211
A:Accession: A35474
A:Molecule type: DNA
A:Residues: 1-99 <SHY>
A:Cross-references: UNIPROT:P13500; UNIPARC:UPI0000000DC9; GB:M37719; NID:g187447; PIDN:
R:Rollins, B.J.; Stier, P.; Ernst, T.; Wong, G.G.
Mol. Cell. Biol. 9, 4687-4695, 1989
A:Title: The human homolog of the JE gene encodes a monocyte secretory protein.
A:Reference number: A33476; MUID:90097880; PMID:2513477
A:Accession: A33476
A:Molecule type: mRNA
A:Residues: 1-99 <ROL>
A:Cross-references: UNIPARC:UPI0000000DC9; GB:M30816; GB:M31625; GB:M31626; NID:g188701;
R:Yoshimura, T.; Yuhki, N.; Moore, S.K.; Appella, E.; Lerman, M.I.; Leonard, E.J.
FEBS Lett. 244, 487-493, 1989
A:Title: Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, exp
A:Reference number: S03339; MUID:89153605; PMID:2465924
A:Accession: S03339
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-99 <VOS>
A:Cross-references: UNIPARC:UPI0000000DC9; GB:X14768; NID:g34513; PIDN:CAA32876.1; PID:9
A:Experimental source: glioma cell line U-105MG
R:Yoshimura, T.; Leonard, E.J.
Adv. Exp. Med. Biol. 305, 47-56, 1991
A:Title: Human monocyte chemoattractant protein-1 (MCP-1).
A:Reference number: I51841; MUID:92095166; PMID:1661560
A:Accession: I51841
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-99 <YO2>
A:Cross-references: UNIPARC:UPI0000000DC9; GB:S71513; NID:g240867; PIDN:AAB20651.1; PID:
R:Botazzi, B.; Colotta, F.; Sica, A.; Nobili, N.; Mantovani, A.
Int. J. Cancer 45, 795-797, 1990

A:Title: A chemoattractant expressed in human sarcoma cells (tumor-derived chemotactic f
-1/MCAF).
A:Reference number: A60299; MUID:90216082; PMID:2182547
A:Accession: A60299
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-99 <BOT>
A:Cross-references: UNIPARC:UPI0000000DC9
R:Furutani, Y.; Nomura, H.; Notake, M.; Oyama, Y.; Fukui, T.; Yamada, M.; Larsen, C.G.
Biochem. Biophys. Res. Commun. 159, 249-255, 1989
A:Title: Cloning and sequencing of the cDNA for human monocyte chemotactic and activatin
A:Reference number: A32300; MUID:89165862; PMID:2923622
A:Accession: A32300
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-99 <FUD>
A:Cross-references: UNIPARC:UPI0000000DC9; GB:M24545; NID:g187434; PIDN:AAAL8164.1; PID:
R:Robinson, E.A.; Yoshimura, T.; Leonard, E.J.; Tanaka, S.; Griffin, P.R.; Shabanowitz,
Proc. Natl. Acad. Sci. U.S.A. 86, 1850-1854, 1989
A:Title: Complete amino acid sequence of a human monocyte chemoattractant, a putative me
A:Reference number: A32396; MUID:89184525; PMID:2648385
A:Accession: A32396
A:Molecule type: protein
A:Residues: 'X', 25-99 <ROB>
A:Cross-references: UNIPARC:UPI00001429D5
R:Decock, B.; Conings, R.; Lenaerte, J.P.; Billiau, A.; Van Damme, J.
Biochem. Biophys. Res. Commun. 167, 904-909, 1990
A:Title: Identification of the monocyte chemotactic protein from human osteosarcoma cell
A:Reference number: A34561; MUID:90211336; PMID:2322286
A:Accession: A34561
A:Molecule type: protein
A:Residues: 29-33 'XX', 36-52; 82-92 <DBC>
A:Cross-references: UNIPARC:UPI000017674D; UNIPARC:UPI000017674E
R:Li, Y.S.; Shyy, Y.J.; Wright, J.G.; Valente, A.J.; Cornhill, J.F.; Kolattukudy, P.E.
Mol. Cell. Biochem. 126, 61-68, 1993
A:Title: The expression of monocyte chemotactic protein (MCP-1) in human vascular endoth
A:Reference number: I57488; MUID:94150478; PMID:8107690
A:Accession: I57488
A:Status: translated from GB/EMBL/DBJ
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A:Cross-references: UNIPARC:UPI0000000DC9; GB:S69738; NID:G545464; PIDN:AAB29926.1; PID:
R:Ye, Q.N.; Su, G.F.; Yuan, Y.; Huang, C.F.
Chinese J. Microbiol. Immunol. 14, 29-32, 1994
A:Title: The PCR, cloning and sequencing of human monocyte chemoattractant protein-1 (MC
A:Reference number: JCI096
A:Accession: JCI096
A:Molecule type: mRNA
A:Residues: 24-28, 'Q', 30-99 <YEQ>
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A:Gene: GDB:SCVA2
A:Cross-references: GDB:125279; OMIM:158105
A:Map position: 17q11.2-17q12
C:Superfamily: macrophage inflammatory protein
C:Keywords: cytokine; glycoprotein; inflammation; pyroglutamic acid
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F:29-99/Product: monocyte chemoattractant protein 1, short form #status experimental <MA
F:24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F:37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. NO. 2.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ISVQRLASYYRITSSK 16
| | | | | | | | | | | | | | | | | |
Db 43 ISVQRLASYYRITSSK 58

RESULT 2
A55984

monocyte chemotactic protein bo-MCP-lb - bovine (fragments)
C/Species: Bos primigenius taurus (cattle)
C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-May-1997
C/Accession: A55984
R/Proost, P.; Wuyts, A.; Lenaerts, J.P.; Van Damme, J.
Biochemistry 33, 13406-13412, 1994
A/Title: Purification, sequence analysis, and biological characterization of a second bovine monocyte chemotactic protein
A/Reference number: A55984; MUID:95034774; PMID:7947749
A/Accession: A55984
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-72 <PRO>
A/Cross-references: UNIPARC:UPI000017674C
C/Superfamily: macrophage inflammatory protein

Query Match 87.7%; Score 64; DB 2; Length 72;
Best Local Similarity 81.2%; Pred. No. 8.1e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
||| ||| ||| ||| |||
Db 18 ISMQRLMSYRRTSSK 33

RESULT 3
JC2136
monocyte chemoattractant protein-1 precursor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C/Accession: JC2136; S57498
R/Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 199, 962-968, 1994
A/Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Analysis of its expression in the luteal phase of the menstrual cycle
A/Reference number: JC2136; MUID:94183284; PMID:7510962
A/Accession: JC2136
A/Molecule type: mRNA
A/Residues: 1-99 <HOS>
A/Cross-references: UNIPROT:P42831; UNIPARC:UPI00001362C7; GB:Z48479; NID:G683716; PIDN:R74ach, O.
A/Reference number: S57497
submitted to the EMBL Data Library, July 1994
A/Accession: S57498
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-99 <ZAC>
A/Cross-references: UNIPARC:UPI00001362C7; EMBL:X79416; NID:g872312; PIDN:CAA55945.1; PF:24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>
P/94/Binding site: carbohydrate (Asn) #status predicted

Query Match 87.7%; Score 64; DB 2; Length 99;
Best Local Similarity 81.2%; Pred. No. 0.00011;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
||| ||| ||| ||| |||
Db 43 ISMQRLMSYRRTSSK 58

RESULT 4
A39296
monocyte chemoattractant protein 1 precursor - bovine
N/Alternate names: monocyte chemoattractant factor 1; seminal plasma protein P6
C/Species: Bos primigenius taurus (cattle)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A39296; B39296
R/Wempe, F.; Henschen, A.; Scheit, K.H.
DNA Cell Biol. 10, 671-679, 1991
A/Title: Gene expression and cDNA cloning identified a major basic protein constituent of human neutrophils
A/Reference number: A39296; MUID:92096117; PMID:1721821
A/Accession: A39296

Query Match 76.7%; Score 56; DB 2; Length 97;
Best Local Similarity 75.0%; Pred. No. 0.0035;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
| : ||| ||||| |
Db 41 IPLQRLSYRITSSK 56

RESULT 7
I46857
monocyte chemoattractant protein-1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46857
R:Yoshimura, T.; Iuhki, N.
J. Immunol. 146, 3483-3488, 1991
A:Title: Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein
A:Reference number: I46857; MUID:91225489; PMID:2026877
A:Accession: I46857
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-125 <YOS>
A:Cross-references: UNIPROT:P28292; UNIPARC:UPI00001362C8; GB:M57440; NID:g165469; PIDN:
C:Superfamily: macrophage inflammatory protein

Query Match 76.7%; Score 56; DB 2; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.0046;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
| : ||| ||||| |
Db 43 ISVRLMSYRINSTK 58

RESULT 8
JC2478
eotaxin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 16-Jul-1999
C:Accession: JC2478
R:Jose, P.J.; Adcock, I.M.; Griffiths-Johnson, D.A.; Berkman, N.; Wells, T.N.C.; Williams
Biochem. Biophys. Res. Commun. 205, 788-794, 1994
A:Title: Eotaxin: Cloning of an eosinophil chemoattractant cytokine and increased mRNA e
A:Reference number: JC2478; MUID:95091818; PMID:7999113
A:Accession: JC2478
A:Molecule type: mRNA
A:Residues: 1-96 <JOS>
A:Cross-references: UNIPARC:UPI000017074E; EMBL:X77603; NID:g602551; PIDN:CAA54698.1; PI
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-96/Product: eotaxin #status predicted <MAT>
F:93/Binding site: carbohydrate (Thr) (covalent) #status predicted

Query Match 71.2%; Score 52; DB 2; Length 96;
Best Local Similarity 75.0%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
| : ||| ||||| |
Db 40 ISFQRLSKYKITSSK 55

RESULT 9
I48099
eotaxin precursor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48099
R:Rothenberg, M.E.; Luster, A.D.; Lilly, C.M.; Drazen, J.M.; Leder, P.
J. Exp. Med. 181, 1211-1216, 1995

Query Match 71.2%; Score 52; DB 2; Length 96;
Best Local Similarity 75.0%; Pred. No. 0.019;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
| : ||| ||||| |
Db 40 ISFQRLSKYKITSSK 55

RESULT 10
A30209
PDGP-inducible JE glycoprotein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A30209; A44771; A30861
R:Rollins, B.J.; Morrison, E.D.; Stiles, C.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988
A:Title: Cloning and expression of JE, a gene inducible by platelet-derived growth facto
A:Reference number: A30209; MUID:88234501; PMID:3287374
A:Accession: A30209
A:Molecule type: DNA
A:Residues: 1-148 <ROL>
A:Cross-references: UNIPROT:P10148; UNIPARC:UPI0000020A69; GB:M19681; NID:g193486; PIDN:
R:Kawahara, R.S.; Deuel, T.P.
J. Biol. Chem. 264, 679-682, 1989
A:Title: Platelet-derived growth factor-inducible gene JE is a member of a family of sma
A:Reference number: A44771; MUID:89093129; PMID:2910858
A:Accession: A44771
A:Molecule type: DNA; mRNA
A:Residues: 1-148 <KA2>
A:Cross-references: UNIPARC:UPI0000020A69; GB:J04467; NID:g193488; PIDN:AAA37685.1; PID:
C:Genetics: JE
A:Gene: JE
A:Introns: 26/1; 65/2
C:Superfamily: macrophage inflammatory protein
C:Keywords: cytokine; glycoprotein
F:116/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.1%; Score 49; DB 1; Length 148;
Best Local Similarity 62.5%; Pred. No. 0.11;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
| : ||| ||||| |
Db 43 IPMSRLSYKRITSSR 58

RESULT 11
A54678
monocyte chemotactic protein 3 precursor - human
N:Alternate names: monocyte chemoattractant protein MCP-3
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C:Accession: A54678; JC1478; S32222
R:Opdenakker, G.; Fiten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys, G.
Genomics 21, 403-408, 1994
A:Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the
A:Reference number: A54678; MUID:94375065; PMID:7916328
A:Accession: A54678
A:Molecule type: DNA
A:Residues: 1-109 <OPD>
A:Cross-references: UNIPARC:UPI00000006BD; GB:X72309
R:Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.
Biochem. Biophys. Res. Commun. 191, 535-542, 1993

A;Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA and
A;Reference number: JCL478; MUID:93213290; PMID:8461011
A;Accession: JCL478
A;Molecule type: mRNA
A;Residues: 1-109 <OP>
A;Cross-references: UNIPARC:UPI00000006BD; GB:X72308; GB:S57464; NID:g3928270; PIDN:CAAS
R;Minty, A.; Chalou, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Miloux,
submitted to the EMBL Data Library, March 1993
A;Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoattract
A;Reference number: S32222
A;Accession: S32222
A;Molecule type: mRNA
A;Residues: 1-109 <MIN>
A;Cross-references: UNIPARC:UPI00000006BD; EMBL:X71087; NID:g288396; PIDN:CAAS0405.1; PI
A;Comment: This protein induces proteinase secretion and chemotaxis by macrophages and m
C;Genetics:
A;Gene: GDB:SCYA7; SCYA6; MCP-3
A;Cross-references: GDB:I38473; OMIM:158106
A;Map position: 17q11-17q12
A;Introns: 36/1, 75/2
C;Superfamily: macrophage inflammatory protein
C;Keywords: cytokine; glycoprotein; inflammation
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-109/Product: monocyte chemotactic protein 3 #status predicted <MAT>
F;39/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.4%; Score 47; DB 2; Length 109;
Best Local Similarity 73.3%; Pred. No. 0.19;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRITSS 15
| ||| ||| ||| |||
Db 53 IPKQRLASYRITSS 67

RESULT 12
S07723
Immediate-early serum-responsive protein JE precursor - rat
N;Alternate names: monocyte chemoattractant protein-1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
A;Accession: S07723; JN0128
R;Timmers, H.T.M.; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
Nucleic Acids Res. 18, 23-34, 1990
A;Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential
A;Reference number: S07723; MUID:90174947; PMID:2106664
A;Accession: S07723
A;Molecule type: DNA
A;Residues: 1-148 <TIM>
A;Cross-references: UNIPROT:P14844; UNIPARC:UPI0000000187; EMBL:X17053; NID:g55530; PIDN
R;Yoshimura, T.; Takeya, M.; Takahashi, K.
Biochem. Biophys. Res. Commun. 174, 504-509, 1991
A;Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its exp
A;Reference number: JN0128; MUID:91128376; PMID:1704226
A;Accession: JN0128
A;Molecule type: mRNA
A;Residues: 1-148 <YOS>
A;Cross-references: UNIPARC:UPI0000000187; GB:IM57441; NID:g205333; PIDN:AAA63496.1; PID:
A;Experimental source: spleen cells
A;Note: the authors translated the codon GAA for residue 62 as Lys and GCT for residue 6
C;Genetics:
A;Introns: 26/1; 65/2
C;Superfamily: macrophage inflammatory protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-148/Product: immediate-early serum-responsive protein JE #status predicted <MAT>

Query Match 63.0%; Score 46; DB 1; Length 148;
Best Local Similarity 56.2%; Pred. No. 0.41;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRITSSK 16
| : || : ||| : ||| :
Db 43 IPKQRLASYRITSSR 58

RESULT 13
A48093
monocytic cytokine FIC - mouse
N;Alternate names: interleukin/chemokine; MARC/FIC protein; monocyte chemotactic protein-
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A;Accession: A48093; JC2452; S30592; I49630
R;Heinrich, J.N.; Ryseck, R.P.; Macdonald-Bravo, H.; Bravo, R.
Mol. Cell. Biol. 13, 2020-2030, 1993
A;Title: The product of a novel growth factor-activated gene, fic, is a biologically act
A;Reference number: A48093; MUID:93204948; PMID:8455595
A;Accession: A48093
A;Molecule type: mRNA
A;Residues: 1-97 <HEI>
A;Cross-references: UNIPROT:Q03366; UNIPARC:UPI000016CCBC; GB:I04694; NID:g192925; PIDN
A;Experimental source: NIH 3T3 cells
R;Thirion, S.; Nys, G.; Fiten, P.; Maure, S.; Damme, J.V.; Opdenakker, G.
Biochem. Biophys. Res. Commun. 201, 493-499, 1994
A;Title: Mouse macrophage derived monocyte chemotactic protein-3: cDNA cloning and ident
A;Reference number: JC2452; MUID:94271193; PMID:8003978
A;Accession: JC2452
A;Molecule type: mRNA
A;Residues: 1-73, 'A', '75-97 <THI>
A;Cross-references: UNIPARC:UPI000000028E; GB:S71251; NID:g547088; PIDN:AAB30997.1; PID:
A;Experimental source: LPS-stimulated WEHI-3 cells
R;Kulmburg, P.A.; Huber, N.E.; Scheer, B.J.; Wrann, M.; Baumruker, T.
J. Exp. Med. 176, 1773-1778, 1992
A;Title: Immunoglobulin E plus antigen challenge induces a novel intercrine/chemokine in
A;Reference number: S30592; MUID:93094785; PMID:1281219
A;Accession: S30592
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-73, 'A', '75-97 <KUL>
A;Cross-references: UNIPARC:UPI000000028E; EMBL:Z12297; NID:g57937; PIDN:CAA78169.1; PID
C;Genetics:
A;Gene: fic
C;Superfamily: macrophage inflammatory protein
C;Keywords: glycoprotein
F;29/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 61.6%; Score 45; DB 2; Length 97;
Best Local Similarity 62.5%; Pred. No. 0.4;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRITSSK 16
| : ||| : ||| : ||| :
Db 41 IPKRLASYRITSSR 56

RESULT 14
JC5295
monocyte chemotactic protein-2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
A;Accession: JC5295
R;Van Coillie, E.; Froyen, G.; Nomiya, H.; Miura, R.; Fiten, P.; Van Aelst, I.; Van Da
Biochem. Biophys. Res. Commun. 231, 726-730, 1997
A;Title: Human monocyte chemotactic protein-2: cDNA cloning and regulated expression of
A;Reference number: JC5295; MUID:97224420; PMID:9070881
A;Accession: JC5295
A;Molecule type: mRNA
A;Residues: 1-99 <VAN>
A;Cross-references: UNIPROT:P80075; UNIPARC:UPI0000030FC6; GB:Y10802; NID:g1924937; PIDN
A;Experimental source: bone marrow
C;Comment: This protein belongs to the beta-chemokine family which is one of the major H
tis and in tumor biology, and contribute to the trafficking and recruitment of the respon
C;Genetics:
A;Gene: mcp-2
C;Superfamily: macrophage inflammatory protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemotactic protein-2 #status predicted <MAT>

Query Match 60.3%; Score 44; DB 2; Length 99;
Best Local Similarity 64.3%; Pred. No. 0.63; Mismatches 2; Gaps 0;
Matches 9; Conservative 2; Indels 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSS 14
| : | | | | | | | | | |
Db 43 IPIQRLESYTRITN 56

RESULT 15
S62188
hypothetical protein 1 - Azotobacter vinelandii (fragment)
C:Species: Azotobacter vinelandii
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S62188
R;Colnaghi, R.; Pagani, S.; Kennedy, C.; Drummond, M.
Eur. J. Biochem. 236, 240-248, 1996
A:Title: Cloning, sequence analysis and overexpression of the rhodanese gene of Azotobacter vinelandii
A:Reference number: S62187; MUID:96184504; PMID:8617271
A:Accession: S62188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-60 <COL>
A:Cross-references: UNIPROT:Q44557; UNIPARC:UPI000013BFD9; EMBL:L42346; NID:g1069990; PMID:8617271

Query Match 57.5%; Score 42; DB 2; Length 60;
Best Local Similarity 60.0%; Pred. No. 0.89; Mismatches 2; Gaps 0;
Matches 9; Conservative 2; Indels 4; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSS 15
| : | | | | | | | | | |
Db 40 IQPQMASYRHILAS 54

RESULT 16
I48147
monocyte chemoattractant protein-1 - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48147
R;Yoshimura, T.
J. Immunol. 150, 5025-5032, 1993
A:Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression of the complementary DNA
A:Reference number: I48147; MUID:93267104; PMID:8496603
A:Accession: I48147
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-120 <RES>
A:Cross-references: UNIPROT:Q08782; UNIPARC:UPI00001362C6; GB:L04985; NID:g349820; PIDN:G349820

C:Genetics:
A:Gene: MCP-1
C:Superfamily: macrophage inflammatory protein

Query Match 56.2%; Score 41; DB 2; Length 120;
Best Local Similarity 50.0%; Pred. No. 2.8; Mismatches 4; Indels 4; Indels 0; Gaps 0;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| : | | | | | | | | | |
Db 41 IPLKRVKGYERITSSR 56

RESULT 17
F83026
conserved hypothetical protein PA4952 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: F83026
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Blevins, L.E.; Brode, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: F83026
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-339 <STO>
A:Cross-references: UNIPROT:Q9HUL3; UNIPARC:UPI000000C5B8F; GB:AE004908; GB:AE004091; NID:G82950
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4952
C:Superfamily: conserved hypothetical protein H11714

Query Match 56.2%; Score 41; DB 2; Length 339;
Best Local Similarity 60.0%; Pred. No. 8.3; Mismatches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSS 15
| : | | | | | | | | | |
Db 319 IMPQMASYRHILAS 333

RESULT 18
S76549
transcription-repair coupling protein - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S76549
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis sp. strain PCC 6803
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76549
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1199 <KAN>
A:Cross-references: UNIPROT:Q55750; UNIPARC:UPI000012F03E; EMBL:D64002; GB:AB001339; NID:G55750
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: transcription-repair coupling protein
C:Keywords: ATP; DNA repair; leucine zipper; nucleotide binding; P-loop; transcription
F;673-680/Region: nucleotide-binding motif A (P-loop)
F;771-776/Region: nucleotide-binding motif B
F;775-778/Region: DEAD/H motif #status atypical

Query Match 56.2%; Score 41; DB 1; Length 1199;
Best Local Similarity 63.6%; Pred. No. 31; Mismatches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QRLASYRRITS 14
| : | | | | | | | | | |
Db 1063 EKMAAYRRITS 1073

RESULT 19
T38233
probable cystathionine gamma-synthase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C:Accession: T38233
R;Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z21780
A:Accession: T38233
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-398 <MUR>
A:Cross-references: UNIPARC:UPI000006C358; EMBL:AL021813; PIDN:CAA16988.1; GSPDB:GN00066
A:Experimental source: strain 972h-; cosmid C23A1
C:Genetics:
A:Gene: SPDB:SPAC23A1.14C
A:Map position: 1

C;Superfamily: cystathionine gamma-synthase

Query Match 53.4%; Score 39; DB 2; Length 398;
Best Local Similarity 53.3%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQLASVRRITSSK 16
||:|:|:|:|:|
Db 354 SVESLIEWRRWTDTSK 368

RESULT 20

F72253
hypochemical protein TM1450 - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72253
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.; C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72253
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-893 <ARN>
A;Cross-references: UNIPROT:Q9XIG2; UNIPARC:UPI00000D38A8; GB:AE001796; GB:AE000512; NID
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1450

Query Match 53.4%; Score 39; DB 2; Length 893;
Best Local Similarity 61.5%; Pred. No. 54;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 VORLASVRRITSS 15
|:|:|:|:|:|
Db 788 VERLRYRLASS 800

RESULT 21

JC2417
monocyte chemoattractant protein-2 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C;Accession: JC2417
R;Hoang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 205, 148-153, 1994
A;Title: Porcine luteal cells express monocyte chemoattractant protein-2 (MCP-2): Analysis
A;Reference number: JC2417; MUID:95091716; PMID:7999015
A;Accession: JC2417
A;Molecule type: mRNA
A;Residues: 1-99 <HOS>
A;Cross-references: UNIPROT:P49873; UNIPARC:UPI00001362D6; GB:Z48480; NID:9683718; PIDN:
A;Experimental source: corpus luteum
C;Superfamily: macrophage inflammatory protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-99/Product: monocyte chemoattractant protein-2 #status predicted <MAT>

Query Match 52.1%; Score 38; DB 2; Length 99;
Best Local Similarity 50.0%; Pred. No. 8.4;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16
|:|:|:|:|:|
Db 43 IPFKKLESYTRITNSQ 58

RESULT 22

A82754
lipoprotein XFO855 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: A82754
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82754
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <SIM>
A;Cross-references: UNIPROT:Q9PP23; UNIPARC:UPI00000C2546; GB:AE003925; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsumura, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XFO855

Query Match 52.1%; Score 38; DB 2; Length 242;
Best Local Similarity 43.8%; Pred. No. 21;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16
::|:|:|:|:|:|
Db 64 VAPQDLAWNRITASK 79

RESULT 23

JC5200
Chemoreceptor TB334 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: JC5200; PC4302
R;Thomas, M.B.; Haines, S.L.; Akesson, R.A.
Gene 178, 1-5, 1996
A;Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.
A;Reference number: JC5200; MUID:97080538; PMID:8921883
A;Accession: JC5200
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-311 <THO1>
A;Cross-references: UNIPROT:Q62942; UNIPARC:UPI00000402D2; GB:U50947; NID:gl256388; PIDN:
A;Accession: PC4302
A;Status: preliminary
A;Molecule type: protein
A;Residues: 146-153; 265-272 <THO2>
A;Cross-references: UNIPARC:UPI0000178381; UNIPARC:UPI0000178382
A;Experimental source: taste bud
C;Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction
C;Genetics:
A;Gene: tb334
C;Superfamily: olfactory receptor OR14
C;Keywords: olfaction; taste bud; transmembrane protein
F;24-47/Domain: transmembrane #status predicted <TM1>
F;56-77/Domain: transmembrane #status predicted <TM2>
F;99-118/Domain: transmembrane #status predicted <TM3>
F;138-162/Domain: transmembrane #status predicted <TM4>
F;195-217/Domain: transmembrane #status predicted <TM5>
F;236-258/Domain: transmembrane #status predicted <TM6>
F;271-291/Domain: transmembrane #status predicted <TM7>

```
Query Match      52.1%; Score 38; DB 2; Length 311;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SVQRLASVRRITSS 15
Db 298 ALKRLSHRRILSS 311
      :|||:|||||
      :|||:|||||

RESULT 24
D37314
regulatory protein lcrR - Yersinia pseudotuberculosis (fragment)
C:Species: Yersinia pseudotuberculosis
C>Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 05-Oct-2004
C:Accession: D37314
R:Bergman, I.; Hakansson, S.; Forsberg, A.; Norlander, L.; Macellaro, A.; Baeckman, A.;
J. Bacteriol. 173, 1607-1616, 1991
A:Title: Analysis of the V antigen lcrGVH-yopBD operon of Yersinia pseudotuberculosis: e
A:Reference number: A37314; MUID:91154114; PMID:1705541
A:Accession: D37314
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-59 <BAR>
A:Cross-references: UNIPROT:P19393; UNIPARC:UPI00001798AE
C:Superfamily: low calcium response locus protein R

Query Match      51.4%; Score 37.5; DB 2; Length 59;
Best Local Similarity 58.8%; Pred. No. 6.1;
Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ISVQRLAS-YRRITSSK 16
Db 14 LSTQRLAHFYRRWTGAK 30
      :|||||:|||||
      :|||||:|||||

RESULT 25
A37774
lcrR protein - Yersinia pestis
C:Species: Yersinia pestis
C>Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 05-Oct-2004
C:Accession: A37774
R:Barve, S.S.; Straley, S.C.
J. Bacteriol. 172, 4661-4671, 1990
A:Title: lcrR, a low-Ca(2+)-response locus with dual Ca(2+)-dependent functions in Yers
A:Reference number: A37774; MUID:90330579; PMID:1695896
A:Accession: A37774
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-146 <BAR>
A:Cross-references: UNIPROT:P19393; UNIPARC:UPI00001798AD; GB:M35740
C:Superfamily: low calcium response locus protein R

Query Match      51.4%; Score 37.5; DB 2; Length 146;
Best Local Similarity 58.8%; Pred. No. 16;
Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ISVQRLAS-YRRITSSK 16
Db 101 LSTQRLAHFYRRWTGAK 117
      :|||||:|||||
      :|||||:|||||

RESULT 26
T43592
low calcium response protein R - Yersinia pestis plasmid pCD1
C:Species: Yersinia pestis
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 05-Oct-2004
C:Accession: T43592; T42887
R:Hu, P.; Elliott, J.; McCreedy, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker
J. Bacteriol. 180, 5192-5202, 1998
A:Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A:Reference number: 222578; MUID:98422474; PMID:9748454
A:Accession: T43592
A:Status: preliminary; translated from GB/EMBL/DBDJ
```

```
A:Molecule type: DNA
A:Residues: 1-146 <HUP>
A:Cross-references: UNIPROT:P19393; UNIPARC:UPI000012E2B8; EMBL:AF053946; MUID:g2996222;
A:Experimental source: strain KIM
R:Perry, R.D.; Straley, S.C.; Fetherston, J.D.; Rose, D.J.; Gregor, J.; Blattner, F.R.
Infect. Immun. 66, 4611-4623, 1998
A:Title: DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of Yersinia p
A:Reference number: 222273; MUID:98427122; PMID:9746557
A:Accession: T42887
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-146 <PER>
A:Cross-references: UNIPARC:UPI000012E2B8; EMBL:AF074612; MUID:g3822037; PIDN:AAC69831.1;
A:Experimental source: strain KIM5
C:Genetics:
A:Gene: lcrR
A:Genome: plasmid pCD1
C:Superfamily: low calcium response locus protein R

Query Match      51.4%; Score 37.5; DB 2; Length 146;
Best Local Similarity 58.8%; Pred. No. 16;
Matches 10; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy 1 ISVQRLAS-YRRITSSK 16
Db 101 LSTQRLAHFYRRWTGAK 117
      :|||||:|||||
      :|||||:|||||

RESULT 27
T19339
hypothetical protein Cl6D2.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19339
R:Lloyd, C.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z19110
A:Accession: T19339
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-194 <WIL>
A:Cross-references: UNIPROT:O62061; UNIPARC:UPI00000805A6; EMBL:AL023810; PIDN:CAA19421.
A:Experimental source: clone Cl6D2
C:Genetics:
A:Gene: CESP:Cl6D2.1
A:Map position: 2
A:Introns: 17/3; 53/2; 86/3; 137/3

Query Match      50.7%; Score 37; DB 2; Length 194;
Best Local Similarity 58.3%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SVQRLASVRRIT 13
Db 182 SEQQLAQFRRTV 193
      |::|:|::|
      |::|:|::|

RESULT 28
T02021
hypothetical protein T9E19.2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
C:Accession: T02021
R:Stromatt, C.; Johnson, D.; Le, T.
submitted to the EMBL Data Library, November 1998
A:Description: The sequence of A. thaliana T9E19.
A:Reference number: Z14496
A:Accession: T02021
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-374 <STR>
A:Cross-references: UNIPROT:Q9ZSH6; UNIPARC:UPI000000A530C; EMBL:AF104920; MUID:g3859610;
A:Experimental source: cultivar Columbia
```

C;Genetics:
A;Map position: 4
A;Introns: 279/3
A;Note: T9E19.2

Query Match 50.7%; Score 37; DB 2; Length 374;
Best Local Similarity 53.3%; Pred. No. 52;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
|:|||||:|:
Db 256 SIHRLASLRITR 270

RESULT 29

C82112
flagellin FlaE VC2144 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82112
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82112
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-378 <HEI>
A;Cross-references: UNIPROT:Q9KQ60; UNIPARC:UPI000012A8A0; GB:AE004287; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2144
A;Map position: 1
C;Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 378;
Best Local Similarity 53.3%; Pred. No. 52;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
|:|||||:|:
Db 28 SLERLSSGNRINSK 42

RESULT 30

G82107
flagellin core protein A VC2188 [Imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82107
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82107
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-379 <HEI>
A;Cross-references: UNIPROT:Q30858; UNIPARC:UPI000012A886; GB:AE004290; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2188
A;Map position: 1
C;Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 379;
Best Local Similarity 53.3%; Pred. No. 52;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
|:|||||:|:
Db 28 SWERLSSGNRINSK 42

RESULT 31

S52444
flagellin - Legionella micdadei
C;Species: Legionella micdadei
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52444
R;Bangsberg, J.; Hindersson, P.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning and expression of Legionella micdadei flagellin.
A;Reference number: S52444
A;Accession: S52444
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474 <BAN>
A;Cross-references: UNIPROT:P53606; UNIPARC:UPI000012A8D4; EMBL:X84699; NID:G673427; PID
C;Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 474;
Best Local Similarity 53.3%; Pred. No. 66;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
|:|||||:|:
Db 28 AIQRLSSGLRINSK 42

RESULT 32

FLEC
flagellin - Escherichia coli (strain K-12)
C;Species: Escherichia coli
A;Variety: strain K-12
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: A37249; JY0018; I41270; H64955; A28187
R;Kuwajima, G.; Asaka, J.I.; Fujiwara, T.; Fujiwara, T.; Kondo, E.
J. Bacteriol. 168, 1479-1483, 1986
A;Title: Nucleotide sequence of the hag gene encoding flagellin of Escherichia coli.
A;Reference number: A37249; MUID:87057066; PMID:3536885
A;Accession: A37249
A;Molecule type: DNA
A;Residues: 1-498 <KUM>
A;Cross-references: UNIPROT:P04949; UNIPARC:UPI00000000AD; GB:M14358; NID:G146311; PIDN:
A;Experimental source: strain K-12
R;Hanafusa, T.; Sakai, A.; Tomimaga, A.; Enomoto, M.
Mol. Gen. Genet. 216, 44-50, 1989
A;Title: Isolation and characterization of Escherichia coli hag operator mutants whose h
A;Reference number: JY0018; MUID:89281489; PMID:2659972
A;Accession: JY0018

A;Molecule type: DNA
A;Residues: 1-284, 'L', 286-498 <HAN>
A;Cross-references: UNIPARC:UPI000016F1F3; GB:X17440; NID:G41649; PIDN:CAA35488.1; PID:G
A;Experimental source: strain K-12
R;Szekely, E.; Simon, M.
J. Bacteriol. 155, 74-81, 1983

A;Title: DNA sequence adjacent to flagellar genes and evolution of flagellar- phase vari
A;Reference number: I41269; MUID:83238225; PMID:6305924
A;Accession: I41270
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-20 <RES>
A;Cross-references: UNIPARC:UPI000016F1F5; GB:J01607; NID:G146315; PIDN:AAA92491.1; PID:
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64955
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

A; Cross-references: UNIPROT:Q06352; UNIPARC:UPI000000B7C73; GB:L07388; NID:G290438; PIDN:
C; Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 584;
Best Local Similarity 53.3%; Pred. No. 82;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
|:|:|:|:|:|:|:
Db 28 SIERLSSGLRINSK 42

RESULT 37
F85809
hypothetical protein flic [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C; Species: Escherichia coli
C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C; Accession: F85809
R; Perla, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Killer, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUID:21074935; PMID:11206551
A; Accession: F85809
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-585 <STO>
A; Cross-references: UNIPROT:Q9K2Y6; UNIPARC:UPI00000165819; GB:AE005174; NID:gl2516024; F:
A; Experimental source: strain O157:H7, substrain EDL933
C; Genetics:
A; Gene: flic
C; Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 585;
Best Local Similarity 53.3%; Pred. No. 82;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
|:|:|:|:|:|:|:
Db 28 SIERLSSGLRINSK 42

RESULT 38
F90961
flagellin [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C; Accession: F90961
R; Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Accession: F90961
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-585 <HAY>
A; Cross-references: UNIPROT:Q9K2Y6; UNIPARC:UPI000000D00B9; GB:BA0000007; PIDN:BA836085.1;
A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; Genetics:
A; Gene: ECa2662
C; Superfamily: flagellin

Query Match 50.7%; Score 37; DB 2; Length 585;
Best Local Similarity 53.3%; Pred. No. 82;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
|:|:|:|:|:|:|:
Db 28 SIERLSSGLRINSK 42

RESULT 39

```
Qy 3 VQRLASYRRITSS 15
   |:|:|:|:|:|
Db 84 VESLSAYRRLSS 96

RESULT 42
D85089
hypothetical protein AT4g08880 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85089
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: D85089
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1175 <STO>
A:Cross-references: UNIPROT:Q9ZPF3; UNIPARC:UPI000009F708; GB:NC_001268; NID:g7267530; E
C:Genetics:
A:Gene: AT4g08880
A:Map position: 4

Query Match 50.7%; Score 37; DB 2; Length 1175;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
   |:|:|:|:|:|
Db 192 SIHRLASLRAITRSR 206

RESULT 43
E86402
hypothetical protein F28J5.2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86402
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86402
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1198 <STO>
A:Cross-references: UNIPROT:Q9C6N9; UNIPARC:UPI00000A5394; GB:AE005172; NID:g10998930; E
C:Genetics:
A:Map position: 1

Query Match 50.7%; Score 37; DB 2; Length 1198;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
   |:|:|:|:|:|
Db 328 SIHRLASLRAITRSR 342

RESULT 44
H85041
hypothetical protein AT4g03300 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85041
```

```
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: H85041
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1285 <STO>
A:Cross-references: UNIPROT:Q9ZR01; UNIPARC:UPI00000A72B2; GB:NC_001268; NID:g7270200; P
C:Genetics:
A:Gene: AT4g03300
A:Map position: 4

Query Match 50.7%; Score 37; DB 2; Length 1285;
Best Local Similarity 53.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
   |:|:|:|:|:|
Db 480 SIHRLASLRAITRSR 494

RESULT 45
H96559
hypothetical protein FSF19.8 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H96559
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96559
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1305 <STO>
A:Cross-references: UNIPROT:Q9ZU21; UNIPARC:UPI00000AA103; GB:AE005173; NID:g4220449; P
C:Genetics:
A:Gene: FSF19.8
A:Map position: 1

Query Match 50.7%; Score 37; DB 2; Length 1305;
Best Local Similarity 53.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
   |:|:~|:|:|:|:|
Db 328 SIHRLASLRAITRSR 342

RESULT 46
D85066
hypothetical protein AT4g05280 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: D85066
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: D85066
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1312 <STO>
A:Cross-references: UNIPROT:Q9M0W7; UNIPARC:UPI00000A5C54; GB:NC_001268; NID:g7267288; P
C:Genetics:
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:09:23 ; Search time 177.048 Seconds
(without alignments)
1106.832 Million cell updates/sec

Title: US-10-644-277-62
Perfect score: 2379
Sequence: 1 QVQLQSGGLVKSQTLISL.....MHEALHHYTKSLSLGK 446

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2379	100.0	446	8 ADK52356	Adk52356 Human ant
2	2197.5	92.4	470	9 AEB45857	Aeb45857 Human mon
3	2187.5	92.0	464	9 AEC20880	Aec20880 Low risk
4	2186	91.9	450	6 ABP96294	Abp96294 4A5-3.1.1
5	2177	91.5	467	9 ADZ51037	Adz51037 Amino aci
6	2171	91.3	467	2 AAW14925	Aaw14925 Human gam
7	2171	91.3	467	2 ADE31589	Ade31589 Gamma 4 h
8	2164	91.0	467	2 AAW14926	Aaw14926 Human gam
9	2164	91.0	467	2 ADE31591	Ade31591 Gamma 4 h
10	2159	90.8	467	2 AAW14927	Aaw14927 Human gam
11	2159	90.8	467	7 ADZ51593	Adz51593 Gamma 4 h
12	2158.5	90.7	480	9 ADZ57697	Adz57697 Anti-cMet
13	2140	90.0	473	4 AAB36206	Aab36206 Human imm
14	2136.5	89.8	580	6 AAO30915	Aao30915 di-NHS76
15	2119	89.1	442	9 ADY74807	Ady74807 Rat anti-
16	2108	88.6	463	9 ADZ57701	Adz57701 Anti-cMet
17	2106.5	88.5	466	7 ADE28479	Ade28479 Human ant
18	2104.5	88.5	466	7 ADE28471	Ade28471 Human ant
19	2096.5	88.1	466	7 ADE28419	Ade28419 Human ant
20	2090	87.9	448	9 ADW11296	Adw11296 Human C-t
21	2088.5	87.8	451	8 ADQ31884	Adq31884 Antibody
22	2088.5	87.8	451	8 ADT77643	Adt77643 Antibody
23	2088.5	87.8	451	9 AEB51162	Aeb51162 Chimeric
24	2088	87.8	448	9 ADW11298	Adw11298 Human C-t

25	2085.5	87.7	451	8 ADT51711	Adt51711 M200 anti
26	2084.5	87.6	464	7 ADE28411	Ade28411 Human ant
27	2083	87.6	442	9 ADY74779	Ady74779 Rat anti-
28	2082.5	87.5	451	8 ADT51709	Adt51709 M200 anti
29	2082.5	87.5	451	8 ADT51710	Adt51710 M200 anti
30	2079.5	87.4	447	9 AEB46954	Aeb46954 CD1a spec
31	2079.5	87.4	451	8 ADT51712	Adt51712 M200 anti
32	2079.5	87.4	541	8 ADR10116	Adr10116 Human pro
33	2078	87.3	448	9 ADW11294	Adw11294 Human C-t
34	2077.5	87.3	451	8 ADT51713	Adt51713 M200 anti
35	2077.5	87.3	462	3 AAB26884	Aab26884 Human imm
36	2075	87.2	471	9 AEB45873	Aeb45873 Human mon
37	2071	87.1	461	9 AEA41062	Aea41062 Human ant
38	2071	87.1	465	9 AEB45849	Aeb45849 Human mon
39	2067	86.9	463	9 AEA41030	Aea41030 Human ant
40	2067	86.9	469	9 AEB45895	Aeb45895 Human mon
41	2065.5	86.8	451	8 ADQ31890	Adq31890 Antibody
42	2065.5	86.8	451	9 AEB51168	Aeb51168 Chimeric
43	2064.5	86.8	462	9 AEB45881	Aeb45881 Human mon
44	2064	86.8	467	9 AEC20877	Aec20877 Low + mod
45	2064	86.8	469	8 ADL93669	Adl93669 Human CD4

ALIGNMENTS

RESULT 1
ADK52356
ID ADK52356 standard; protein; 446 AA.
XX
AC ADK52356;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region heavy chain #16.
XX
KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; Neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN WQ2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52355.
XX
PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
PS Claim 1; SEQ ID NO 62; 154pp; English.
XX
CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,

CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region heavy chain sequence.
XX
SQ Sequence 446 AA;

Query Match 100.0%; Score 2379; DB 8; Length 446;
Best Local Similarity 100.0%; Pred. No. 3e-135;
Matches 446; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVQLQESGFLVKPSQTLSTCTVSGSISGCGNYNNIRQHPGKLEWIGYIYSGNTY 60
Db 1 QVQLQESGFLVKPSQTLSTCTVSGSISGCGNYNNIRQHPGKLEWIGYIYSGNTY 60

Qy 61 YNPISLKRITISIDTSKNQFSLTSSVTAADTAVVYCARDGGDDAFDIWGQTMVTVSSA 120
Db 61 YNPISLKRITISIDTSKNQFSLTSSVTAADTAVVYCARDGGDDAFDIWGQTMVTVSSA 120

Qy 121 STKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180
Db 121 STKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG 180

Qy 181 LYSLSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPAPPEFLGSPVF 240
Db 181 LYSLSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPAPPEFLGSPVF 240

Qy 241 LPPPKPDTLMSRTPETCVVVDVSDPEVQFNWYDGEVHNAKTPREEQFNSTYR 300
Db 241 LPPPKPDTLMSRTPETCVVVDVSDPEVQFNWYDGEVHNAKTPREEQFNSTYR 300

Qy 301 VVSVLTVLHQDWLNGEKVKCKVSNKGLPSSIEKTIISKAGQPREPQVYTLPPSQEEMTKN 360
Db 301 VVSVLTVLHQDWLNGEKVKCKVSNKGLPSSIEKTIISKAGQPREPQVYTLPPSQEEMTKN 360

Qy 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGN 420
Db 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGN 420

Qy 421 VFSCSWMEALHNHYTQKSLSLGLK 446
Db 421 VFSCSWMEALHNHYTQKSLSLGLK 446

RESULT 2
AEB45857
XX ID AEB45857 standard; protein; 470 AA.
XX AC AEB45857;
XX DT 06-OCT-2005 (first entry)
XX DE Human monoclonal anti-MadCAM antibody #11.
XX KW Monoclonal antibody; mucosal addressin cell adhesion molecule; MadCAM;
KW inflammation; inflammatory bowel disease; Crohn's disease;
KW ulcerative colitis; diverticular disease; gastritis; liver disease;
KW primary biliary cirrhosis; primary sclerosing cholangitis;
KW insulin dependent diabetes; graft versus host disease; antiinflammatory;
KW gastrointestinal-gen.; antidiabetic; hepatotropic; antidiabetic;
KW immunosuppressive; antibody.
XX OS Homo sapiens.
XX PN WO2005067620-A2.
XX PD 28-JUL-2005.
XX PF 07-JAN-2005; 2005WO-US000370.
XX

PR 09-JAN-2004; 2004US-0535490P.
XX (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
PA (PFIZ) PFIZER LTD.
XX
PI Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendscho M;
XX WPI; 2005-554958/56.
DR N-PSDB; AEB45856.
XX
PT New antibody to Mucosal Addressin Cell Adhesion Molecule, useful for
PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel
PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or
PT graft versus host disease.
XX
PS Claim 8; SEQ ID NO 22; 167pp; English.
XX
CC The invention relates to a human monoclonal antibody or its antigen-
CC binding portion that specifically binds to mucosal addressin cell
CC adhesion molecule (MADCAM). The invention also relates to a hybridoma
CC cell line that produces the human monoclonal antibody, a pharmaceutical
CC composition comprising an amount of the monoclonal antibody or its
CC antigen-binding portion and a pharmaceutical carrier, a method of
CC treating inflammatory disease in a subject, an isolated cell line that
CC produces the monoclonal antibody or its antigen-binding portion or the
CC heavy chain or light chain of the antibody or of its portion, an isolated
CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy
CC chain or its antigen-binding portion or the light chain or its antigen-
CC binding portion of an antibody described above, a vector comprising the
CC nucleic acid molecule, where the vector optionally comprises an
CC expression control sequence operably linked to the nucleic acid molecule,
CC a host cell comprising the vector or the nucleic acid molecule above, a
CC method of producing a human monoclonal antibody or its antigen-binding
CC portion that specifically binds MadCAM, a method of isolating an antibody
CC or its antigen-binding portion that specifically binds to MadCAM, a
CC method of treating a subject in need of a human antibody or its antigen-
CC binding portion that specifically binds to MadCAM and inhibits binding to
CC MadCAM, a method of inhibiting alpha4beta7 binding to cells
CC expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte
CC endotheial cell adhesion, migration and infiltration into tissues, a
CC method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion,
CC inhibiting the MadCAM-mediated recruitment of lymphocytes to
CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder
CC characterized by circulating soluble human MadCAM and detecting
CC inflammation in a subject. The antibody, composition and methods are
CC useful for diagnosing and treating inflammatory disease, e.g.
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC diverticular disease, gastritis, liver disease, primary biliary
CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
CC graft versus host disease. This sequence represents a human monoclonal
CC anti-MadCAM antibody of the invention.
XX
SQ Sequence 470 AA;

Query Match 92.4%; Score 2197.5; DB 9; Length 470;
Best Local Similarity 92.9%; Pred. No. 2.8e-124;
Matches 421; Conservative 5; Mismatches 18; Indels 9; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGCGNYNNIRQHPGKLEWIGYIYSGNTY 60
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGSISGCGNYNNIRQHPGKLEWIGYIYSGNTY 77

Qy 61 YNPISLKRITISIDTSKNQFSLTSSVTAADTAVVYCARDG-----GDADFIDWGQGT 113
Db 78 SNPSLRGRVTILADTSKNQFSLSSVTAADTAVVYCARDRTITIRGLIPSFDFYWGQGT 137

Qy 114 MVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
Db 138 LVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 197

Qy 174 AVLQSSGLYLSVSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVESKYGPPCPAPPEF 233
XX

198 AVLQSSGLYSLSSVWTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYPGPPCPAPDF 257
234 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNNYDGVVHNAKTPREE 293
258 LGGPSVFLPPPKDPTLMISRTPEVTCVVVDVSQEDPEVQFNNYDGVVHNAKTPREE 317
294 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKAKGQPREPQVYTLPPS 353
318 QFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKAKGQPREPQVYTLPPS 377
354 QEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGFFLYSRLTVDK 413
378 QEEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGFFLYSRLTVDK 437
414 SRWQEGNVFSCSVMHALHNHYTKLSLSLKG 446
438 SRWQEGNVFSCSVMHALHNHYTKLSLSLKG 470

RESULT 3
AEC20880
ID AEC20880 standard; protein; 464 AA.
XX AEC20880;
XX
XX 20-OCT-2005 (first entry)
XX
XX Low risk humanized RX1 antibody heRX1-1.IgG4.
XX endocrine-gen.; antiarthritic; antibacterial; antiinflammatory;
XX antirheumatic; antithyroid; bone metastases; calcium antagonist; cancer;
XX cardiovascular-gen.; degeneration; eating-disorders-gen.; gastrointestinal-gen.;
XX endocrine disease; endocrine-gen.; endocrine-gen.; immune disorder;
XX genetic disorder; hepatotropic; hypercalcemia; mouth disease;
XX immunotherapy; inflammation; monoclonal antibody; osteopathic;
XX musculoskeletal disease; neoplasm; nephrotropic; osteoporosis;
XX osteopetrosis; osteoporosis; pagets disease; periodontal disease;
XX pharmaceutical; rheumatoid arthritis; RX1.
XX
XX Homo sapiens.
XX Mus musculus.
XX Synthetic.
XX
XX W02005068503-A2.
XX
XX 28-JUL-2005.
XX
XX 06-JAN-2005; 2005WO-US000546.
XX
XX 07-JAN-2004; 2004US-0535181P.
XX 02-JUN-2004; 2004US-0576417P.
XX
XX (CHIR) CHIRON CORP.
XX (XOMA) XOMA TECHNOLOGY LTD.
XX
XX Liu C, Zimmerman DL, Harrowe GM, Koehs K, Kavanaugh WM, Long L;
XX Calderon-Cacia M, Horwitz AH;
XX WPI; 2005-597707/61.
XX N-PSDB; AEC20878, AEC20879.
XX
XX Novel non-murine antibody that competes with monoclonal antibody RX1 for
XX binding to macrophage colony stimulating factor, useful for treating
XX hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer,
XX osteoporosis.
XX
XX Claim 53; SEQ ID NO 119; 269pp; English.
XX
XX The invention describes a non-murine antibody (I) that competes with
XX monoclonal antibody RX1 for binding to macrophage colony stimulating
XX factor (M-CSF) by more than 75%, where the monoclonal antibody RX1 has
XX the heavy chain and light chain amino acid sequences having a fully
XX defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)

sequences given in the specification, respectively. (I) is useful for preventing a subject afflicted with a disease that causes or contributes to osteolysis, where the antibody effectively reduces the severity of bone loss associated with the disease. The disease is chosen from metabolic bone diseases associated with relatively increased osteoclast activity, including endocrinopathies, hypercalcemia, deficiency states, chronic diseases, and hereditary diseases, cancer, osteoporosis, osteopetrosis, inflammation of bone associated with arthritis and/or rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or Paget's disease. (I) is useful for preventing or treating metastatic cancer. Antibodies of the invention are useful for preventing or reducing bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is useful for manufacturing a medicament for preventing or reducing bone loss in a patient exhibiting osteolysis, manufacturing a medicament for treating a patient afflicted with a disease that causes or contributes to osteolysis, and metastatic cancer to bone in a patient suffering from metastatic cancer, for manufacturing a medicament for treating a patient having cancer. (I) in synergistic combination, is useful for preparing a medicament for treating a patient exhibiting osteolysis. This is the amino acid sequence of a low risk humanized M-CSF specific murine antibody RX1.

Query Match 92.0%; Score 2187.5; DB 9; Length 464;
Best Local Similarity 93.9%; Pred. No. 1.1e-123;
Matches 419; Conservative 6; Mismatches 18; Indels 3; Gaps 2;
XX Sequence 464 AA;
SQ

QY 2 VOLQSGPGLVKPSQTLSTCTVSGSGSISSGGNY--NNWIRHPGKLEWIGYVYSGNTY 60
DB 21 VOLQSGPGLVKPSQTLSTCTVTDYSITS--DYANNWIRQPPGKLEWVGYSYSGSTS 78
QY 61 YNPSLKSRTISIDTSKNQFSLTSSVTAADTAVYACARDGGDDAFDIWGQGTMTVTVSSA 120
DB 79 YNPSLKSRTISIDTSKNQFSLTSSVTAADTAVYACARDGGDDAFDIWGQGTMTVTVSSA 138
QY 121 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTTTPAVLQSSG 180
DB 139 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSNVNSGALTSGVHTTTPAVLQSSG 198
QY 181 LYSLSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYPGPPCPAPDFLGGPSVP 240
DB 199 LYSLSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYPGPPCPAPDFLGGPSVP 258
QY 241 LFPKPDKDTLMISRTPEVTCVVVDVSQEDPEVQFNNYDGVVHNAKTPREEQFNSTYR 300
DB 259 LFPKPDKDTLMISRTPEVTCVVVDVSQEDPEVQFNNYDGVVHNAKTPREEQFNSTYR 318
QY 301 VVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKAKGQPREPQVYTLPPSQEEMTKN 360
DB 319 VVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKSKAKGQPREPQVYTLPPSQEEMTKN 378
QY 361 QVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGFFLYSRLTVDKSRWQEGN 420
DB 379 QVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPPVLDSDGFFLYSRLTVDKSRWQEGN 438
QY 421 VFSCSVMHALHNHYTKLSLSLKG 446
DB 439 VFSCSVMHALHNHYTKLSLSLKG 464

RESULT 4
ABP96294
ID ABP96294 standard; protein; 450 AA.
XX ABP96294;
XX AC
XX 20-MAY-2003 (first entry)
XX
XX 4A5-3.1.1-B4 antibody amino acid sequence #1.
DE
XX
XX Anti-hTNFSF13b human antibody; antibody; human; TNFSF13b; antiulcer;
KW immunosuppressive; antiinflammatory; dermatological; antirheumatic;

KW antiarthritic; antiaethmatic; antiallergic; antiparasitic; antiparasitic;
KW antiinfertility; antithyroid; thyromimetic; haemostatic; cytostatic;
KW tumour necrosis factor antagonist; TNF antagonist; rheumatoid arthritis;
KW systemic lupus erythematosus; juvenile chronic arthritis; Lyme arthritis;
KW Crohn's disease; ulcerative colitis; inflammatory bowel disease; asthma;
KW allergic disease; psoriasis; immune disease; organ transplant rejection;
KW graft-versus-host disease; sarcoidosis; infectious disease; cancer;
KW parasitic disease; female infertility; autoimmune thrombocytopenia;
KW autoimmune thyroid disease; Hashimoto's disease; Sjogren's syndrome.

OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 24..34
FT /label= CDR1
FT Region 50..56
FT /label= CDR2
FT Region 89..97
FT /label= CDR3

XX WO2003016468-A2.
XX 27-FEB-2003.
XX 15-AUG-2002; 2002WO-US021842.
XX 16-AUG-2001; 2001US-0312808P.
XX (ELIL) LILLY & CO ELI.

XX Gelfanova VP, Hale JE, Kikly KK, Witcher DR, Rathnachalam R;
XX WPI; 2003-268308/26.

XX New anti-HTNFS13b human antibody, useful in manufacturing a medicament
PT for inhibiting TNFSF13b activity in a subject suffering from a disorder
PT in which TNFSF13b activity is detrimental, e.g. asthma, cancer or
PT rheumatoid arthritis.

XX Example 7; Page 33; 52pp; English.

XX The present invention describes an anti-HTNFSF13b human antibody (I). (I)
CC has immunosuppressive, antiinflammatory, dermatological, antiulcer,
CC antirheumatic, antiarthritic, antiaethmatic, antiallergic, antiparasitic,
CC antiparasitic, antiinfertility, antithyroid, thyromimetic, haemostatic
CC and cytostatic activities, and can be used as a tumour necrosis factor
CC (TNF) antagonist. The anti-HTNFSF13b human antibody or an antibody that
CC neutralises TNFSF13b activity by binding an epitope of TNFSF13b is useful
CC in manufacturing a medicament for administering to a subject suffering
CC from a disorder in which TNFSF13b activity is detrimental, e.g. systemic
CC lupus erythematosus, rheumatoid arthritis, juvenile chronic arthritis,
CC Lyme arthritis, Crohn's disease, ulcerative colitis, inflammatory bowel
CC disease, asthma, allergic diseases, psoriasis, acute or chronic immune
CC disease associated with organ transplantation, organ transplant
CC rejection, graft-versus-host disease, sarcoidosis, infectious diseases,
CC parasitic diseases, female infertility, autoimmune thrombocytopenia,
CC autoimmune thyroid disease, Hashimoto's disease, Sjogren's syndrome, or
CC cancer. The present sequence represents a 4A5-3.1.1-B4 antibody amino
CC acid sequence, which is used in an example from the present invention

XX Sequence 450 AA;

Query Match 91.9%; Score 2186; DB 6; Length 450;
Best Local Similarity 92.3%; Pred. No. 1.3e-123;
Matches 417; Conservative 9; Mismatches 18; Indels 8; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLISLTCTVSGSISGCGYVWVWIRHQPGKLEWIGYVYSGNTY 60
DB 1 QVQLQQWAGLTKPSETLSLTCAVYGGSF--GYVWSWIRPPGKLEWIGVNHSGSTN 58
QY 61 YNPSLKSRITTSIDTSKQFSLTSSVTAADTAVVYCARGDYDILTGYYVDFYWGQGT 114

Db 59 YNPSLKSRVTSVDTSKNQFSLKLSVTAADTAVVYCARGDYDILTGYYVDFYWGQGT 118
QY 115 VTSSASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPEPPTVYVWNSGALTSGVHTPE 174
Db 119 VTSSASTKGPSVPPLAPCSRSTSESTAALGCLVKDYFPEPPTVYVWNSGALTSGVHTPE 178
QY 175 VLQSSGLYSLSVVTVPSSSSLGTQYTCNVVDHKPSNTKVDKRVESKYGPPCPAPPEFL 234
Db 179 VLQSSGLYSLSVVTVPSSSSLGTQYTCNVVDHKPSNTKVDKRVESKYGPPCPAPPEFL 238
QY 235 GGPSVFLFPKPKDMLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNNAKTKPREQ 294
Db 239 GGPSVFLFPKPKDMLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNNAKTKPREQ 298
QY 295 FNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQ 354
Db 299 FNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQ 358
QY 355 EEMTKNOVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSRLTVDKS 414
Db 359 EEMTKNOVSLTCLVKGFVPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSRLTVDKS 418
QY 415 RWQEGNVFSCVMHEALHNHYTQKSLSLGLK 446
Db 419 RWQEGNVFSCVMHEALHNHYTQKSLSLGLK 450

RESULT 5
ADZ51037
ID ADZ51037 standard; protein; 467 AA.
XX
AC ADZ51037;
XX
DT 30-JUN-2005 (first entry)
XX
DE Amino acid sequence of heavy chain of anti-H4-1BB antibody.
XX
KW antibody therapy; H4-1BB; CD137; IgG4; cytostatic; immunosuppressive;
KW antiinflammatory; antimicrobial; gene therapy;
KW T cell mediated autoimmune disease; cancer; neoplasm; autoimmune disease;
KW inflammatory disease; infectious disease; heavy chain.

OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..19
FT /note= "leader peptide"
XX
PN WO200503584-A1.

XX 21-APR-2005.
XX 12-OCT-2004; 2004WO-US033587.
XX 10-OCT-2003; 2003US-0510193P.
XX 08-OCT-2004; 2004US-00961567.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Jure-Kunkel M, Hefta LJ, Santoro M, Ganguly S;
XX WPI; 2005-296269/30.
XX N-PSDB; ADZ51035.

XX New monoclonal antibody that specifically binds to 4-1BB comprises a
PT light chain variable region and a heavy chain variable region, useful for
PT treating cancer, autoimmune diseases, inflammatory diseases, or
PT infectious diseases.

XX Claim 3; SEQ ID NO 3; 92pp; English.
XX The specification describes fully human antibodies against human 4-1BB
CC (CD137) (H4-1BB). These antibodies are especially IgG4 antibodies.

CC Antibodies for human 4-1BB are useful as immuno-enhancers of an anti-
CC tumor or anti-viral immune response, or as immunomodulators of T cell
CC mediated autoimmune disease. They can also be used as diagnostic tools
CC for the detection of H4-1BB in blood or tissues of patients with cancer,
CC autoimmune, or other disease. The antibody can also be used for treating
CC cancer (prostate cancer, melanoma, or epithelial cancer), autoimmune
CC diseases (multiple sclerosis, rheumatoid arthritis, systemic lupus
CC erythematosus, or myasthenia gravis), inflammatory diseases, and
CC infectious diseases. AD251035, AD251036, and AD251037 represent the
CC coding strand, complementary strand, and encoded protein of a plasmid.
CC This plasmid encodes the heavy chain of an antibody of the invention.
XX
XX Sequence 467 AA;

Query Match 91.5%; Score 2177; DB 9; Length 467;
Best Local Similarity 92.0%; Pred. No. 4.7e-123;
Matches 414; Conservative 11; Mismatches 19; Indels 6; Gaps 2;
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYVSGNTY 60
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYVSGNTY 77
QY 61 YNPISLKRITISIDTSKNQPSLTSSTVTAADTAIVYCARDGG---DDAFDINGQGTMT 116
DB 78 YNPISLKRITISIDTSKNQPSLTSSTVTAADTAIVYCARDGG---DDAFDINGQGTMT 137
QY 117 VSSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYPPEVTVSWNSGALTSGVHTPPAVL 176
DB 138 VSSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYPPEVTVSWNSGALTSGVHTPPAVL 197
QY 177 QSSGLYSLGSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGPPCPAPFELGG 236
DB 198 QSSGLYSLGSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGPPCPAPFELGG 257
QY 237 PSVFLPFPKPKDLMISRTPEVTVSVVDSQEDPEVQFNWYDGVVHNAKTKPREQFN 296
DB 258 PSVFLPFPKPKDLMISRTPEVTVSVVDSQEDPEVQFNWYDGVVHNAKTKPREQFN 317
QY 297 STYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEE 356
DB 318 STYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEE 377
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRTVDSKRW 416
DB 378 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRTVDSKRW 437
QY 417 QEGNVFSCSVHMEALHNHYTQKSLSLSLGK 446
DB 438 QEGNVFSCSVHMEALHNHYTQKSLSLSLGK 467

RESULT 6
AAW14925
ID AAW14925 standard; protein; 467 AA.
XX
XX AAW14925;
XX
XX 18-OCT-1997 (first entry)
XX
XX Human gamma-4 heavy chain.
XX
XX CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
XX cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia;
XX lymphoma; graft-versus-host disease; asthma; transplant rejection; HIV;
XX therapy; CE9 gamma 4.
XX
XX Homo sapiens.
XX
XX WO9709351-A1.
XX
XX 13-MAR-1997.
XX
XX 05-SEP-1996; 96WO-US014324.

XX 06-SEP-1995; 95US-00523894.
XX (IDEC-) IDEC PHARM CORP.
XX Hanna N, Newman RA, Reff ME;
XX WPI; 1997-201913/18.
XX N-PSDB; AAT62868.
XX Chimeric antibody comprising monkey variable domains and human constant
XX domains - affects CD4-mediated immune functions, esp. useful for
XX treatment of auto-immune disease, e.g. rheumatoid arthritis.
XX
XX Claim 6; Page 82-84; 155pp; English.
XX 3 Polypeptides (AAW14925-27) respectively comprise the heavy chain
XX regions of human gamma-4, gamma-4E carrying an L236E mutation in the
XX hinge region, and gamma-4PE carrying L236E and S229P mutations. They can
XX be incorporated into novel monoclonal and chimeric antibodies, e.g. CE9
XX gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human IgG4 FC
XX binding domain framework is combined with the antigen binding domains
XX (see also AAW14922-23) of macaque anti- human CD4 monoclonal antibody
XX E9.1. These antibodies show high affinity to human CD4, have little or no
XX immunogenicity in humans and show reduced or absence of effector
XX function. They can be used to treat autoimmune diseases such as
XX rheumatoid arthritis

Query Match 91.3%; Score 2171; DB 2; Length 467;
Best Local Similarity 91.7%; Pred. No. 1.1e-122;
Matches 418; Conservative 7; Mismatches 13; Indels 18; Gaps 4;
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYVSGNTY 59
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYVSGGNT 78
QY 60 YNPISLKRITISIDTSKNQPSLTSSTVTAADTAIVYCARDGGDDAFDI-----WG 110
DB 79 YNPISLKRITISIDTSKNQPSLTSSTVTAADTAIVYCARDGGDDAFDI-----NLT 131
QY 111 QGTMTVTSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYPPEVTVSWNSGALTSGVH 170
DB 132 QGVLTVTSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYPPEVTVSWNSGALTSGVH 191
QY 171 TTPAVLQSSGLYSLGSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 230
DB 192 TTPAVLQSSGLYSLGSVTVTPSSSLGKTYYTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 251
QY 231 PEFLLGSPVFLPFPKPKDLMISRTPEVTVSVVDSQEDPEVQFNWYDGVVHNAKTKP 290
DB 252 PEFLLGSPVFLPFPKPKDLMISRTPEVTVSVVDSQEDPEVQFNWYDGVVHNAKTKP 311
QY 291 REEQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAKGQPREPQVYTL 350
DB 312 REEQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTSKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRT 410
DB 372 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRT 431
QY 411 VDKSRWQEGNVFSCSVHMEALHNHYTQKSLSLSLGK 446
DB 432 VDKSRWQEGNVFSCSVHMEALHNHYTQKSLSLSLGK 467

RESULT 7
ADE31589
ID ADE31589 standard; protein; 467 AA.
XX
XX ADE31589;
XX

CC function. The gamma-4E and -4PE mutations confer activity enhanced
CC stability and eliminate depleting activity. The antibodies can be used to
CC treat autoimmune diseases such as rheumatoid arthritis
XX
SQ Sequence 467 AA;

Query Match	91.0%;	Score 2164;	DB 2;	Length 467;
Best Local Similarity	91.4%;	Pred. No. 2.9e-122;		
Matches 417;	Conservative 7;	Mismatches 14;	Indels 18;	Gaps 4;
QY 1	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNWIRQHPGKLEWIGYIYYS-GNT 59			
DB 20	QVQLQESGPGLVKPSQTLSTCTVSGGSI-SGDYYFWIRQHPGKLEWIGYIYSGGGT 78			
QY 60	YNPISLKRITISIDTSKNQFSLTSSVTAADTAVYVCARDGGDDAFDI-----WG 110			
DB 79	NTNPSLNRRVSIIDTSKNLFSKLRSVTAADTAVYVCAS-----NILKYLHMLLYWG 131			
QY 111	QGTMTVTSSASTKGPSPVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170			
DB 132	QGVLTVTSSASTKGPSPVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 191			
QY 171	TPPAVLQSSGLYSLSSVTVTPSSSLGKTITTCNVDRHKPSNTKYDKRVESKYGPPCPSCPA 230			
DB 192	TPPAVLQSSGLYSLSSVTVTPSSSLGKTITTCNVDRHKPSNTKYDKRVESKYGPPCPSCPA 251			
QY 231	PFELGSPVFLPPPKPDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNATKP 290			
DB 252	PEFEGGSPVFLPPPKPDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNATKP 311			
QY 291	REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350			
DB 312	REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371			
QY 351	PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 410			
DB 372	PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 431			
QY 411	VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLSLGK 446			
DB 432	VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLSLGK 467			

RESULT 9
ADE31591
ID ADE31591 standard; protein; 467 AA.
XX
AC ADE31591;
XX
DT 29-JAN-2004 (first entry)
XX
DE Gamma 4 heavy chain variable/constant domains E mutant.
XX
KW chimeric antibody; CD4 antibody; Old World monkey monoclonal antibody;
KW immunostimulant; antiasthmatic; immunosuppressive; antiarthritic;
KW antirheumatic; cytostatic; anti-HIV; CD4 related condition;
KW autoimmune disorder; rheumatoid arthritis; non-autoimmune disorder;
KW leukaemia; lymphoma; graft-versus-host diseases; asthma;
KW transplant rejection; HIV infection; CE9.1; human; gamma 4;
KW heavy chain variable domain; heavy chain constant domain; E mutant.
XX
OS Homo sapiens.
XX
PN US2003077275-A1.
XX
PD 24-APR-2003.
XX
XX 05-AUG-2002; 2002US-00211357.
XX
XX 25-JUL-1991; 91US-00735064.
PR 23-MAR-1992; 92US-00856281.
PR 10-JUL-1992; 92US-00912292.
PR 25-JAN-1995; 95US-00379072.

PR 07-JUN-1995; 95US-00476237.
PR 06-SEP-1995; 95US-00523894.
PR 10-JUL-2000; 2000US-00612914.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
XX Hanna N, Newman RA, Reff ME;
XX
XX WPI; 2003-625537/59.
DR N-PSDB; ADE31590.
XX
XX New chimeric anti-CD4 antibodies, useful for treating or preventing a CD4
PT related conditions, e.g. rheumatoid arthritis, leukemia, lymphoma, graft-
PT versus-host diseases, asthma, transplant rejection or HIV infection.
XX
PS Disclosure; SEQ ID NO 10; 85pp; English.
XX
CC The invention describes a chimeric antibody, which is specific to human
CC CD4. The chimeric antibody comprises the variable heavy and light chain
CC sequences of an Old World monkey monoclonal antibody produced against
CC human CD4, and human constant heavy and light domain sequences. The
CC chimeric antibody has immunostimulant, antiasthmatic, immunosuppressive,
CC antiarthritic, antirheumatic, cytostatic and anti-HIV properties. The
CC chimeric antibody is useful in therapy or prophylaxis, particularly for
CC treating or preventing a CD4 related condition. This condition includes
CC an autoimmune disorder (e.g. rheumatoid arthritis), a non-autoimmune
CC disorder (e.g. leukaemia, lymphoma, graft-versus-host diseases, asthma,
CC transplant rejection or HIV infection), or a condition mediated by or
CC involving CD4+ cells. This is the amino acid sequence of human gamma 4
CC heavy chain variable and constant domains E mutant associated with
CC creation of CE9.1, a monkey/human chimeric antibody with specificity for
CC CD4.
XX
SQ Sequence 467 AA;

Query Match	91.0%;	Score 2164;	DB 7;	Length 467;
Best Local Similarity	91.4%;	Pred. No. 2.9e-122;		
Matches 417;	Conservative 7;	Mismatches 14;	Indels 18;	Gaps 4;
QY 1	QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNWIRQHPGKLEWIGYIYYS-GNT 59			
DB 20	QVQLQESGPGLVKPSQTLSTCTVSGGSI-SGDYYFWIRQHPGKLEWIGYIYSGGGT 78			
QY 60	YNPISLKRITISIDTSKNQFSLTSSVTAADTAVYVCARDGGDDAFDI-----WG 110			
DB 79	NTNPSLNRRVSIIDTSKNLFSKLRSVTAADTAVYVCAS-----NILKYLHMLLYWG 131			
QY 111	QGTMTVTSSASTKGPSPVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170			
DB 132	QGVLTVTSSASTKGPSPVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 191			
QY 171	TPPAVLQSSGLYSLSSVTVTPSSSLGKTITTCNVDRHKPSNTKYDKRVESKYGPPCPSCPA 230			
DB 192	TPPAVLQSSGLYSLSSVTVTPSSSLGKTITTCNVDRHKPSNTKYDKRVESKYGPPCPSCPA 251			
QY 231	PFELGSPVFLPPPKPDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNATKP 290			
DB 252	PEFEGGSPVFLPPPKPDTLMISRTPEVTCVVDVVSQEDPEVQFNWYVDGVEVHNATKP 311			
QY 291	REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350			
DB 312	REEQFNSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371			
QY 351	PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 410			
DB 372	PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 431			
QY 411	VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLSLGK 446			
DB 432	VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLSLGK 467			

CC	chimeric antibody has immunostimulant, antiaethmatic, immunosuppressive,	
CC	antiarthritic, antirheumatic, cytostatic and anti-HIV properties. The	
CC	chimeric antibody is useful in therapy or prophylaxis, particularly for	
CC	treating or preventing a CD4 related condition. This condition includes	
CC	an autoimmune disorder (e.g. rheumatoid arthritis), a non-autoimmune	
CC	disorder (e.g. leukaemia, lymphoma, graft-versus-host diseases, asthma,	
CC	transplant rejection or HIV infection), or a condition mediated by or	
CC	involving CD4+ cells. This is the amino acid sequence of human gamma 4	
CC	heavy chain variable and constant domains PE mutant associated with	
CC	creation of CE9.1, a monkey/human chimeric antibody with specificity for	
CC	CD4.	
XX		
SQ	Sequence 467 AA;	
	Query Match 90.8%; Score 2159; DB 7; Length 467;	
	Best Local Similarity 91.2%; Pred. No. 5.7e-122;	
	Matches 416; Conservative 7; Mismatches 15; Indels 18; Gaps 4;	
Qy	1 QVQLQESGCLVKPSQTLSTCTVSGSISSGNGYNWIRQHPGKLEWIGYIYYS-GNT 59	
Db	20 QVQLQESGPGLVKPSQTLSTCTVSGSI-SGDYYFWIRQSPGKLEWIGYIYSGGDT 78	
Qy	60 YNPISLKRITISIDTSKQFSLTSSVTAADTAVYYCARDGDDAFDI-----WG 110	
Db	79 NYPISLNRVSIIDTSKSLFSLKLSVTAADTAVYYCAS-----NILKYLHLLYWG 131	
Qy	111 QGTMTVSSASTKGPSVFPPLACSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVH 170	
Db	132 QGVLTVTSSASTKGPSVFPPLACSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVH 191	
Qy	171 TFPVAVLQSSGLYSLSSVTVFPSSSLGKTKYTCNVHDKPSNTKYDKVESKYGPCCPCA 230	
Db	192 TFPVAVLQSSGLYSLSSVTVFPSSSLGKTKYTCNVHDKPSNTKYDKVESKYGPCCPCA 251	
Qy	231 PEFGLGPSVLPFPKPKDLMISRTPEVTCVVDVDSQEDPEVQFNMYVDGVEVHNARTKP 290	
Db	252 PEFEGGPSVLPFPKPKDLMISRTPEVTCVVDVDSQEDPEVQFNMYVDGVEVHNARTKP 311	
Qy	291 REQFNSTYRVSVLTVLHQDLNGLKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 350	
Db	312 REQFNSTYRVSVLTVLHQDLNGLKEYCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 371	
Qy	351 PPQSEMTKQVSLTCLVKGFYPSDIAVEFESGQENNNYKTPPVLDSDGSPFLYSRLT 410	
Db	372 PPQSEMTKQVSLTCLVKGFYPSDIAVEFESGQENNNYKTPPVLDSDGSPFLYSRLT 431	
Qy	411 VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 446	
Db	432 VDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 467	
	RESULT 12	
ID	ADZ57697 standard; protein; 480 AA.	
XX		
AC	ADZ57697;	
XX		
DT	30-JUN-2005 (first entry)	
XX		
DE	Anti-cMet antibody 9.1.2 heavy chain protein.	
XX		
KW	antibody engineering; cytostatic; vulnary; vasotropic; cardiant;	
KW	monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer;	
KW	gastrointestinal ulcer; ischemia; transplant rejection;	
KW	myocardial infarction; reperfusion injury; restenosis; angioplasty;	
KW	vascular disease; cancer; retinopathy; endometriosis; arthritis;	
KW	Alzheimers disease; tumor; Glioblastoma; sarcoma; carcinoma; diagnosis;	
KW	antibody.	
OS	Homo sapiens.	
XX		
Key	Location/Qualifiers	
Peptide	1. .19	

FT	Protein	/note= "signal peptide"
FT	20. .480	
FT	Region	/note= "mature antibody 9.1.2. heavy chain protein 1"
FT	50. .56	
FT	Region	/note= "complementarity determining region 1"
FT	71. .86	
FT	Region	/note= "complementarity determining region 2"
FT	119. .143	
FT	Region	/note= "complementarity determining region 3"
PN	GB2404660-A.	
XX		
PD	09-FEB-2005.	
XX		
PF	04-AUG-2004; 2004GB-00017384.	
XX		
PR	04-AUG-2003; 2003US-0492432P.	
XX		
PA	(PFIZ) PFIZER PROD INC.	
PA	(ABGE-) ABGENIX INC.	
XX		
PI	Michaud NR, Kajiji S, Borzillo G, Bedian V, Coleman K, Green LB;	
PI	Jia X;	
XX		
DR	WPI; 2005-145169/16.	
DR	N-PSDB; ADZ57696.	
XX		
CC	Human monoclonal antibody or antigen-binding portion that specifically	
CC	binds to c-Met, useful for treating cancer by inhibiting c-Met or for	
CC	promoting tissue regeneration and wound healing by activating c-Met.	
CC	Claim 6; SEQ ID NO 6; 128pp; English.	
CC	The invention relates to a human monoclonal antibody (I) or its antigen-	
CC	binding portion that specifically binds to c-Met, comprises a heavy chain	
CC	having a fully defined sequence (S1) of 13.3.2 heavy chain, where X2 is	
CC	lysine and X4 is threonine, and a light chain having a fully defined	
CC	sequence (S2) of 13.3.2 light chain, where X8 is threonine, where both	
CC	chains are without a signal sequence. All the sequences are fully defined	
CC	in the specification. (I) is useful for the manufacture of a medicament	
CC	for treating a hyperproliferative disorder in a subject, where the	
CC	antibody or its portion is a c-Met antagonist. (I) is useful for	
CC	manufacture of a medicament for promoting wound healing or tissue	
CC	regeneration in a subject, where the antibody, antigen-binding portion or	
CC	the composition activates c-Met. (I) which has a c-Met agonist activity	
CC	is useful in tissue regeneration or wound healing (skin ulcers or gastric	
CC	ulcers), or treating ischemia associated with kidney transplant	
CC	rejection, for attenuating toxicity associated with cyclosporin treatment	
CC	after transplant surgery, for treating myocardial infarction, cardiac	
CC	ischemia due to reperfusion injury, restenosis after angioplasty or	
CC	vascular diseases (I) which has a c-Met antagonist activity is useful	
CC	for treating cancers of brain, lung, squamous cell, bladder, neck, liver,	
CC	prostate, etc., proliferative vitreoretinopathy, proliferative plaque	
CC	retinopathy, endometriosis, and arthritis, for inhibiting cellular mitogenic	
CC	formation in Alzheimer's disease, inhibiting cellular mitogenic	
CC	responses, or for treating tumor, glioblastoma, sarcomas, or carcinomas.	
CC	(I) is useful for detecting c-Met in a biological sample in vitro or in	
CC	vivo, thus useful for diagnosing c-Met-expressing tumor. (I) has	
CC	selectivity for c-Met that is at least 100 times greater than their	
CC	selectivity for insulin like growth factor I receptor. This sequence	
CC	corresponds to the antibody 9.1.2 heavy chain used in the invention.	
XX		
SQ	Sequence 480 AA;	
	Query Match 90.7%; Score 2159.5; DB 9; Length 480;	
	Best Local Similarity 88.5%; Pred. No. 6.3e-122;	
	Matches 409; Conservative 17; Mismatches 19; Indels 17; Gaps 3;	
Qy	1 QVQLQESGCLVKPSQTLSTCTVSGSISSGNGYNWIRQHPGKLEWIGYIYYSQNTY 60	
Db	20 QVQLQESGPGLVKPSQTLSTCTVSGSISSGNGYNWIRQHPGKLEWIGYIYYSQNTY 79	
Qy	61 YNPISLKRITISIDTSKQFSLTSSVTAADTAVYYCARDG-----GDADF- 106	

Db 80 YNPSLKSRVTIISVDTSKNQFSLKLSVTHADTAVYICARDGPGLCSSCTSCVTCGEYYY 139
QY 107 --DINGQGTMTVSSASTKGPSVFLPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA 164
Db 140 GMDVNGQGTTVTVSSASTKGPSVFLPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGA 199
QY 165 LTSGVHTPFAVLQSSGLYSLSSVTVVPSSSLGKTYYTCNVDHKPSNTKVDKVERKCCVE 224
Db 200 LTSGVHTPFAVLQSSGLYSLSSVTVVPSVSNFGTQTYTCNVDHKPSNTKVDKVERKCCVE 259
QY 225 CPSCAPEPLGGPSVFLPPPKDILMISRTPEVTCVVVDVSOEDPEVQFNWYVDGVEVH 284
Db 260 CPFCAPP-VAGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVH 318
QY 285 NAKTPREBQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKQGP 344
Db 319 NAKTPREBQFNSTFRVVSFLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPRE 378
QY 345 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFF 404
Db 379 PQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPMLDSDGSFF 438
QY 405 LYSRLTVDKSRWQEGNVFSCSVWHEALHNHYTQKSLSLGLK 446
Db 439 LYSKLTVDKSRWQGNVFSCSVWHEALHNHYTQKSLSLSPGK 480

RESULT 13

AAAB36206
ID AAB36206 standard; protein; 473 AA.
XX AAB36206;
XX US6135941-A.
PD 24-OCT-2000.
XX 27-MAR-1998; 98US-00049672.
PR 27-MAR-1998; 98US-00049672.
XX (INCY-) INCYTE PHARM INC.
PI Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
XX WPI; 2001-030926/04.
DR N-PSDB; AAC66522.
XX New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing immune
PT or cell proliferative disorders or infections.
XX Claim 1; Col 53-56; 54pp; English.

CC The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer

XX Sequence 473 AA;
SQ Query Match 90.0%; Score 2140; DB 4; Length 473;
Best Local Similarity 89.2%; Pred. No. 8.1e-121;
Matches 405; Conservative 18; Mismatches 23; Indels 8; Gaps 2;
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWMIROHPGKLEWIGYIYSGNTY 60
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWMIROHPGKLEWIGYIYSGNTL 79
QY 61 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYICARD----GGDAFDIMGQGTMY 115
Db 80 YNPSLKSRVTIISVDTSKNQFSLKLSVTAADTAVYICARDVDVGLRGNYGNDVWGQGTLV 139
QY 116 TVSSASTKGPSVFLPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTPFAV 175
Db 140 TVSSASTKGPSVFLPLAPSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTPFAV 199
QY 176 LQSSGLYSLSSVTVVPSSSLGKTYYTCNVDHKPSNTKVDKRVESK---YGPFCPCPAPE 232
Db 200 LQSSGLYSLSSVTVVPSSSLGKTQTYICNVNHKPSNTKVDKRVESKCDKTHTCPPCPAPE 259
QY 233 FLGGPSVFLPPPKDILMISRTPEVTCVVVDVSOEDPEVQFNWYVDGVEVHNAKTGP 292
Db 260 LLGGPSVFLPPPKDILMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTGP 319
QY 293 EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKQGPPEQVYTLPP 352
Db 320 EQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPAPIEKTISKAKQGPPEQVYTLPP 379
QY 353 SQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLTV 412
Db 380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLTV 439
QY 413 KSRWQEGNVFSCSVWHEALHNHYTQKSLSLGLK 446
Db 440 KSRWQGNVFSCSVWHEALHNHYTQKSLSLSPGK 473

RESULT 14

AAO30915
ID AAO30915 standard; protein; 580 AA.
XX AAO30915;
XX 22-SEP-2003 (first entry)
DE dI-NHS76 (gamma4h) (FN>AQ) -ala-IL2 (D20T) variant protein.
XX Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;
KW gene therapy; immunoglobulin; Ig; fusion protein; human; variant.
XX Homo sapiens.
OS Unidentified.
OS Chimeric.
XX WO2003048334-A2.
XX 12-JUN-2003.
PD 04-DEC-2002; 2002WO-US038780.
PF 04-DEC-2001; 2001US-0337113P.
PR 12-APR-2002; 2002US-0371966P.
XX (EMDL-) EMD LEXIGEN RES CENT CORP.
XX Gillies SD;
XX WPI; 2003-513757/48.
XX New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2
PT

Qy	301	VVS	VT	VL	VL	HQ	DL	NG	KE	YK	CV	SN	KL	PS	IE	KT	IS	KA	GO	PR	PO	VY	TL	PP	SO	EE	MT	KN	360				
Db	297	VVS	VT	VL	VL	HQ	DL	NG	KE	YK	CV	SN	KL	PS	IE	KT	IS	KA	GO	PR	PO	VY	TL	PP	SO	EE	MT	KN	356				
Qy	361	QV	SL	TCL	VK	GF	YP	SD	IA	VE	WE	SN	GO	PEN	NY	KT	TP	PP	VL	DS	DG	SD	FF	FL	YS	RL	TV	DK	SR	WO	EG	N	420
Db	357	QV	SL	TCL	VK	GF	YP	SD	IA	VE	WE	SN	GO	PEN	NY	KT	TP	PP	VL	DS	DG	SD	FF	FL	YS	RL	TV	DK	SR	WO	EG	N	416
Qy	421	VF	CS	VM	HE	AL	HN	HY	TQ	KS	LS	LS	LG	K																			
Db	417	VF	CS	VM	HE	AL	HN	HY	TQ	KS	LS	LS	LG	K																			

Search completed: December 17, 2005, 01:18:31
Job time : 180.048 secs

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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:10:58 ; Search time 33.7879 Seconds
(without alignments)
1270.061 Million cell updates/sec

Title: US-10-644-277-62
Perfect score: 2379
Sequence: 1 QVQLQESGPGLVKPSQTLSL.....MHEALHNHYTQKSLSLGLK 446

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1743	73.3	327	1 G4HU	Ig gamma-4 chain C
2	1605.5	67.5	326	1 G2HU	Ig gamma-2 chain C
3	1590.5	66.9	330	1 GHU	Ig gamma-1 chain C
4	1585	66.6	377	2 A60764	Ig gamma-3 chain C
5	1575	66.2	377	2 A23511	Ig gamma-3 chain C
6	1562.5	65.7	470	2 S22080	Ig heavy chain pre
7	1521.5	64.0	472	2 S31459	Ig gamma-1 chain r
8	1427.5	60.0	374	2 S69339	Ig heavy chain V r
9	1422	59.8	469	2 S37483	Ig gamma-2a chain
10	1411.5	59.3	446	2 S40295	Ig gamma-2a chain
11	1367	57.5	444	2 PC4336	monoclonal antibody
12	1311.5	55.1	474	1 G2M511	Ig gamma-2b chain
13	1303	54.8	475	2 S01321	Ig gamma-2b chain
14	1289.5	54.2	328	2 I47159	Ig gamma 2a chain
15	1283.5	54.0	328	2 I47160	Ig gamma 2b chain
16	1264.5	53.2	328	2 I47161	Ig gamma 3 chain c
17	1240.5	52.1	328	2 I47158	Ig gamma 1 chain c
18	1199	50.4	323	1 GHRB	Ig gamma chain C r
19	1162	48.8	329	1 G2GP	Ig gamma-2 chain C
20	1147	48.2	308	2 C30554	Ig heavy chain C r
21	1139.5	47.9	255	4 S31866	Ig gamma-1 chain C
22	1129.5	47.5	234	2 PT0207	Ig gamma chain C r
23	1124	47.2	333	2 PS0018	Ig gamma-2b chain
24	1118.5	47.0	326	2 PS0017	Ig gamma-1 chain C
25	1108.5	46.6	289	1 G3HUM1	Ig gamma-3 heavy c
26	1108	46.6	329	2 S00847	Ig gamma-2c chain
27	1106.5	46.5	324	1 G1MS	Ig gamma-1 chain C
28	1106.5	46.5	330	1 G2MSA	Ig gamma-2a chain
29	1103	46.4	327	2 S06611	Ig gamma-2 chain C

30	1101.5	46.3	393	1 G1MSM	Ig gamma-1 chain C
31	1101.5	46.3	399	1 G2MSAM	Ig gamma-2a chain
32	1099	46.2	335	1 G2MSAB	Ig gamma-2a chain
33	1098.5	46.2	329	1 G3MSC	Ig gamma-3 chain C
34	1090.5	45.8	398	1 G3MSM	Ig gamma-3 chain C
35	1085.5	45.6	277	2 I47162	Ig gamma 4 chain C
36	1084.5	45.6	322	2 PS0019	Ig gamma-2a chain
37	1049.5	44.1	405	1 G2MSBM	Ig gamma-2b chain
38	921.5	38.7	548	2 S38864	Ig epsilon chain C
39	908	38.2	220	2 A49444	Ig gamma-1 heavy c
40	822	34.6	549	2 S04845	Ig heavy chain pre
41	816.5	34.3	592	2 S25705	Ig mu chain - shee
42	765	32.2	241	2 S69131	Ig heavy chain (DO
43	735	30.9	249	2 S69340	Ig heavy chain VHI
44	734.5	30.9	246	2 S38950	Ig gamma chain - m
45	727	30.6	572	2 B46529	Ig Y heavy chain (

ALIGNMENTS

RESULT 1

G4HU

Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104; PMID:6299662
A:Accession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELL>
A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A>Note: the sequence was determined from the germline gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A:Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant r
A:Reference number: A90249; MUID:70207560; PMID:4192699
A:Accession: A90249
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
A:Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C:Genetics:

A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 111/1; 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	73.3%	Score 1743;	DB 1;	Length 327;
Best Local Similarity	100.0%;	Pred. No. 3.3e-93;		
Matches 327;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	120	ASTKGPSVFPLA	PCSRSTSESTAALGCLVKDYFPEPTVWSN	SGALTSGVHTFPAVLQSS 179
Db	1	ASTKGPSVFPLA	PCSRSTSESTAALGCLVKDYFPEPTVWSN	SGALTSGVHTFPAVLQSS 60
Qy	180	GLYSLSSVTVF	SSSLGTYTTCNVDPKPSNTKVDKRVESKY	GPPCPAPFELGGPSV 239
Db	61	GLYSLSSVTVF	SSSLGTYTTCNVDPKPSNTKVDKRVESKY	GPPCPAPFELGGPSV 120

QY 240 FLPPPKPDTLMISRTPEVTCVVVDVSDDEPQVNFVYVGVVHNAKTKPREQFNSTY 299
DB 121 FLPPPKPDTLMISRTPEVTCVVVDVSDDEPQVNFVYVGVVHNAKTKPREQFNSTY 180
QY 300 RVSVLTVLHODWLNKGYCKVSNKGLPSSITEKTSKAKGQPREPQVYVTLPPSQEEMTK 359
DB 181 RVSVLTVLHODWLNKGYCKVSNKGLPSSITEKTSKAKGQPREPQVYVTLPPSQEEMTK 240
QY 360 NQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPPVLDSDGSFPLYSLRTVDKSRWQEG 419
DB 241 NQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPPVLDSDGSFPLYSLRTVDKSRWQEG 300
QY 420 NVFSCSVNHEALHNHYTQKSLSLGLK 446
DB 301 NVFSCSVNHEALHNHYTQKSLSLGLK 327

RESULT 2
G2HU
Ig gamma-2 chain C region - human
A:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
A:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFCC; GB:V00554; GB:J00230; NID:g32
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A:Cross-references: UNIPARC:UPI0000173791
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'B',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198-
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
A:Cross-references: UNIPARC:UPI0000173794
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds

R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lai
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,140-200,246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.5%; Score 1605.5; DB 1; Length 326;
Best Local Similarity 92.4%; Pred. No. 2.6e-85;
Matches 302; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 120 ASTKGPSVFLPAPCSRSTSESTAALGLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLOSS 179
DB 1 ASTKGPSVFLPAPCSRSTSESTAALGLVKDYFPEPVTVSNWNSGALTSGVHTFPAVLOSS 60
QY 180 GLYSLSVVTVPSSSLGKTTCNVNHHKPSNTKVDKRVESKYGPPCPCPAPEFLGGPSV 239
DB 61 GLYSLSVVTVPSSNFGTQYTCNVNHHKPSNTKVDKTVKCCVCEPCAPP-VAGPSV 119
QY 240 FLPPPKPDTLMISRTPEVTCVVVDVSDDEPQVNFVYVGVVHNAKTKPREQFNSTY 299
DB 120 FLPPPKPDTLMISRTPEVTCVVVDVSDDEPQVNFVYVGVVHNAKTKPREQFNSTF 179
QY 300 RVSVLTVLHODWLNKGYCKVSNKGLPSSITEKTSKAKGQPREPQVYVTLPPSQEEMTK 359
DB 180 RVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTSIKTKGQPREPQVYVTLPPSQEEMTK 239
QY 360 NQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPPVLDSDGSFPLYSLRTVDKSRWQEG 419
DB 240 NQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTPPPVLDSDGSFPLYSLRTVDKSRWQOG 299
QY 420 NVFSCSVNHEALHNHYTQKSLSLGLK 446
DB 300 NVFSCSVNHEALHNHYTQKSLSLSPGK 326

RESULT 3
G2HU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A93433; S36861; S3887; B90563; A90564; B91688; A91723; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370
A:Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, ;
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

F;103/Disulfide bonds: interchain (to light chain) #status experimental	
F;109,I112/Disulfide bonds: interchain (to heavy chain) #status experimental	
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental	
Query Match	66.9%; Score 1590.5; DB 1: Length 330;
Best Local Similarity	90.9%; Pred. No. 1.9e-84;
Matches 300; Conservative	12; Mismatches 15; Indels 3; Gaps 1;
QY	120 ASTKGPSVFPPLAPCSRSTSESTAALGLVKDYFPPEVTVSWNSGALTSGVHHTFPAVLQSS 179
DB	1 ASTKGPSVFPPLAPSSKSTSGTAAALGLVKDYFPPEVTVSWNSGALTSGVHHTFPAVLQSS 60
QY	180 GLYSLSVVTVPSSSLGTTKYTCNVDPKPSNTKVDKRVESK---YGPCCSCPAPEFLGG 236
DB	61 GLYSLSVVTVPSSSLGTTQTYICNVNHPKPSNTKVDKRVESKCDKTHTCPCPAPELLGG 120
QY	237 PSVFLPPPKPKDTLMSIRTPTEVTCVVVDVDSQEDPEVQFNMYVDGVEVHNNAKTKPREBQFN 296
DB	121 PSVFLPPPKPKDTLMSIRTPTEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREBQYN 180
QY	297 STYRVVSVLTVLHODWLNGKEYKCKVSNKGLPSSIEKTTISKAKGQPREPOVYTLPPSQEE 356
DB	181 STYRVVSVLTVLHODWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREPOVYTLPPSRDE 240
QY	357 MYKQVSVLCLVKGFYPSDIAVESWESNGPENNYKTPPVLDSDGSFPLYSLRTVDSKSRW 416
DB	241 LTKNQVSVLCLVKGFYPSDIAVESWESNGPENNYKTPPVLDSDGSFPLYSLRTVDSKSRW 300
QY	417 QEGNVFSCSVMHREALNNHYTKLSLSLQK 446
DB	301 QQGVFSCSVMHREALNNHYTKLSLSLPGK 330
RESULT 4	
A60764	
Ig gamma-3 chain C region, form IaT - human	
C;Species: Homo sapiens (man)	
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004	
C;Accession: A60764	
R;Huck, S.; Lefranc, G.; Lefranc, M.P.	
Immunogenetics 30, 250-257, 1989	
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG	
A;Reference number: A60764; MUID: 90007613; PMID: 2571587	
A;Accession: A60764	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-377 <HUC>	
A;Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI00000176F0B	
C;Superfamily: immunoglobulin homology	
C;Keywords: immunoglobulin	
F;20-85/Domain: immunoglobulin homology <IMM>	
Query Match	66.6%; Score 1585; DB 2: Length 377;
Best Local Similarity	80.6%; Pred. No. 4.6e-84;
Matches 304; Conservative	8; Mismatches 15; Indels 50; Gaps 1;
QY	120 ASTKGPSVFPPLAPCSRSTSESTAALGLVKDYFPPEVTVSWNSGALTSGVHHTFPAVLQSS 179
DB	1 ASTKGPSVFPPLAPCSRSTSGTAAALGLVKDYFPPEVTVSWNSGALTSGVHHTFPAVLQSS 60
QY	180 GLYSLSVVTVPSSSLGTTKYTCNVDPKPSNTKVDKRVESK----- 220
DB	61 GLYSLSVVTVPSSSLGTTQTYICNVNHPKPSNTKVDKRVELKTPPLGDTTHTCPCPEPKSC 120
QY	221 -----YGPCCSCPAPEFLGGSVFLFPKPKDT 249
DB	121 DTPPPCPCPEPKSCDTPPPCPCPEPKSCDTPPPCPCPAPELLGGSVFLFPKPKDT 180
QY	250 LMTSRTPEVTCVVVDVDSQEDPEVQFNWYVDGVEVHNNAKTKPREBQFNSTYRWSVLTVLH 309
DB	181 LMTSRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNNAKTKPREBQYNSTPRVSVLTVLH 240
QY	310 QDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYTLPPSQEEMTKNQVSLTCLVK 369

Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISTKGPREFQVYTLPPSREEMTKQVSLTCLVK 300
QY 370 GYPGSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNMFVSCVMHE 429
Db 301 GFYPGSDIAVEWESSGQPENNYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNMFVSCVMHE 360
QY 430 ALHNHYTQKSLSLGLK 446
Db 361 ALHNRFQKSLSLSPGK 377

RESULT 5
A23511
Ig gamma-3 chain C region (allotype G3m(b)) - human
C:Species: Homo sapiens (man)
C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
C:Accession: A23511
R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
Nucleic Acids Res. 14, 1779-1789, 1986
A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c
A:Reference number: A23511; MUID:86148507; PMID:3081877
A:Accession: A23511
A:Keywords: immunoglobulin
A:Molecule type: DNA
A:Residues: 1-377 <HUC>
A:Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12958; NID:G33070; PIDN:CAA272

C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 66.2%; Score 1575; DB 2; Length 377;
Best Local Similarity 79.6%; Pred. No. 1.7e-83;
Matches 300; Conservative 12; Mismatches 15; Indels 50; Gaps 1;

QY 120 ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSS 179
Db 1 ASTKGPSVFPLAPCSRSTSGGTAAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAVLQSS 60
QY 180 GLYSLSVVTVPSLSLGYTKYTCNVVDHKPSNTKVDKRVESK----- 220
Db 61 GLYSLSVVTVPSLSLGTQYTCNVNHRKPSNTKVDKRVELKTPLDGDTHTTCPRCEPKSC 120
QY 221 -----YGPSPCPAPPEFLGGPSVFLFPPPKPDT 249
Db 121 DTPPPCPCEPKSCDTPPPCPCEPKSCDTPPPCPAPPEFLGGPSVFLFPPPKPDT 180

QY 250 LMISRTPEVTCVVVDVSDPEQFNWYVDGVEFHNAKTKPREEQFNSTYRVSVSLTVLH 309
Db 181 LMISRTPEVTCVVVDVSHEDPEVQFKWYVDGVEFHNAKTKPREEQFNSTYRVSVSLTVLH 240
QY 310 QDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGPRFPQVYTLPPSREEMTKQVSLTCLVK 369
Db 241 QDWLNGKEYKCKVSNKALPAPIEKTISTKGPREFQVYTLPPSREEMTKQVSLTCLVK 300

QY 370 GYPGSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSRLTVDKSRWQEGNMFVSCVMHE 429
Db 301 GFYPGSDIAVEWESSGQPENNYNTTPPVLDSDGSFFLYSRLTVDKSRWQEGNMFVSCVMHE 360
QY 430 ALHNHYTQKSLSLGLK 446
Db 361 ALHNRFQKSLSLSPGK 377

RESULT 6
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (clone 8.10)
C:Species: Bos primigenius taurus (cattle)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080
A:Accession: S22080
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-470 <SAN>
A:Cross-references: UNIPARC:UPI0000116007; EMBL:X62916; NID:G439; PIDN:CAA44699.1; PID:G4
R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma
A:Reference number: S06610; MUID:90097956; PMID:2513487
A:Accession: S06610
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: UNIPARC:UPI0000176F36; EMBL:X16701
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: IG CH gamma-1
A:Introns: 98/1; 111/1; 221/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F:161-225/Domain: immunoglobulin homology <IMM>
F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.7%; Score 1562.5; DB 2; Length 470;
Best Local Similarity 66.5%; Pred. No. 1.2e-82;
Matches 302; Conservative 49; Mismatches 92; Indels 11; Gaps 6;

QY 1 QVQLQESGPGLVKPSQTLSTLTCTVSGGSISSGGNWNWIRHCPGLEWICVIYSGNTY 60
Db 20 QVQLRESGPSLVKPSQTLSTLTCTVSGFSLSSYA--LTWVROAPKALEWVGGITSGGT 77

QY 61 YNPALKSRITISIDTSKNQFSLTLSSVTAADTAVVYCAR----DGGDDAF-DINGQGTMV 115
Db 78 YNPALKSRLSITKENSQSVLSVSVTPEDTATYYCARSTYGEVGDGAIADANGQGLLV 137

QY 116 TVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWMNSGALTSGVHTFPAV 175
Db 138 TVSSASTTAPKVPYPLSLSCCGDKSSSTVTLGCLVSYMPPEPTVTWNSGALKSGVHTFPAV 197

QY 176 LQSSGLYSLSVVTVPSLSLGTQYTCNVVDHKPSNTKVDKVESEKYP-PCPSCPAPEFL 234
Db 198 LQSSGLYSLSVMVTVPGSTSG-QTFTCNVAPASSTKVDKAVDPTCKPSPCDCCPPPELP 256

QY 235 GGPSVFLFPPPKPDKDTLMISRTPEVTCVVVDVSDPEQFNWYVDGVEFHNAKTKPREEQ 294
Db 257 GGPSVFLFPPPKPDKDTLISGTPETVTCVVVDGHDDEPKFSWFDVVDVNTATTKPREEQ 316

QY 295 FNSTYRVSVSLTVLHQDLNKGKYCKVSNKGLPSSIEKTIISKAKGPRFPQVYTLPPSQ 354
Db 317 FNSTYRVVSALRIHQDWTGGKPKVHNEGLPAPIVTRTISRKTGPAREPVVYVLAPPQ 376

QY 355 EEMTKNQVSLTCLVKGYFPPSDIAVEWESNGCP--ENNYKITPPVLDSDGSFSLSLTVTD 412
Db 377 EELSKSTVSLTCMWTSFYPPDYIAVEWQRNGQPESEDKYGTTPPQLDADSSVFLYSKLKRD 436

QY 413 KSRWQEGNFSVCSVMHEALHNHYTQKSLSLGLK 446
Db 437 RNSWQEGDGYTCVVMHEALHNHYTQKSLSKAGK 470

RESULT 7
S31459
Ig gamma-1 chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31459
R:Patrici, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A:Reference number: S31459

A:Accession: S31459
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-472 <PAT>
A:Cross-references: UNIPARC:UPI0000176F35; EMBL:X69797
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 64.0%; Score 1521.5; DB 2; Length 472;
Best Local Similarity 63.6%; Pred. No. 2.6e-80;
Matches 293; Conservative 54; Mismatches 93; Indels 21; Gaps 5;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSGSISSGNGYNWIRQHPGKLEWIGYIYSGNTY 60
DB 18 QVRLQESGSLATLLQTLSTVCTCTSSLNNG--VDWVRQAPGKALEWIGSGYDEID 75
QY 61 YNPISLRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGGD-----AFDIWGQT 113
DB 76 YNPVLSRLSITKDTSKSQVSLTSLVTTEDTAAYVYCARVDYDSSHAPAYASYDFMG 135
QY 114 MVTVSASTKGPSVFPPLAPCSRSTSSSTAALGCLVKDYPPPEPTVSWNSGALTS 173
DB 136 LISVLSASTTPPKVYELTSCGDTSSIVTLGCLVSSYMPPEPTVVTWNSGALTS 195
QY 174 AVLOSGLYSLSSVTVPPSSLTGKTYTCNVDRHKPSNTKVDKVESKYGPPCP 227
DB 196 AILQSSGLYSLSSVTVPPASTSGAQTFCINVAHPASSTKVDKRVE-----PGCPDPCKHCR 251
QY 228 CPAPEFLGGPSVFLFPKPKDLMISRTPEVTCVVVDVSDPEVDQFNWYVDGVEVHNAK 287
DB 252 CPPPELPGGPSVFIFFPKPKDILITISGTEVTCVVVDVQDDPEVQSFNVDNVEV 311
QY 288 TKPREQFNSTYRWVSVLTVLHODWLNKGYCKVKNKGLPSSIETKISKAKGQPRE 347
DB 312 TKPREQFNSTFRVVSALPIQHODWGTGKEFKCKVHNEALPAPIVRTISRTKGQARE 371
QY 348 YTLPPQSEMTKNQVSLTCLVKGFYPSDIAVEVSNQGP--ENNYKTPPPVLDSDGSP 405
DB 372 YVLAPEQELSKSTLSVTCLVTFYFDYIAVEQKNGQPESEDKYGTITTSQLDADGS 431
QY 406 YSRLTVDKSRWQNGVFNCSVMEALHNYTKSLSLGK 446
DB 432 YSRLRVDKNSWQEGDYACVVMHEALHNYTKSLSPCK 472

RESULT 8
S69339
IG heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C:Accession: S69339; S72664
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; PMID:95262687; PMID:7744049
A:Accession: S69339
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
R:Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140, 'C', 142-374 <KH2>
A:Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 60.0%; Score 1427.5; DB 2; Length 374;
Best Local Similarity 62.7%; Pred. No. 5e-75;

Matches 282; Conservative 27; Mismatches 42; Indels 99; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSGSISSGNGYNWIRQHPGKLEWIGYIYSGNTY 60
DB 20 QITLKESGPTLVKPTQTLTCTTSGFSLSKSGVGVIRQPPGQALEWALIFWDDDKR 79
QY 61 YNPISLRITISIDTSKNQFSLTSSVTAADTAAYVYCARD-----GGDAFDIWGQ 116
DB 80 YSPSLRTRLTITKDTSKNQVVLTMVNDPADTATYCYGYSVEGYGQYRFHSGQGT 139
QY 117 VSSASTKGPSVFPPLAPCSRSTSSSTAALGCLVKDYFPEPTVTVSWNSGALTS 176
DB 140 VSS-----EPKSCD----- 148
QY 177 QSSGLYSLSSVTVPPSSLTGKTYTCNVDRHKPSNTKVDKVESKYGPPCPSP 236
DB 149 -----KTHT-----CPPCPAPPELLGG 164
QY 237 PSVFLFPPPKDLMISRTPEVTCVVVDVSDPEVDQFNWYVDGVEVHNAKTPRE 296
DB 165 PSVFLFPPPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPRE 224
QY 297 STYRVSVLTVLHODWLNKGYCKVKNKGLPSSIETKISKAKGQPREQV 356
DB 225 STYRVSVLTVLHODWLNKGYCKVKNKGLPSSIETKISKAKGQPREQV 284
QY 357 MTKNQVSLTCLVKGFYPSDIAVEVSNQGPENNYKTPPPVLDSDGSPFLYSL 416
DB 285 MTKNQVSLTCLVKGFYPSDIAVEVSNQGPENNYKTPPPVLDSDGSPFLYSL 344
QY 417 QSGNVFSCVSMHEALHNYTKSLSLGK 446
DB 345 QSGNVFSCVSMHEALHNYTKSLSLGK 374

RESULT 9
S37483
IG gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: UNIPARC:UPI000002FB47; EMBL:X70423; NID:G406252; PIDN:CAA49868.1; PII:61
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 59.8%; Score 1422; DB 2; Length 469;
Best Local Similarity 59.7%; Pred. No. 1.3e-74;
Matches 271; Conservative 71; Mismatches 100; Indels 12; Gaps 7;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSGSISSGNGYNWIRQHPGKLEWIGYIYSGNT 59
DB 20 QIQLOQSGPELVKPGASVKISCKASGYTFD--YYINWVKQKPGQGLKIGWIPAS 77
QY 60 YNPISLRITISIDTSKNQFSLTSSVTAADTAAYVYCARDGGDDA--FDI 117
DB 78 KYNENFKGATLTVDTSSSTAYMQLSSLTSEDYAVFCARAMGATATLLDYGQ 137
QY 118 SSASTKGPSVFPPLAPCSRSTSSSTAALGCLVKDYFPEPTVTVSWNSGALTS 177
DB 138 SSAKTTPASVYPLAPVCGDTGSSVTGLCLVKGYFPEPTVTLWNSGSLSSG 197
QY 178 SGLYSLSSVTVPPSSLTGKTYTCNVDRHKPSNTKVDKVESKYGP---PCP-- 232
DB 198 SD-LYTLSSSVTVTSWPSQITCNVAHPASSTKVDKIEPR-GPTIKPCPPCK 255

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QY 233 FLGGPSVFLFPKPKDQTLMIKSRTEVTCVVVDVSDQEDPEVQFNWYVDGVGVHNAKTKPRE 292
Db 256 LUGGSPVFIFFPKIKDKVLMISLSPITVCVVVDVSDDDPDQVQISWVFNNVVHTAQQTQHR 315
QY 293 EGFNSTYRVVSVLTCLVKGFPSPDIAVEWESNGQPNENYKTTTPVLDSDGSGFFLYSRLTVDK 352
Db 316 EDYNSLTRVVSALPIQHODWMSGKFKCKVNNKDLPAPIERTISKPKSVRAQVYVVLPP 375
QY 353 SOEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSGFFLYSRLTVD 412
Db 376 PREEMTKQVLTLCMTDPMEDIVYVETWNGKTELNYKNTPEVLDSDGSGYFMYSKLRVE 435
QY 413 KRWQEGNVFSCVMHEALHNNHYTKOKLSLSLKG 446
Db 436 KQWVERNSYSCSVVHGLEHNNHHTTKFSRTPGK 469

RESULT 10
S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: S40295
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bi
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
A:Cross-references: UNIPROT:Q99L25; UNIPARC:UPI0000176F38
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMW>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Aen) (covalent) #status experimental

Query Match 59.3%; Score 1411.5; DB 2; Length 446;
Best Local Similarity 59.6%; Pred. No. 5.1e-74;
Matches 269; Conservative 71; Mismatches 100; Indels 11; Gaps 7;

QY 1 QVQLQESGGLVKPSQTLISLTCTVSGGSISSGGNYNNIRQHPGKLEWIGYIY-YSQNT 59
Db 1 QIQLOQSGPELVRPGASVKISCKASGYFTD--YIHWVKORPGGLEWIGWYIPGSGNT 58
QY 60 YNPISLKSRIITISIDTSKNQFSLTSSVTAADTAIVYICARDGGDDAFDIWGQGTMTVYSS 119
Db 59 KYNEKFKGKATLTVDTSSSTAYMQLSLTSEDSAVYFCAR--GGKFAMDYWGQGTMTVYSS 117
QY 120 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 179
Db 118 AKTTAPSVYPLAPVCGDITGSSVTLGCLVKGYFPEPTVTLWNSGSLSSGVHTFPAVLQSD 177
QY 180 GLYSLSVVTVPSSSLGKTKYTCNVDHKPSNTKVDKRVESKGP---PCP--SCPAPDFL 234
Db 178 -LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKLEPR--GPTIKPCPCPKCPAPNLL 235
QY 235 GGPSVFLFPKPKDQTLMIKSRTEVTCVVVDVSDQEDPEVQFNWYVDGVGVHNAKTKPREEQ 294
Db 236 GGPSVFIFFPKIKDKVLMISLSPMTVCVVVDVSDDDPDQVQISWVFNNVVHTAQQTQHR 295
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QY 295 FNSTYRVVSVLTCLVKGFPSPDIAVEWESNGQPNENYKTTTPVLDSDGSGFFLYSRLTVDK 354
Db 296 YNSTLTRVVSALPIQHODWMSGKFKCKVNNKDLPAPIERTISKPKSVRAQVYVVLPPPE 355
QY 355 EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTTPVLDSDGSGFFLYSRLTVDK 414
Db 356 EEMTKQVLTLCMTDPMEDIVYVETWNGKTELNYKNTPEVLDSDGSGYFMYSKLRVEK 415
QY 415 RWQEGNVFSCVMHEALHNNHYTKOKLSLSLKG 445
Db 416 NWVERNSYSCSVVHGLEHNNHHTTKFSRTPG 446

RESULT 11
PC4336
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: PC4436
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kanachi, M.; Harada, A.;
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277; PMID:9398605
A:Accession: PC4436
A:Molecule type: protein
A:Residues: 1-444 <AKA>
A:Cross-references: UNIPARC:UPI0000176F41
C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:251-320/Domain: immunoglobulin homology <IMW>
F:22/Disulfide bonds: interchain (to 98) #status predicted
F:99/Disulfide bonds: interchain (to 109) #status predicted

Query Match 57.5%; Score 1367; DB 2; Length 444;
Best Local Similarity 58.0%; Pred. No. 1.8e-71;
Matches 262; Conservative 69; Mismatches 107; Indels 14; Gaps 7;

QY 1 QVQLQESGGLVKPSQTLISLTCTVSGGSISSGGNY--NNIRQHPGKLEWIGYIYSGNT 59
Db 1 EVQXVETGGGLVRPQNSKLSLTSGTFTFS---NYRMHLRQPPGKRLIEWIAVITVKSDN 57
QY 60 Y---YNPISLKSRIITISIDTSKNQFSLTSSVTAADTAIVYICARDGGDDAFDIWGQGTMTV 116
Db 58 YGAKYAESVGRFTISRDDSKSVYLQWNLREEDTAIYCCRTPTWYVYAMDCWQGTSTVI 117
QY 117 VSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVL 176
Db 118 VSSAKTTPPSVYPLAPGSAQTNSMVTLGCLVKGYFPEPTVTVWNSGSLSSGVHTFPAVL 177
QY 177 QSGLYLSLVTVPSSSLGKTKYTCNVDHKPSNTKVDKRVESK--YGPSPCPAPDFL 234
Db 178 QSD--LYTLSSSVTVPSSTWPSSTETVCNVAHPASSTKVDKIVPRDCGCKPC-ICTVPEV- 234
QY 235 GGPSVFLFPKPKDQTLMIKSRTEVTCVVVDVSDQEDPEVQFNWYVDGVGVHNAKTKPREEQ 294
Db 235 --SSVFIFFPKPKDQTLITTPKVICVVVDLSKDDPEVQFSWFVDDVEVHTAQTPREEQ 292
QY 295 FNSTYRVVSVLTCLVKGFPSPDIAVEWESNGQPNENYKTTTPVLDSDGSGFFLYSRLTVDK 354
Db 293 FNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPAPAPIEKTISKTKGRKAPQVVTIPPK 352
QY 355 EEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPNENYKTTTPVLDSDGSGFFLYSRLTVDK 414
Db 353 EQMAKDKVSLTMITDFPEDITVEWQMGQPAENYKNTQIMDTDGSYFYYSKLNVOQS 412
QY 415 RWQEGNVFSCVMHEALHNNHYTKOKLSLSLKG 446
Db 413 NWEAGNTFTCSVLHGLEHNNHHTTKSLSHSPGK 444

RESULT 12
G2MS11
Ig gamma-2b chain - mouse
```

Query Match	55.1%	Score 1311.5	DB 1	Length 474
Best Local Similarity	55.0%	Pred. No. 38-68		
Matches 252	Conservative	72	Mismatches 119	Indels 15
Gaps				5
QY	1	QVQLQESGPGLVKPKSQTLSLCTVTSGGSISSGGNYWNWIRHQHPGKLGLEWIGYIY-YSGNT	59	
DB	20	EVQLQSGPELVPCGASVKMSCKASGYTFIT-VYMHVVKQPKGQGLEWIGYINPNKDKGT	77	
QY	60	YYPNPLSKRITISIDTSKNQPSLTLSVTAADTAATVYVCARDGGDDAFDIWGQGTMTVTVSS	119	
DB	78	KNEKFKGKATITSDKSSNTAYMELSSLTSEDSAVYICARDYDYDMFAYWGQGLVTVSA	137	
QY	120	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQSS	179	
DB	138	AKTTPSVYPLAPGCGDITGSSVTSCLVKGYFPEPVTVTWNSGSLSSVHTLSQALLQS	197	
QY	180	GLYSLSVVTVTPSSSLGTITCTYCNVDHKPSNTKVDKRVESKYGP-----PCP-----SC	228	
DB	198	GLYTWSSSVTVPSSTWPSQTVCVAHPASSITVDVKKLEPS-GPISITINPCPCKECHKC	256	
QY	229	PAPEFLGSPSVLPFPKPKDTLMISPTPEVTCVVDVDSQSDPEVQFNWYDGVGVHNAKT	288	
DB	257	PAPNLEGSPSVIFPPNIKIDVLMISLTPKVCVVDVSEDDPDVQISFWVNNVEVHTAQT	316	
QY	289	KPREQFNSITYRWVSVLVTLVHODWLNGKEYCKVSNKGLPSSIEKTIISKAKGQPREPQVY	348	
DB	317	QTHREDYNTIRVSVTLPTQHODMWSGKEFKCKVNKKLPSPITERTISKIKGLVRAPOVY	376	
QY	349	TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLVDSGDSFPFLYSR	408	
DB	377	ILPPAPAEQLSRKDVSLTCLVGVNPGPDISVEWTSNGHTTEENYKDTAPVLDSGDSGYFIYSK	436	
QY	409	LTVDSKRWQEGVNFVSCSVVMEALHNHYTOKSLSLSLCK 446		
DB	437	LNWKTSKWEKTDTSFCNVRHGLKNYLLKTTISRSPGK 474		
RESULT 13				
S01321				
Ig gamma-2b chain precursor - mouse				
C:Species: Mus musculus (house mouse)				
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999				
C:Accession: S01321				
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.				
Eur. J. Biochem. 176, 287-295, 1988				
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin				
A:Reference number: S01320; PMID:88329081; PMID:3138116				
A:Accession: S01321				
A:Molecule type: mRNA				
A:Residues: 1-475 <DE1>				
A:Cross-references: UNIPARC:UPI0000115DDDB; EMBL:X13188; NID:G51780; PIDN:CAA315				
F:1-19/Domain: signal sequence #status predicted <SIG>				
F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>				
F:159-223/Domain: immunoglobulin homology <IMM>				
C:Superfamily: immunoglobulin C region; immunoglobulin homology				
C:Keywords: immunoglobulin				

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:10:08 ; Search time 204.079 Seconds
(without alignments)
1541.883 Million cell updates/sec

Title: US-10-644-277-62
Perfect score: 2379
Sequence: 1 QVQLQESGGLVKPSQTLSL.....MHEALNNHYTKSLSLGK 446

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2146	90.2	476	2	Q6MXZ7_HUMAN	Q6mxz7 homo sapien
2	2144.5	90.1	473	2	Q8TC63_HUMAN	Q8tc63 homo sapien
3	2127.5	89.4	476	2	Q6GMX1_HUMAN	Q6gmxi homo sapien
4	2074	87.2	465	2	Q6GMX6_HUMAN	Q6gmxi6 homo sapien
5	1919.5	80.7	466	2	Q6IN78_HUMAN	Q6in78 homo sapien
6	1918.5	80.6	470	2	Q6PJA4_HUMAN	Q6pj44 homo sapien
7	1900	79.9	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
8	1896.5	79.7	464	2	Q6MZU6_HUMAN	Q6mzu6 homo sapien
9	1893.5	79.6	478	2	Q6PI81_HUMAN	Q6pi81 homo sapien
10	1893	79.6	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
11	1892	79.5	475	2	Q5EP85_HUMAN	Q5ef85 homo sapien
12	1886.5	79.3	470	2	Q7Z5W1_HUMAN	Q7z5w1 homo sapien
13	1883	79.2	469	2	Q569F4_HUMAN	Q569f4 homo sapien
14	1880.5	79.0	472	2	Q6N089_HUMAN	Q6n089 homo sapien
15	1879	79.0	475	2	Q6MZQ6_HUMAN	Q6mzq6 homo sapien
16	1875.5	78.8	480	2	Q6N094_HUMAN	Q6n094 homo sapien
17	1874	78.8	544	2	Q6PJ95_HUMAN	Q6pj95 homo sapien
18	1871.5	78.7	482	2	Q7Z3S1_HUMAN	Q7z3s1 homo sapien
19	1863.5	78.3	466	2	Q6N096_HUMAN	Q6n096 homo sapien
20	1862.5	78.3	470	2	Q68CN4_HUMAN	Q68cn4 homo sapien
21	1859	78.1	473	2	Q6P055_HUMAN	Q6p055 homo sapien
22	1855	78.0	475	2	Q6GMW7_HUMAN	Q6gmw7 homo sapien
23	1850	77.8	521	2	Q8N4Y9_HUMAN	Q8n4y9 homo sapien
24	1844	77.5	417	2	Q6N093_HUMAN	Q6n093 homo sapien
25	1839.5	77.3	518	2	Q6N030_HUMAN	Q6n030 homo sapien
26	1838.5	77.3	480	2	Q6PJF1_HUMAN	Q6pjf1 homo sapien
27	1835	77.1	475	2	Q6N095_HUMAN	Q6n095 homo sapien
28	1830	76.9	469	2	Q7Z7P5_HUMAN	Q7z7p5 homo sapien
29	1826	76.8	519	2	Q5EBM2_HUMAN	Q5ebm2 homo sapien
30	1804	75.8	475	2	Q3RE17_PONPY	Q3re17 pongo pygma
31	1804	75.8	481	2	Q6N097_HUMAN	Q6n097 homo sapien

32	1743	73.3	327	1	IGHG4_HUMAN	P01861 homo sapien
33	1661.5	69.8	348	2	Q6PYX1_HUMAN	Q6pyx1 homo sapien
34	1605.5	67.5	326	1	IGHG2_HUMAN	P01859 homo sapien
35	1590.5	66.9	230	1	IGHG1_HUMAN	P01857 homo sapien
36	1571	66.0	509	2	Q8NF17_HUMAN	Q8nf17 homo sapien
37	1501	63.1	469	2	Q8M839_RAT	Q8m839 rattus norv
38	1470	61.8	354	2	Q86TT2_HUMAN	Q86tt2 homo sapien
39	1450.5	61.0	458	2	Q5M842_RAT	Q5m842 rattus norv
40	1416	59.5	467	2	Q4VBH1_RAT	Q4vbh1 rattus norv
41	1408	59.2	465	2	Q5I0J0_RAT	Q5i0j0 rattus norv
42	1407	59.1	473	2	Q9D8L4_MOUSE	Q9d8l4 mus musculu
43	1405.5	59.1	468	2	Q569B4_RAT	Q569b4 rattus norv
44	1399.5	58.8	468	2	Q569W9_MOUSE	Q569w9 mus musculu
45	1395	58.6	463	2	Q99LC4_MOUSE	Q99lc4 mus musculu

ALIGNMENTS

RESULT 1
Q6MXZ7_HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6MXZ7;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686M24218.
GN Name=DKFZp686M24218;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Robo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640824; CAE45900.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6MXZ7; 28-472.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00230; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52420 MW; 0D3D1FFE5853958F CRC64;

Query Match 90.2%; Score 2146; DB 2; Length 476;
Best Local Similarity 89.8%; Pred. No. 3.2e-143;
Matches 404; Conservative 13; Mismatches 29; Indels 4; Gaps 1;

QY	1	QVQLQESGGLVKPSQTLSLTCTVSGGISSSGGYNNWIRQHPGKGLIEWIGIYYSGNTY	60
DB	27	QLQLQESGGLVKASQTLSLTCSVPGYISDSSSYGWINRQPPGQGLIEWIGTVSYSGTPY	86
QY	61	YNPSLKSRITISIDTSKNQFSLTSSVTADTAVYYCARDGG-----DDAPDIWGQGTMTV	116
DB	87	YTFSLKSLRTHIVDPSKSIQIFNLTSVTADTAVYYCVRHGGYSFASAYPFPGQCAPVT	146
QY	117	VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL	176
DB	147	VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVL	206

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QY 177 QSSGLYSSVVTVPSSSISLGTQTYTCNVHDHPSNTKVDKRVESKYGPCCPAPERFGLG 236
Db 207 QSSGLYSSVVTVPSSSISLGTQTYTCNVHDHPSNTKVDKRVESKYGPCCPAPERFGLG 266
QY 237 PSVFLFPKPKDMLMSRTPEVTCVVVDVDSQEDPEVQFNWYVDGVEVHNATKPREEQFN 296
Db 267 PSVFLFPKPKDMLMSRTPEVTCVVVDVDSQEDPEVQFNWYVDGVEVHNATKPREEQFN 326
QY 297 STYRVVSVTLVHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEE 356
Db 327 STYRVVSVTLVHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEE 386
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKYKTPPVLDSDGSPFLYSRLTVDKSRW 416
Db 387 MTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKYKTPPVLDSDGSPFLYSRLTVDKSRW 446
QY 417 QGNNVFSVSMHEALHNHYTQKSLSLGLK 446
Db 447 QGNNVFSVSMHEALHNHYTQKSLSLGLK 476

RESULT 2
Q8TC63 HUMAN
ID Q8TC63 HUMAN PRELIMINARY; PRT; 473 AA.
AC Q8TC63
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.C1.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
```

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DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Immunoglobulin domain.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;

Query Match 90.1%; Score 2144.5; DB 2; Length 473;
Best Local Similarity 90.6%; Pred. No. 4e-143;
Matches 405; Conservative 14; Mismatches 27; Indels 1; Gaps 1;

QY 1 QVQLQESGPGLVKPQSQTLSLTCTVSGGSISSGGYNNWIRHQHKGLEWIGYIYSGNTY 60
Db 27 RLQLQESGPGLVKPQSQTLSLTCTVSGGSISSGGYNNWIRHQHKGLEWIGYIYSGNTY 86
QY 61 YNPISLKRITISIDTSKNQPSLTLSSTVAADTAIYICARDGGDDAFDI-WQOQTMTVVS 119
Db 87 YSPSLRSRVTSADMSSENFYKLDLSVTAADTAIYICAAAGHLVNGFGAHWGQGLVSVSP 146
QY 120 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 179
Db 147 ASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 206
QY 180 GLYSLSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPCCPAPERFGLGSPV 239
Db 207 GLYSLSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPCCPAPERFGLGSPV 266
QY 240 FLPPPKPKDMLMSRTPEVTCVVVDVDSQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 299
Db 267 FLPPPKPKDMLMSRTPEVTCVVVDVDSQEDPEVQFNWYVDGVEVHNATKPREEQFNSTY 326
QY 300 RVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 359
Db 327 RVSVLTVLHQDLWNGKEYCKVSNKGLPSSIEKTSKAKGQPREPQVYTLPPSQEEMTK 386
QY 360 NQVSLTCLVKGFYPSDIAVEWESNGOPENNPKYKTPPVLDSDGSPFLYSRLTVDKSRWQEG 419
Db 387 NQVSLTCLVKGFYPSDIAVEWESNGOPENNPKYKTPPVLDSDGSPFLYSRLTVDKSRWQEG 446
QY 420 NVFSCSVSMHEALHNHYTQKSLSLGLK 446
Db 447 NVFSCSVSMHEALHNHYTQKSLSLGLK 473

RESULT 3
Q6GMX1 HUMAN
ID Q6GMX1 HUMAN PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AAH25985.1; -, mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.C1.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
```


RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 89.4%; Score 2127.5; DB 2; Length 476;
Best Local Similarity 88.2%; Pred. No. 6.5e-142;
Matches 403; Conservative 20; Mismatches 23; Indels 11; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNWIROHPGKGLEWIGIYYSGNTY 60
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNWIROHPGKGLEWIGIYYSGNTY 79

QY 61 YNPILSKRITISIDTSKNQFSLTSSVTAADTAAYVCARDG-----GDDAFDIWGOG 112
DB 80 YNPILSKRITISIDTSKNQFSLTSSVTAADTAAYVCARDG-----GDDAFDIWGOG 139

QY 113 TMTVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTF 172
DB 140 TMTVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTF 199

QY 173 PAVLQSGSLYSLSVTVTPSSSLGKTYYTNCVNHKPSNTKVDKRVESK---YGPCCPSCP 229
DB 200 PAVLQSGSLYSLSVTVTPSSSLGKTYYTNCVNHKPSNTKVDKRVESK---YGPCCPSCP 259

QY 230 APFLGSGPSVFLPAPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNAKTK 289
DB 260 APFLGSGPSVFLPAPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNAKTK 319

QY 290 PREEQFNSTYRVSVLTFLVLDHQLNGKEYKCKVSNKGLPSSIEKTIKAKQGPPEQVYT 349
DB 320 PREEQFNSTYRVSVLTFLVLDHQLNGKEYKCKVSNKGLPSSIEKTIKAKQGPPEQVYT 379

QY 350 LPSPQEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSRL 409
DB 380 LPSPQEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSRL 439

QY 410 TVDKSRWQEGNVFSCSVNHEALHNYTKQSLSLGK 446
DB 440 TVDKSRWQEGNVFSCSVNHEALHNYTKQSLSLGK 476

RESULT 4
Q6GMX6 HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766.1; -; mRNA.
GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 87.2%; Score 2074; DB 2; Length 465;
Best Local Similarity 88.4%; Pred. No. 3.8e-138;
Matches 397; Conservative 19; Mismatches 27; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNWIROHPGKGLEWIGIYYSGNTY 60
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNWIROHPGKGLEWIGIYYSGNTY 77

QY 61 YNPILSKRITISIDTSKNQFSLTSSVTAADTAAYVCARDGDDAFDIWGQTMVTVSSA 120
DB 78 YNPILSKRITISIDTSKNQFSLTSSVTAADTAAYVCARDGDDAFDIWGQTMVTVSSA 136

QY 121 STKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
DB 137 STKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 196

QY 181 LYSLSVTVTPSSSLGKTYYTNCVNHKPSNTKVDKRVESK---YGPCCPSCPAPFLGGP 237
DB 197 LYSLSVTVTPSSSLGKTYYTNCVNHKPSNTKVDKRVESK---YGPCCPSCPAPFLGGP 256

QY 238 SVFLPFPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNAKTKPREQFN 297
DB 257 SVFLPFPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNAKTKPREQFN 316

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QY 298 TYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAGOPREPQVYTLPPSOBEM 357
Db |||||
QY 317 TYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAGOPREPQVYTLPPSRDEL 376
Db |||||
QY 358 TKNOVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTTPPVLDSGDSFFLYSLRLTVDKSRWQ 417
Db |||||
QY 377 TKNOVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTTPPVLDSGDSFFLYSKLTVDKSRWQ 436
Db |||||
QY 418 EGNVFCSCVMHEALHNHYTKSLSLSGK 446
Db :|||||
QY 437 QGNVFCSCVMHEALHNHYTKSLSLSPGK 465
Db :|||||

RESULT 5
Q6IN78 HUMAN
ID Q6IN78_HUMAN PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHI1 protein.
GN Name=IGHI1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -; mRNA.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG-LIKE; 2.
SQ SEQUENCE 466 AA; 50854 MW; 53EB0BCDE81076E CRC64;

Query Match 80.7%; Score 1919.5; DB 2; Length 466;
Best Local Similarity 81.5%; Pred. No. 3.2e-127;

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Matches 366; Conservative 28; Mismatches 50; Indels 5; Gaps 2;
QY 1 QVQLQESGPGLVKPQSQTLSLTCTVSGSISGGNYWMIROHPKGLGWIIYISGNTY 60
Db |||||
QY 20 EVQLVESGGGLIQPGGSLTSLCAASGLTSS--NYMHWVRQAPGKGLWVSVLYIGGATY 77
Db |||||
QY 61 YNPGLKRIITISIDTSKNQPSLTSSVTAADTA VYVCARDGGDDAFDIWGCGTWTVSSA 120
Db |||||
QY 78 YADSVKGRFTLIRDSNKNTLYLQWNSLR AEDTA VYVCARGNYVVPAPWGQGTIVTSSA 137
Db |||||
QY 121 STKGPSVFP LAPCSRSTSESTAALGCLVKDYFPPEPVTVMNSGALTSVHTFPVAVLQSSG 180
Db |||||
QY 138 STKGPSVFP LAPSSKSTSGGTAALGCLVKDYFPPEPVTVMNSGALTSVHTFPVAVLQSSG 197
Db |||||
QY 181 LYSLSVVTVPSSSLGTYTTCNVNDHPSNTKVDKRVESK---YGPCPCSPCAPPEFLGGP 237
Db |||||
QY 198 LYSLSVVTVPSSSLGTQTICNVNHRKPSNTKVDKRVKPSKCDTKTHTCCPCPAPELLGGP 257
Db |||||
QY 238 SVFLFPPPKDPTLMISRTPEVTCVVVDVSDRPQVFNWYVDGVVEHNATKTPREEQFNS 297
Db |||||
QY 258 SVFLFPPPKDPTLMISRTPEVTCVVVDVSDRPQVFNWYVDGVVEHNATKTPREEQFNS 317
Db |||||
QY 298 TYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAGOPREPQVYTLPPSOBEM 357
Db |||||
QY 318 TYRVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIISKAGOPREPQVYTLPPSRDEL 377
Db |||||
QY 358 TKNOVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTTPPVLDSGDSFFLYSLRLTVDKSRWQ 417
Db |||||
QY 378 TKNOVSLTCLVKGFYPSDIAVEWESNGQPNENYKTTTPPVLDSGDSFFLYSKLTVDKSRWQ 437
Db |||||
QY 418 EGNVFCSCVMHEALHNHYTKSLSLSGK 446
Db :|||||
QY 438 QGNVFCSCVMHEALHNHYTKSLSLSPGK 466
Db :|||||

RESULT 6
Q6PJN4 HUMAN
ID Q6PJN4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q6PJN4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHI1 protein.
GN Name=IGHI1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

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OX	NCB
RN	[1]


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QY 345 PQVYTLPPSQBETKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTTPPVLDSDGSPF 404
DB 377 PQVYTLPPSREBETKNOVSLTCLVKGFPSPDI AVEWESNGQPENNYKTTTPPVLDSDGSPF 436
QY 405 LYSRLTVDKSRQEGNVFSCVMHEALHNHYTKSLSLGK 446
DB 437 LYSKLTVDKSRQEGNVFSCVMHEALHNHYTKSLSLSPGK 478

RESULT 10
Q6P6C4_HUMAN
ID Q6P6C4_HUMAN PRELIMINARY; PRT; 465 AA.
AC Q6P6C4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAI62335.1; -; mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6P6C4; 20-465.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDD89348ADC37E6D CRC64;

Query Match 79.6%; Score 1893; DB 2; Length 465;
Best Local Similarity 80.7%; Pred. No. 2.4e-125;
Matches 363; Conservative 28; Mismatches 51; Indels 8; Gaps 5;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSSGSISSGGNYW-NWIRQHPGKGLEWIIYYISGN- 58
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DB 20 EVQLMESAGLVKPGGSLRLSCLAASGFFFS---EYMSWVRQAPGKGLEWVANIKDDGSA 76
QY 59 TYYPNLSKRLTITSDTSKNQFSLTSSVTAADTAIVYCARD--GGDDAFDIWGGGTWVT 116
DB 77 TYHDSVKGRTTISRDNARNTLYLQMSLRVEDTANYICAREIPGRCFYDFWGHGTLVT 136
QY 117 VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVVMNSGALTSGVHTFPAVL 176
DB 137 VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVVMNSGALTSGVHTFPAVL 196
QY 177 QSSGLYSLSVTVTPSSSLGTYTCNDVDPKPSNTKVDKRVESKYGPCCPAPCFEFLGG 236
DB 197 QSSGLYSLSVTVTPSSNFGTQTYTCNDVDPKPSNTKVDKRVESKYGPCCPAPCFEFLGG 255
QY 237 PSVFLPPKPKDLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVEVHNATKPREEQFN 296
DB 256 PSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNATKPREEQFN 315
QY 297 STYRVSVSLTVLHQDLNKGKEYCKVSNKGLPSSIEKTSKAKGQPRFPQVYTLPPSOEE 356
DB 316 STFRVSVSLTVVHQDLNKGKEYCKVSNKGLPAIEKTSKTKGQPRFPQVYTLPPSREE 375
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLTKVDKSRW 416
DB 376 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSPFLYSLTKVDKSRW 435
QY 417 QEGNVFSCVMHEALHNHYTKSLSLGK 446
DB 436 QQGNVFSCVMHEALHNHYTKSLSLSPGK 465

RESULT 11
QSEFES_HUMAN
ID QSEFES_HUMAN PRELIMINARY; PRT; 475 AA.
AC QSEFES;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 gammal heavy chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Gaucher C., Klein P., Beliard R.;
RT "Sequence determination of the recombinant human anti-Rhd monoclonal
antibody T125.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894992; AAW82028.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW SIGNAL.
FT SIGNAL.
FT CHAIN 1 19 Potential.
FT CHAIN 20 475 anti-Rhd monoclonal T125 gammal heavy
chain.
SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

Query Match 79.5%; Score 1892; DB 2; Length 475;
Best Local Similarity 80.0%; Pred. No. 2.9e-125;
Matches 367; Conservative 27; Mismatches 49; Indels 16; Gaps 5;
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QY 60 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVVYCARDDGDDAFDI-----WG 110
Db 79 NYNPSLNKRVSIIDTSKNLFSKLRSVTAADTAVVYCAS-----NILKYLHLLYWG 131
QY 111 QGTMTVTSASATKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
Db 132 QGVLTVTSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 191
QY 171 TPAVLQSSGLYSLSSVTVTPSSSLGTKTTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 230
Db 192 TPAVLQSSGLYSLSSVTVTPSSSLGTKTTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 251
QY 231 PEFLLGSPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 290
Db 252 PEFLLGSPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 311
QY 291 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350
Db 312 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLT 410
Db 372 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLT 431
QY 411 VDKSRWQEGNVFSCSVMHREALHNYHTOKSLSLSLGK 446
Db 432 VDKSRWQEGNVFSCSVMHREALHNYHTOKSLSLSLGK 467
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RESULT 2

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US-08-523-894-10
; Sequence 10, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-10
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Query Match 91.0%; Score 2164; DB 2; Length 467;
Best Local Similarity 91.4%; Pred. No. 2.9e-160;
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Matches 417; Conservative 7; Mismatches 14; Indels 18; Gaps 4;
QY 1 QVQLQESGPGLVKPSQTLSLTCTVSGSGSISSGNGYNWIRQHPGKGLEWIGYIYS-GNT 59
Db 20 QVQLQESGPGLVKPSETLSLTCSVSGSI-SGDYWFMIROSPGKLEWIGYIYSGGGT 78
QY 60 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVVYCARDDGDDAFDI-----WG 110
Db 79 NYNPSLNKRVSIIDTSKNLFSKLRSVTAADTAVVYCAS-----NILKYLHLLYWG 131
QY 111 QGTMTVTSASATKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
Db 132 QGVLTVTSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 191
QY 171 TPAVLQSSGLYSLSSVTVTPSSSLGTKTTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 230
Db 192 TPAVLQSSGLYSLSSVTVTPSSSLGTKTTCNVDPKPSNTKVDKRVESKYGPPCPSCPA 251
QY 231 PEFLLGSPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 290
Db 252 PEFLLGSPSVFLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKP 311
QY 291 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 350
Db 312 REEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLT 410
Db 372 PPSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLT 431
QY 411 VDKSRWQEGNVFSCSVMHREALHNYHTOKSLSLSLGK 446
Db 432 VDKSRWQEGNVFSCSVMHREALHNYHTOKSLSLSLGK 467

RESULT 3
US-08-523-894-12
; Sequence 12, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
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Mon Dec 19 14:40:27 2005

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-12

Query Match      90.8%; Score 2159; DB 2; Length 467;
Best Local Similarity 91.2%; Pred. No. 7.1e-160;
Matches 416; Conservative 7; Mismatches 15; Indels 18; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYYSGNTY 59
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYYSGNTY 78
QY 60 YNPSSLKSRITISIDTSKNQFSLTSSVTAADTAATVAVYCARDGDDAFDI-----WG 110
DB 79 YNPSSLKSRITISIDTSKNQFSLTSSVTAADTAATVAVYCARDGDDAFDI-----WG 131
QY 111 QGTMVTVSSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVH 170
DB 132 QGVLTVTVSSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVH 191
QY 171 TTPAVLQSSGLYSLSVTVTPSSSLGTQYTCNVVDHKKPNTKVDKRVESKYGPPCPSCPA 230
DB 192 TTPAVLQSSGLYSLSVTVTPSSSLGTQYTCNVVDHKKPNTKVDKRVESKYGPPCPSCPA 251
QY 231 PFLGSPSVFLPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTP 290
DB 252 PFLGSPSVFLPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTP 311
QY 291 REQFNSTYRVVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 350
DB 312 REQFNSTYRVVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 371
QY 351 PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 410
DB 372 PPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 431
QY 411 VDKSRWQEGNVFSCSVWHEALHNHYTQKSLSLGLK 446
DB 432 VDKSRWQEGNVFSCSVWHEALHNHYTQKSLSLGLK 467

RESULT 4
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Certone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANTU01
; CLONE: 1513264
; US-09-049-672A-4

Query Match      90.0%; Score 2140; DB 2; Length 473;
Best Local Similarity 89.2%; Pred. No. 2.2e-158;
Matches 405; Conservative 18; Mismatches 23; Indels 8; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYYSGNTY 60
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIHQHPGKLEWIGIYYSGNTY 79
QY 61 YNPSSLKSRITISIDTSKNQFSLTSSVTAADTAATVAVYCARD-----GGDDAFDIWGGTMY 115
DB 80 YNPSSLKSRITISIDTSKNQFSLTSSVTAADTAATVAVYCARD-----GGDDAFDIWGGTMY 139
QY 116 TVSSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 175
DB 140 TVSSASTKGPSVFPPLAPCSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 199
QY 176 LOSSGLYSLSVTVTPSSSLGTQYTCNVVDHKKPNTKVDKRVESK---YGPCCPCPAPE 232
DB 200 LOSSGLYSLSVTVTPSSSLGTQYTCNVVDHKKPNTKVDKRVESK---YGPCCPCPAPE 259
QY 233 FLGGPSVFLPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTPRE 292
DB 260 FLGGPSVFLPPPKPDTLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTPRE 319
QY 293 EQFNSTYRVVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLTVD 352
DB 320 EQFNSTYRVVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLTVD 379
QY 353 SOEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLTVD 412
DB 380 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLTVD 439
QY 413 KSRWQEGNVFSCSVWHEALHNHYTQKSLSLGLK 446
DB 440 KSRWQEGNVFSCSVWHEALHNHYTQKSLSLGLK 473

RESULT 5
PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felte & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-13152-4
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Query Match 86.7%; Score 2062.5; DB 4; Length 443;

Best Local Similarity 88.1%; Pred. No. 2.1e-152;
Matches 393; Conservative 16; Mismatches 34; Indels 3; Gaps 2;

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Qy 1 QVQLQESGPGLVKPSQTLTLCTVSGGISGSGNYWNIHQHPGKLEWIGYVSGNTY 60
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTSTYIA--MSWVRQAPGKLEWVASISTGGSTY 58
Qy 61 YNPISLKSRTITSIDTSKNQFSLTSSVTAADTAVYYCARDGGDDAFDIWGQGTWVTVSSA 120
Db 59 YPDSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCARD-YDGYFDYWGQGTWVTVSSA 117
Qy 121 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 180
Db 118 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 177
Qy 181 LYSLSVSVTVPSSSISLGTYYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSVF 240
Db 178 LYSLSVSVTVPSSSISLGTYYTCNVDPKPSNTKVDKRVESKYGPPCPSPCPAPEFLGGPSVF 237
Qy 241 LFPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR 300
Db 238 LFPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYR 297
Qy 301 VSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPRPQVYTLPPSQQEEMTKN 360
Db 298 VSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPRPQVYTLPPSQQEEMTKN 357
Qy 361 QVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRTVDDKSRWQEGN 420
Db 358 QVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRTVDDKSRWQEGN 417
Qy 421 VFSCSWMEALHNHYTQKSLSLGLK 446
Db 418 VFSCSWMEALHNHYTQKSLSLGLK 443
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RESULT 6

US-08-704-744-81

; Sequence 81, Application US/08704744

; Patent No. 5705154

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; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-704-744-81
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Query Match 86.5%; Score 2057; DB 1; Length 467;

Best Local Similarity 87.6%; Pred. No. 6.2e-152;
Matches 395; Conservative 13; Mismatches 35; Indels 8; Gaps 4;

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Qy 1 QVQLQESGPGLVKPSQTLTLCTVSGGISGSGNYW--NIHQHPGKLEWIGYIYVSG-N 58
Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFSFRS--YWMTWVRQAPGKLEWVASISISGDN 76
Qy 59 TYNPISLKSRTITSIDTSKNQFSLTSSVTAADTAVYYCARDG---GDADFINGQGTWV 115
Db 77 TYYPDSVKGRFTISRDDSKSTLYLQMNLSRAEDTAVYYCVRDPYFSGHYDFWQGQTLV 136
Qy 116 TVSSASTKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 175
Db 137 TVSSASTKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 196
Qy 176 LQSSGLYSLSVTVPSSSISLGTYYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPEFLG 235
Db 197 LQSSGLYSLSVTVPSSSISLGTYYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPEFLG 256
Qy 236 GPSVFLFPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQF 295
Db 257 GPSVFLFPPPKDPTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKPREEQF 316
Qy 296 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPRPQVYTLPPSQE 355
Db 317 NSTYRVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIKAKGQPRPQVYTLPPSQE 376
Qy 356 EMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLRTVDDKSR 415
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Db 377 EMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSLFLYSLRLTVDKSR 436
Qy 416 WQEGNVFSCVMHEALHNNHYTKQSLSLGK 446
Db 437 WQEGNVFSCVMHEALHNNHYTKQSLSLGK 467
RESULT 7
US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-487-550-12
Query Match 85.9%; Score 2044.5; DB 2; Length 476;
Best Local Similarity 85.6%; Pred. No. 5.9e-151;
Matches 392; Conservative 21; Mismatches 32; Indels 13; Gaps 4;
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNWIHQHPGKLEWIGYIY-YSGNT 59
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNWIHQHPGKLEWIGYIY-YSGNT 78
Qy 60 YNPSLKSRTITSDTSKNQFSLTSSVTAADTAIVYCVDRDLFSVVGMYNNWFDVWGP 111
Db 79 YNPSLKSQVTTISDTSKNQFSLKLSNMTAADTAIVYCVDRDLFSVVGMYNNWFDVWGP 138
Qy 112 GTMTVTSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVYSWNSGALTSGVHT 171
Db 139 GVLTVTSASTKGPSVFPPLAPCSRSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHT 198
Qy 172 FPAVLQSGSLYSLSSVTVTPSSSLGTQTYTCNVDPKFSNTKVDKRVESK---YCPPCPC 228
Db 199 FPAVLQSGSLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKAEPKSCDKTHTTCCPC 258
Qy 229 PAPEFLGGPSVFLPPPKQDTLMISRTPEVTCVVVDYSDQEDPEVOFQNNYVDGVVHNAKT 288
Db 259 PAPELGGPSVFLPPPKQDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNAKT 318

Qy 289 KPRBEQFNSTYRVSVLTFLVHQDMLNGKEYKCKVSNKGLPSSIEKTIISKAKGPPEQVY 348
Db 319 KPREQYNSTYRVSVLTFLVHQDMLNGKEYKCKVSNKALPAPIEKTIISKAKGPPEQVY 378
Qy 349 TLPSPQEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSLFLYSR 408
Db 379 TLPSPRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLDSDGSLFLYSK 438
Qy 409 LTVDKSRWQEGNVFSCVMHEALHNNHYTKQSLSLGK 446
Db 439 LTVDKSRWQEGNVFSCVMHEALHNNHYTKQSLSLSPGK 476
RESULT 8
US-09-526-098-12
; Sequence 12, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-526-098-12
Query Match 85.9%; Score 2044.5; DB 2; Length 476;
Best Local Similarity 85.6%; Pred. No. 5.9e-151;
Matches 392; Conservative 21; Mismatches 32; Indels 13; Gaps 4;
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNWIHQHPGKLEWIGYIY-YSGNT 59
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNWIHQHPGKLEWIGYIY-YSGNT 78
Qy 60 YNPSLKSRTITSDTSKNQFSLTSSVTAADTAIVYCVDRDLFSVVGMYNNWFDVWGP 111
Db 79 YNPSLKSQVTTISDTSKNQFSLKLSNMTAADTAIVYCVDRDLFSVVGMYNNWFDVWGP 138

QY 112 GTWTVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYRPPVTVSWNSGALTSQVHT 171
Db 139 GVLTVSSASTKGPSVFLPAPCSKSTSGTAALGCLVKDYRPPVTVSWNSGALTSQVHT 198
QY 172 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVHKSNTKVDKRVESK---YGPPCPC 228
Db 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVHKSNTKVDKKAEPKSCDKTHTCCPC 258
QY 229 PAPEFLGGPSVFLPAPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNMYVDGVEVHNAKT 288
Db 259 PAPELLGGPSVFLPAPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 318
QY 289 KPREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPOVY 348
Db 319 KPREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVY 378
QY 349 TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR 408
Db 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
QY 409 LTVDKSRWQGNVFCSCVMHEALHNYTKQSLSLSGK 446
Db 439 LTVDKSRWQGNVFCSCVMHEALHNYTKQSLSLSPGK 476
RESULT 9
US-09-383-916-12
; Sequence 12, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-383-916-12
Query Match 85.9%; Score 2044.5; DB 2; Length 476;
Best Local Similarity 85.6%; Pred. No. 5,9e-151;
Matches 392; Conservative 21; Mismatches 32; Indels 13; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNNIRQHPGKLEWICVYI-YSNGT 59
Db 20 QVQLQESGPGLVKPSQTLSTCAVSGSI-SGGYWGMIQPPGKLEWIGSFYSSNGT 78
QY 60 YNPNSLKSRIITISIDTSKNQFSLTSSVTAADTAAYVYCARDG-----GDDAFDIWGP 111
Db 79 YNPNSLKSQVITISIDTSKNQFSLKLSNMTAATAAYVYCVDRDLFSVGVYNNWFDWGP 138
QY 112 GTWTVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYRPPVTVSWNSGALTSQVHT 171
Db 139 GVLTVSSASTKGPSVFLPAPCSKSTSGTAALGCLVKDYRPPVTVSWNSGALTSQVHT 198
QY 172 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVHKSNTKVDKRVESK---YGPPCPC 228
Db 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVHKSNTKVDKKAEPKSCDKTHTCCPC 258
QY 229 PAPEFLGGPSVFLPAPKDTLMISRTPEVTCVVVDVSDQEDPEVQFNMYVDGVEVHNAKT 288
Db 259 PAPELLGGPSVFLPAPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKT 318
QY 289 KPREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKGLPSSIEKTIKAKGQPREPOVY 348
Db 319 KPREEQFNSTYRVSVLTVLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVY 378
QY 349 TLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR 408
Db 379 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
QY 409 LTVDKSRWQGNVFCSCVMHEALHNYTKQSLSLSGK 446
Db 439 LTVDKSRWQGNVFCSCVMHEALHNYTKQSLSLSPGK 476
RESULT 10
US-09-758-173-12
; Sequence 12, Application US/09758173
; Patent No. 6893638
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,173
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021

Db 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFS----DYWMSVNRQAPCKGLEWVADIKNDGSY 76
QY 59 TYNPSLKSRIITISIDTSKNQFSLTSSVTAADTAAYKCYCARDGGDDAFDINGQGGMVTVS 118
Db 77 TNYAPSLNRFITSRDANKNSLYLQWNSLRABEDTAAYTCAR----ELTGTWGGQGMVTVS 132
QY 119 SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 178
Db 133 SASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 192
QY 179 SGLYSLSVVTVPPSSSLGTTKTYTCNVDHKPSNTKVDKRVESYGPFCPCPAPEFLGGPS 238
Db 193 SGLYSLSVVTVPPSSSLGTTKTYTCNVDHKPSNTKVDKRVESYGPFCPCPAPEFLGGPS 252
QY 239 VFLFPPKPKDTLMISRTPEVTCVVVDVQEDDEVDQFNQVNNVYDGVVEVHNATKTPREEQFNST 298
Db 253 VFLFPPKPKDTLMISRTPEVTCVVVDVQEDDEVDQFNQVNNVYDGVVEVHNATKTPREEQFNST 312
QY 299 YRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMT 358
Db 313 YRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPOVYTLPPSQEEMT 372
QY 359 KNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSRLLTVDKSRWQE 418
Db 373 KNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSRLLTVDKSRWQE 432
QY 419 GNVFCSVMHEALHNHYTQKSLSLGLK 446
Db 433 GNVFCSVMHEALHNHYTQKSLSLGLK 460

RESULT 13

US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHAABIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-8

Query Match 84.8%; Score 2018.5; DB 2; Length 472;

Best Local Similarity 85.1%; Pred. No. 6.2e-149;
Matches 387; Conservative 22; Mismatches 35; Indels 11; Gaps 3;

QY 1 QVQLQESGPGLVKPQSQTLSLTCTVSGSISGGNYYWNIHQHPKGLIEWIGIYYSGNTY 60
Db 20 QVQLQEQWAGLLKPKSETLSLTCTVYGGFS--GYWWSWIRQPGKGLIEWIGIINHSSTN 77
QY 61 YNPSLKSRIITISIDTSKNQFSLTSSVTAADTAAYTCAR-----DGDGDAFDLWGGTGM 114
Db 78 YNPSLKSRIITISIDTSKNQFSLKLVNVAADTAAYTCARPEYKWKYHGMDFDPWQGT 137
QY 115 VTVSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174
Db 138 VTVSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 197
QY 175 VLOSGLYSLSVVTVPPSSSLGTTKTYTCNVDHKPSNTKVDKRVESK---YGPFCPCPAP 231
Db 198 VLOSGLYSLSVVTVPPSSSLGTTQTYICNVNHPKPSNTKVDKKAEPKSCDKTQTCCPCPAP 257
QY 232 EFLGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVQEDDEVDQFNQVNNVYDGVVEVHNATKTPR 291
Db 258 ELLGGSPSVFLFPPKPKDTLMISRTPEVTCVVVDVQEDDEVDQFNQVNNVYDGVVEVHNATKTPR 317
QY 292 EEQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPOVYTL 351
Db 318 EEQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREPOVYTL 377
QY 352 PSQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSRLLTV 411
Db 378 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTV 437
QY 412 DKSRWQGNVFCSCVMHEALHNHYTQKSLSLGLK 446
Db 438 DKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 472

RESULT 14

US-07-916-098A-45
; Sequence 45, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843

FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-916-098A-45

Query Match 84.3%; Score 2005; DB 1; Length 467;
Best Local Similarity 85.4%; Pred. No. 6.9e-148;
Matches 385; Conservative 22; Mismatches 36; Indels 8; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNNWIRQHPGKGLEWIGYIY-YSGNT 59
DB 20 QVQLQESGAEVKKPGASVKVSCKASGYTFTS--YVIRHWVRQAPFGQGLEWIGIYINPYNDGT 77

QY 60 YNPISLKRITISIDTSKQFSLTSSVTAADTAATVAVYCARDDGDDA---FDIWGGQTMV 115
DB 78 DYDEKFKGKATVLDPSNTAYWELSSLRSEDATVAVYCARDKDNYATGAWFAYWGQGLV 137

QY 116 TVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAV 175
DB 138 TVSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAV 197

QY 176 LQSSGLYSLSSVTVPSSSISLGTITTCNVDPKPSNTKVDKRVESKYGPPCPAPAEFLG 235
DB 198 LQSSGLYSLSSVTVPSSSISLGTITTCNVDPKPSNTKVDKRVESKYGPPCPAPAEFLG 257

QY 236 GPSVFLPPPKPKDTLMISRTPEVTCVVDVYSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 295
DB 258 GPSVFLPPPKPKDTLMISRTPEVTCVVDVYSQEDPEVQFNWYVDGVEVHNAKTKPREEQF 317

QY 296 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGPQPREQVYTLPPSQE 355
DB 318 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAK-QPREQVYTLPPSQE 376

QY 356 EMTKNQVSLTCLVKGFYPSDIAEVWESNGQPENNYKTPPVLDSDGSGFFLYSRLTVDKSR 415
DB 377 EMTKNQVSLTCLVKGFYPSDIAEVWESNGQPENNYKTPPVLDSDGSGFFLYSRLTVDKSR 436

QY 416 WQGNVFSCSVMHEALHNHYTQKSLSLGLK 446
DB 437 WQGNVFSCSVMHEALHNHYTQKSLSLGLK 467

RESULT 15
US-08-030-175-42
; Sequence 42, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington

STATE: D. C.
COUNTRY: U.S.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage
COMPUTER: IBM AT compatible
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2
SOFTWARE: WordPerfect 5.0 (dos Text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/030,175
FILING DATE: 17-MAY-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01578
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Ernst, Barbara G.
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1768-113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)783-6040
TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-030-175-42

Query Match 83.6%; Score 1990; DB 2; Length 467;
Best Local Similarity 84.7%; Pred. No. 1e-146;
Matches 381; Conservative 26; Mismatches 37; Indels 6; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNNWIRQHPGKGLEWIGYIYSG-NT 59
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGFTSFNYG--MAWVRQPPGRGLEWIGTISHDGS 77

QY 60 YNPISLKRITISIDTSKQFSLTSSVTAADTAATVAVYCARDDGDDA---FDIWGGQTMV 119
DB 78 YFRDSVKGKATVLDPSNTAYWELSSLRSEDATVAVYCARQGTIAGIRHWGQSLTVSS 137

QY 120 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQSS 179
DB 138 ASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTFPAVLQSS 197

QY 180 GLYSLSVTVPSSSISLGTITTCNVDPKPSNTKVDKRVESK---YGPCCPAPAEFLG 236
DB 198 GLYSLSVTVPSSSISLGTITTCNVDPKPSNTKVDKRVESK---YGPCCPAPAEFLG 257

QY 237 PSVFLPPPKPKDTLMISRTPEVTCVVDVYSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 296
DB 258 PSVFLPPPKPKDTLMISRTPEVTCVVDVYSQEDPEVQFNWYVDGVEVHNAKTKPREEQFN 317

QY 297 STYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGPQPREQVYTLPPSQE 356
DB 318 STYRVVSVLTVLHQDWLNGKEYCKVSNKGLPSSIEKTIISKAKGPQPREQVYTLPPSRDE 377

QY 357 MTKNQVSLTCLVKGFYPSDIAEVWESNGQPENNYKTPPVLDSDGSGFFLYSRLTVDKSRW 416
DB 378 LTKNQVSLTCLVKGFYPSDIAEVWESNGQPENNYKTPPVLDSDGSGFFLYSRLTVDKSRW 437

QY 417 QEGNVFSCSVMHEALHNHYTQKSLSLGLK 446
DB 438 QEGNVFSCSVMHEALHNHYTQKSLSLSPGK 467

Search completed: December 17, 2005, 01:25:45
Job time : 46.6 secs

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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:14:05 ; Search time 147.315 Seconds
(without alignments)
1264.988 Million cell updates/sec

Title: US-10-644-277-62
Perfect score: 2379
Sequence: 1 QVQLQSGPGLVKPQTSL.....MHEALHNHYTKLSLSLCK 446

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA Main:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pap:*
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pap:*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap:*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap:*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2379	100.0	446	5	US-10-644-277-62
2	2197.5	92.4	470	6	US-11-031-485-22
3	2180	91.6	450	5	US-10-484-790A-17
4	2177	91.5	467	5	US-10-961-567A-3
5	2171	91.3	467	4	US-10-211-357-8
6	2164	91.0	467	4	US-10-211-357-10
7	2159	90.8	467	4	US-10-211-357-12
8	2158.5	90.7	480	5	US-10-910-901-6
9	2136.5	89.8	580	4	US-10-310-719-37
10	2119	89.1	442	5	US-10-937-596-32
11	2108	88.6	463	5	US-10-910-901-10
12	2106.5	88.5	466	4	US-10-292-088-86
13	2104.5	88.5	466	4	US-10-292-088-70
14	2098.5	88.1	466	4	US-10-292-088-30
15	2088.5	87.8	451	5	US-10-818-068-25
16	2088.5	87.8	451	5	US-10-724-274-25
17	2088.5	87.8	451	5	US-10-830-956-25
18	2085.5	87.7	451	5	US-10-822-300-144
19	2084.5	87.6	464	4	US-10-292-088-22
20	2083	87.6	442	5	US-10-937-596-4
21	2082.5	87.5	451	5	US-10-822-300-142
22	2082.5	87.5	451	5	US-10-822-300-143
23	2079.5	87.4	451	5	US-10-822-300-145
24	2077.5	87.3	451	5	US-10-822-300-146
25	2075	87.2	471	6	US-11-031-485-38
26	2071	87.1	461	5	US-10-938-353-70
27	2071	87.1	465	6	US-11-031-485-14

28	2067	86.9	463	5	US-10-938-353-18	Sequence 18, Appl
29	2067	86.9	469	6	US-11-031-485-60	Sequence 60, Appl
30	2065.5	86.8	451	5	US-10-724-274-31	Sequence 31, Appl
31	2065.5	86.8	451	5	US-10-830-956-31	Sequence 31, Appl
32	2064.5	86.8	462	6	US-11-031-485-46	Sequence 46, Appl
33	2064	86.8	469	4	US-10-663-244-164	Sequence 164, Appl
34	2062.5	86.7	443	3	US-09-917-410-4	Sequence 4, Appl
35	2062.5	86.7	462	5	US-10-938-353-46	Sequence 46, Appl
36	2060	86.6	469	5	US-10-805-177-137	Sequence 137, Appl
37	2059	86.5	444	5	US-10-492-228-57	Sequence 57, Appl
38	2059	86.5	469	4	US-10-663-244-157	Sequence 157, Appl
39	2059	86.5	469	6	US-11-031-485-18	Sequence 18, Appl
40	2057.5	86.5	462	5	US-10-938-353-86	Sequence 86, Appl
41	2055.5	86.4	462	5	US-10-938-353-50	Sequence 50, Appl
42	2054.5	86.4	466	4	US-10-663-244-162	Sequence 162, Appl
43	2054	86.3	461	5	US-10-938-353-38	Sequence 38, Appl
44	2054	86.3	461	5	US-10-938-353-78	Sequence 78, Appl
45	2049.5	86.1	464	4	US-10-663-244-158	Sequence 158, Appl

ALIGNMENTS

RESULT 1
US-10-644-277-62
; Sequence 62, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudae, Jean M.
; APPLICANT: Haak-Frendscho, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kitan
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
; FILE REFERENCE: ABGENIX.091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-62

Query Match	100.0%	Score 2379;	DB 5;	Length 446;
Best Local Similarity	100.0%	Pred. No. 1.7e-152;		
Matches	446;	Conservative	0;	Mismatches
			0;	Indels
			0;	Gaps
				0;
Qy	1	QVQLQSGPGLVKPQTSLTCTVSGGSISSGGNYNNWIRQHPGKLEWIGIYYISGNTY	60	
Db	1	QVQLQSGPGLVKPQTSLTCTVSGGSISSGGNYNNWIRQHPGKLEWIGIYYISGNTY	60	
Qy	61	YNPILSKRITISDTSKNQFSLTSSVTADTAIVYCARDGGDDAFDIWGQGTMTVSSA	120	
Db	61	YNPILSKRITISDTSKNQFSLTSSVTADTAIVYCARDGGDDAFDIWGQGTMTVSSA	120	
Qy	121	STKGPVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG	180	
Db	121	STKGPVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG	180	
Qy	181	LXSLSSVTVTPSSSLTKTYTCNVDRKPKNTKVDKRVESKYGPCCSCPAPELGGPSVF	240	
Db	181	LXSLSSVTVTPSSSLTKTYTCNVDRKPKNTKVDKRVESKYGPCCSCPAPELGGPSVF	240	
Qy	241	LFPKPKDILMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNKTKPREEQFNSTYR	300	
Db	241	LFPKPKDILMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNKTKPREEQFNSTYR	300	

QY 301 VVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREQVYTLPPSQBEMTKN 360
DB 301 VVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREQVYTLPPSQBEMTKN 360
QY 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDKSRWQGN 420
DB 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDKSRWQGN 420
QY 421 VFSCVMHEALHNHYTQKSLSLGLK 446
DB 421 VFSCVMHEALHNHYTQKSLSLGLK 446
RESULT 2
US-11-031-485-22
; Sequence 22, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRIENDSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MadCAM
; FILE REFERENCE: ABX-PF6
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; PRIOR FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 22
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-485-22

Query Match 92.4%; Score 2197.5; DB 6; Length 470;
Best Local Similarity 92.9%; Pred. No. 3.2e-140;
Matches 421; Conservative 5; Mismatches 18; Indels 9; Gaps 2;
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYMNIROHPGKLEWIGVIYYSNTY 60
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGDSLSS--NYWSWIRQAPAGKLEWIGRIYTSGGTN 77
QY 61 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDG-----GDDAFDIWGQGT 113
DB 78 SNPSLRGRVTILADTSKNQFSLKLSVTAADTAVYYCARDRTIIRGLIPSFDDYWGQGT 137
QY 114 MVTVSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
DB 138 LVTVSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 197
QY 174 AVQLQSGLYSLSSVTVTPSSSLGTITYTCNVDPKSNKTKVDKRVESKYGPPCPSPAPEF 233
DB 198 AVQLQSGLYSLSSVTVTPSSSLGTITYTCNVDPKSNKTKVDKRVESKYGPPCPSPAPEF 257
QY 234 LGGPSVFLLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNNAKTKPREE 293
DB 258 LGGPSVFLLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNNAKTKPREE 317
QY 294 QNSTYRVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREQVYTLPPS 353
DB 318 QNSTYRVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREQVYTLPPS 377
QY 354 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDK 413
DB 378 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDK 437
QY 414 SRWQEGNVFSCVMHEALHNHYTQKSLSLGLK 446
DB 438 SRWQEGNVFSCVMHEALHNHYTQKSLSLGLK 470

RESULT 3
US-10-484-790A-17
; Sequence 17, Application US/10484790A
; Publication No. US20050070694A1
; GENERAL INFORMATION:
; APPLICANT: Gelfanova, et al., Valentina
; TITLE OF INVENTION: Antagonistic Anti-hTNFSF13b Human Antibodies
; FILE REFERENCE: X-15239
; CURRENT APPLICATION NUMBER: US/10/484,790A
; CURRENT FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 17
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-484-790A-17

Query Match 91.6%; Score 2180; DB 5; Length 450;
Best Local Similarity 92.0%; Pred. No. 4.7e-139;
Matches 416; Conservative 9; Mismatches 19; Indels 8; Gaps 2;
QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYMNIROHPGKLEWIGVIYYSNTY 60
DB 1 QVQLQEWAGAGLKPSETLSLTCAVYGGFS--GYTWSWIRQPPGKLEWIGEINHSGSTN 58
QY 61 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDGDDA-----FDIWGQGT 114
DB 59 YNPSLKSRVTISVDTSKNQFSLKLSVTAADTAVYYCARGYYDILTGYYYFDYWGQGT 118
QY 115 VTVSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 174
DB 119 VTVSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 178
QY 175 VLQSSGLYSLSSVTVTPSSSLGTITYTCNVDPKSNKTKVDKRVESKYGPPCPSPAPEFL 234
DB 179 VLQSSGLYSLSSVTVTPSSSLGTITYTCNVDPKHSQTKVDKRVESKYGPPCPSPAPEFL 238
QY 235 GGPSVFLLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNNAKTKPREQ 294
DB 239 GGPSVFLLPPPKPDTLMISRTPEVTCVVVDVSQEDPEVQFNWYDGVGVHNNAKTKPREQ 298
QY 295 FNSTYRVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREQVYTLPPSQ 354
DB 299 FNSTYRVVSVLTVLHODWLNGKEYCKVSNKGLPSSIEKTIKAKGQPREQVYTLPPSQ 358
QY 355 BEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDKS 414
DB 359 BEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSRLTVDKS 418
QY 415 RWQEGNVFSCVMHEALHNHYTQKSLSLGLK 446
DB 419 RWQEGNVFSCVMHEALHNHYTQKSLSLGLK 450

RESULT 4
US-10-961-567A-3
; Sequence 3, Application US/10961567A
; Publication No. US20050095244A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Hefta, Laura
; APPLICANT: Santoro, Marc
; APPLICANT: Ganguly, Subinay
; TITLE OF INVENTION: FULLY HUMAN ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: 10060 NP
; CURRENT APPLICATION NUMBER: US/10/961,567A
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US 60/510193
; PRIOR FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.2

SEQ ID NO 3
LENGTH: 467
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: pd17-20H4.9.h4a amino acid sequence
US-10-961-567A-3

Query Match
Best Local Similarity 91.5%; Score 2177; DB 5; Length 467;
Matches 414; Conservative 11; Mismatches 19; Indels 6; Gaps 2;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGSGNYMIRQHPGKLEWIGYIYSGNTY 60
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGSISGSGNYMIRQHPGKLEWIGYIYSGNTY 77
QY 61 YNPISLKRITISIDTSKNQFSLTSSVTAADTAVVYCARDGG---DDAFDIWGQTMVT 116
DB 78 YNPISLKRITISIDTSKNQFSLTSSVTAADTAVVYCARDGG---DDAFDIWGQTMVT 137
QY 117 VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 176
DB 138 VSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 197
QY 177 QSSGLYSLSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVSKEYGPPCPAPPEFLGG 236
DB 198 QSSGLYSLSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVSKEYGPPCPAPPEFLGG 257
QY 237 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNMYVDGVEVHNAKTKPREEQFN 296
DB 258 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNMYVDGVEVHNAKTKPREEQFN 317
QY 297 STYRVVSVLTVLDHQMVLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEE 356
DB 318 STYRVVSVLTVLDHQMVLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSQEE 377
QY 357 MTNQVSLTCLVKGFPSPDIKAVESNGQPNYKTTTPVLDSDGSFFLYSLRTVDDKSRW 416
DB 378 MTNQVSLTCLVKGFPSPDIKAVESNGQPNYKTTTPVLDSDGSFFLYSLRTVDDKSRW 437
QY 417 QEGNVFSCSVMEALHNHYTQKSLSLGLK 446
DB 438 QEGNVFSCSVMEALHNHYTQKSLSLGLK 467

RESULT 5
US-10-211-357-8
Sequence 8, Application US/10211357
Publication No. US2003007275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-211-357-8

Query Match
Best Local Similarity 91.3%; Score 2171; DB 4; Length 467;
Matches 418; Conservative 7; Mismatches 13; Indels 18; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGSGNYMIRQHPGKLEWIGYIYSGNT 59
DB 20 QVQLQESGPGLVKPSQTLSTCTVSGSISGSGNYMIRQHPGKLEWIGYIYSGNT 78
QY 60 YNPISLKRITISIDTSKNQFSLTSSVTAADTAVVYCARDGGDAFDI-----WG 110
DB 79 YNPISLKRITISIDTSKNQFSLTSSVTAADTAVVYCARDGGDAFDI-----WG 131
QY 111 QGTMVTVSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 170
DB 132 QGTMVTVSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVH 191
QY 171 TTPAVLQSSGLYSLSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVSKEYGPPCPSCPA 230
DB 192 TTPAVLQSSGLYSLSVTVTPSSSLGTITTCNVDPKPSNTKVDKRVSKEYGPPCPSCPA 251
QY 231 PEFGLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNMYVDGVEVHNAKTKP 290
DB 252 PEFGLGSPVFLPPPKPKDTLMISRTPEVTCVVVDVSDPEQVFNMYVDGVEVHNAKTKP 311
QY 291 REEQFNSTYRVVSVLTVLDHQMVLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 350
DB 312 REEQFNSTYRVVSVLTVLDHQMVLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNQVSLTCLVKGFPSPDIKAVESNGQPNYKTTTPVLDSDGSFFLYSLRT 410
DB 372 PPSQEMTKNQVSLTCLVKGFPSPDIKAVESNGQPNYKTTTPVLDSDGSFFLYSLRT 431
QY 411 VDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK 446
DB 432 VDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK 467

RESULT 6
US-10-211-357-10
Sequence 10, Application US/10211357
Publication No. US2003007275A1
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA

```
;
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/211,357
; FILING DATE: 05-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/612,914A
; FILING DATE: 10-Jul-2000
; APPLICATION NUMBER: US 08/523,894
; FILING DATE: 06-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-211-357-10
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Query Match 91.0%; Score 2164; DB 4; Length 467;
Best Local Similarity 91.4%; Pred. No. 5,9e-138;
Matches 417; Conservative 7; Mismatches 14; Indels 18; Gaps 4;
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QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYS-GNT 59
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQESGPGLVKPSQTLSTCTVSGGSI-SGDYYWFMIROSPGKLEWIGYIYSGGGT 78
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 YNPPLSKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDGGDAFDI-----WG 110
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 NYNPSLNRRVSIIDTSKNLFSKLRSVTAADTAVYYCAS-----NILKYLHWLLYWG 131
QY 111 QGTWTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVH 170
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
132 QGVLTVTSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVH 191
QY 171 TFPVAVLQSSGLYSLSVTVTPSSSLGTQTYTCNVDPKPSNTKVDKRVSKEYGPPCPSCPA 230
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
192 TFPVAVLQSSGLYSLSVTVTPSSSLGTQTYTCNVDPKPSNTKVDKRVSKEYGPPCPSCPA 251
QY 231 PFLGSGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 290
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
252 PFEFGSPVFLFPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 311
QY 291 REEQFNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 350
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
312 REEQFNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 410
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
372 PPSQEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 431
QY 411 VDKSRWQEGNVFSCSWMEALHNHYTQKSLSLSLGK 446
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
432 VDKSRWQEGNVFSCSWMEALHNHYTQKSLSLSLGK 467
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RESULT 7
US-10-211-357-12
; Sequence 12, Application US/10211357
; Publication No. US20030077275A1
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;
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; Newman, Roland A.
; Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/211,357
; FILING DATE: 05-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/612,914A
; FILING DATE: 10-Jul-2000
; APPLICATION NUMBER: US 08/523,894
; FILING DATE: 06-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-211-357-12
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Query Match 90.8%; Score 2159; DB 4; Length 467;
Best Local Similarity 91.2%; Pred. No. 1.3e-137;
Matches 416; Conservative 7; Mismatches 15; Indels 18; Gaps 4;
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QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYS-GNT 59
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVQLQESGPGLVKPSQTLSTCTVSGGSI-SGDYYWFMIROSPGKLEWIGYIYSGGGT 78
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 YNPPLSKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDGGDAFDI-----WG 110
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 NYNPSLNRRVSIIDTSKNLFSKLRSVTAADTAVYYCAS-----NILKYLHWLLYWG 131
QY 111 QGTWTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVH 170
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
132 QGVLTVTSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVH 191
QY 171 TFPVAVLQSSGLYSLSVTVTPSSSLGTQTYTCNVDPKPSNTKVDKRVSKEYGPPCPSCPA 230
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
192 TFPVAVLQSSGLYSLSVTVTPSSSLGTQTYTCNVDPKPSNTKVDKRVSKEYGPPCPSCPA 251
QY 231 PFLGSGPSVFLPPPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 290
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
252 PFEFGSPVFLFPKPDTLMISRTPEVTCVVVDVSDPEVQFNWYVDGVEVHNAKTKP 311
QY 291 REEQFNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 350
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
312 REEQFNSTYRVVSVLTVLHQLDNLNGKEYKCKVSNKGLPSSIEKTIKAKGQPREPQVYTL 371
QY 351 PPSQEMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSRLT 410
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Db 372 PPSQEMTKNQVSLTCLVKGFPSPDI AVEWESNGQPNKYKTPPVLDSGSGFFLYSLRT 431
Qy 411 VDKSRWQEGNVFSCSVMEALHNNHYTKSLSLGK 446
Db 432 VDKSRWQEGNVFSCSVMEALHNNHYTKSLSLGK 467
RESULT 8
US-10-910-901-6
; Sequence 6, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO c-MET
; FILE REFERENCE: ABX-PF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; PRIOR FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-6
Query Match 90.7%; Score 2158.5; DB 5; Length 480;
Best Local Similarity 88.5%; Pred. No. 1.4e-137;
Matches 409; Conservative 17; Mismatches 19; Indels 17; Gaps 3;
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNNWIRQHPGKGLEWIGYIYSGNTY 60
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNNWIRQHPGKGLEWIGYIYSGNTY 79
Qy 61 YNPISLKRITISIDTSKQFSLTSSVTAADTAIVYCARDG-----GDADF- 106
Db 80 YNPISLKRITISIDTSKQFSLTSSVTAADTAIVYCARDGPGLYGCSSTSCPTVGTYYY 139
Qy 107 --DIWGQGTMTVTVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSVNSGA 164
Db 140 GMDVWGQGTMTVTVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSVNSGA 199
Qy 165 LTSGVHTFPAPVAVLQSSGLYSLSSVTVVPSNFGITQYTCNVDPKPSNTKVDKRVESKGGPP 224
Db 200 LTSGVHTFPAPVAVLQSSGLYSLSSVTVVPSNFGITQYTCNVDPKPSNTKVDKRVESKGGPP 259
Qy 225 CPSCPAPEFLGGPSVFLPAPKPDTLMSRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVH 284
Db 260 CPSCPAPEFLGGPSVFLPAPKPDTLMSRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVH 318
Qy 285 NAKTKPREQFNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTSISKAGQPRE 344
Db 319 NAKTKPREQFNSTYRVVSVLTVLHQDLNKGKEYCKVSNKGLPAPLEKTSISKAGQPRE 378
Qy 345 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNKYKTPPVLDSGSGFF 404
Db 379 PQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNKYKTPPVLDSGSGFF 438
Qy 405 LYSRLTVDKSRWQEGNVFSCSVMEALHNNHYTKSLSLGK 446
Db 439 LYSRLTVDKSRWQEGNVFSCSVMEALHNNHYTKSLSPGK 480

RESULT 9
US-10-310-719-37
; Sequence 37, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020

; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-NHS76(gamma4h) (FN>AQ) -ala-IL2 (D20T) heavy chain fused to
; OTHER INFORMATION: IL-2 variant
US-10-310-719-37
Query Match 89.8%; Score 2136.5; DB 4; Length 580;
Best Local Similarity 91.3%; Pred. No. 5.5e-136;
Matches 409; Conservative 11; Mismatches 23; Indels 5; Gaps 3;
Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNNWIRQHPGKGLEWIGYIYSGNTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYNNWIRQHPGKGLEWIGYIYSGNTY 59
Qy 61 YNPISLKRITISIDTSKQFSLTSSVTAADTAIVYCARDGDDAFDIWGQGTMTVTVSSA 120
Db 60 YNPISLKRITISIDTSKQFSLTSSVTAADTAIVYCAR-GKWSKFDYWGQGTMTVTVSSA 118
Qy 121 STKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSVNSGALTSGVHTTTPAVLQSSG 180
Db 119 STKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPVTVSVNSGALTSGVHTTTPAVLQSSG 178
Qy 181 LYSLSAVTVVPSNFGITQYTCNVDPKPSNTKVDKRVESK---YGPCCPCPAPEFLGGP 237
Db 179 LYSLSAVTVVPSNFGITQYTCNVDPKPSNTKVDKRVESKCDKTHCTCCPAPEFLGGP 238
Qy 238 SVFLPAPKPDTLMSRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTTPREEQNS 297
Db 239 SVFLPAPKPDTLMSRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTTPREEQNS 298
Qy 298 TYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTSISKAGQPREQVYTLPPSQEEM 357
Db 299 TYRVVSVLTVLHQDLNKGKEYCKVSNKGLPSSIEKTSISKAGQPREQVYTLPPSQEEM 358
Qy 358 TKNQVSLTCLVKGFYPSDIAVEWESNGQPNKYKTPPVLDSGSGFFLYSLTVDKSRMQ 417
Db 359 TKNQVSLTCLVKGFYPSDIAVEWESNGQPNKYKTPPVLDSGSGFFLYSLTVDKSRMQ 418
Qy 418 EGNVFSQVMEALHNNHYTKSLSLG 445
Db 419 QGNIFSCSVMEALHNNHYTKSATATPG 446

RESULT 10
US-10-937-596-32
; Sequence 32, Application US/10937596
; Publication No. US2005018169A1
; GENERAL INFORMATION:
; APPLICANT: BARTKE, ILSE
; APPLICANT: CARR, FRANCIS
; APPLICANT: CHIZZONITE, RICHARD ANTHONY
; APPLICANT: EUGUI, ELSIE M.
; APPLICANT: FERTIG, GEORG
; APPLICANT: HAMILTON, ANITA
; APPLICANT: LANZENDOERFER, MARTIN
; APPLICANT: RUEGER, PETRA
; APPLICANT: SCHUMACHER, RALF
; APPLICANT: TRUITT, THERESA PATRICIA
; TITLE OF INVENTION: ANTIBODIES AGAINST INTERLEUKIN-1 RECEPTOR AND USES THEREOF
; FILE REFERENCE: CD21842-US1
; CURRENT APPLICATION NUMBER: US/10/937,596
; CURRENT FILING DATE: 2004-09-09

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; PRIOR APPLICATION NUMBER: 60/501,681
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: EP 03029659.4
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
; OTHER INFORMATION: Chain of DEI 5/8
US-10-937-596-32

Query Match      89.1%; Score 2119; DB 5; Length 442;
Best Local Similarity 90.8%; Pred. No. 6.1e-135;
Matches 405; Conservative 16; Mismatches 21; Indels 4; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYSGNTY 60
Db 1 QVQLQESGPGLVKPSQTLSTCTVSGGLSLS--NSITWIRQPPGKPEMGMINSNGD 58
Qy 61 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDGGDDAFDIWGQGTMTV 120
Db 59 YSTLSKSRITISIDTSKNSQVLTMTNMDPVDATYYCAR--YNYFDYWGQGTMTV 116
Qy 121 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPA 180
Db 117 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTF 176
Qy 181 LYSLSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPEFL 240
Db 177 LYSLSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPE 236
Qy 241 LPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPRE 300
Db 237 LPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPRE 296
Qy 301 VVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKQPREPQVYTLPPS 360
Db 297 VVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKQPREPQVYTLPP 356
Qy 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSLRTVDK 420
Db 357 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSLRTVD 416
Qy 421 VFSCSVMEALHNHYTQKSLSLGLK 446
Db 417 VFSCSVMEALHNHYTQKSLSLGLK 442

RESULT 11
US-10-910-901-10
; Sequence 10, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-PF5
; CURRENT APPLICATION NUMBER: US/10/910,901
; CURRENT FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-910-901-10

Query Match      88.6%; Score 2108; DB 5; Length 463;
Best Local Similarity 89.3%; Pred. No. 4.5e-134;
Matches 402; Conservative 16; Mismatches 25; Indels 7; Gaps 3;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYSG 60
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSIR--GYVSWIRQPPGKLEWIGYIYSG 77
Qy 61 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDGG---DDAFDIWGQ 116
Db 78 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARRGGLGYDYGWFWG 137
Qy 117 VSSASTKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSG 176

Best Local Similarity 89.7%; Pred. No. 3.6e-134;
Matches 400; Conservative 16; Mismatches 28; Indels 2; Gaps 2;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYSG 60
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSISSSSYGGWIRQPPGKGLDWIGSIY 79
Qy 61 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDGGDDAFDIWGQGT 120
Db 80 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARHSW--DYFDYWGQ 138
Qy 121 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTF 180
Db 139 STKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHT 198
Qy 181 LYSLSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPE 240
Db 199 LYSLSVTVTPSSSLGTTKTYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPP 257
Qy 241 LPPPKPKDTLMISRTPEVTCVVDVDSQEDPEVQFNWYVDGVEVHNAKTKPRE 300
Db 258 LPPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVEVHNAKTKPRE 317
Qy 301 VVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKQPREPQVYTLPP 360
Db 318 VVSVLTVLHODWLNKGEYKCKVSNKGLPAPIEKTIISKAKQPREPQVYTLPP 377
Qy 361 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSLRTVD 420
Db 378 QVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSPFLYSLRTVD 437
Qy 421 VFSCSVMEALHNHYTQKSLSLGLK 446
Db 438 VFSCSVMEALHNHYTQKSLSLSPGK 463

RESULT 12
US-10-292-088-86
; Sequence 86, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-86

Query Match      88.5%; Score 2106.5; DB 4; Length 466;
Best Local Similarity 89.3%; Pred. No. 4.5e-134;
Matches 402; Conservative 16; Mismatches 25; Indels 7; Gaps 3;

Qy 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYWNIROHPGKLEWIGYIYSG 60
Db 20 QVQLQESGPGLVKPSQTLSTCTVSGGSIR--GYVSWIRQPPGKLEWIGYIYSG 77
Qy 61 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARDGG---DDAFDIWGQ 116
Db 78 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYYCARRGGLGYDYGWFWG 137
Qy 117 VSSASTKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSG 176
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Db 138 VSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 197
QY 177 QSSGLYSLSSVVTVPSSSLGTITTCNVDPKPSNTKVDKRVSKEYGPPCPAPFELGG 236
Db 198 QSSGLYSLSSVVTVPSSNFGTQITTCNVDPKPSNTKVDKTVRKKCCVECPCPAPP-VAG 256
QY 237 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTKPREEQFN 296
Db 257 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTKPREEQFN 316
QY 297 STYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSREE 356
Db 317 STYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAKGQPREPQVYTLPPSREE 376
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRTVDDKSRW 416
Db 377 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRTVDDKSRW 436
QY 417 QEGNVFSCSMHEALHNNHYTQKSLSLSGK 446
Db 437 QCGNVFSCSMHEALHNNHYTQKSLSLSPGK 466

RESULT 13
US-10-292-088-70
; Sequence 70, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-70

Query Match 88.5%; Score 2104.5; DB 4; Length 466;
Best Local Similarity 89.1%; Pred. No. 6.2e-134;
Matches 401; Conservative 17; Mismatches 25; Indels 7; Gaps 3;

QY 1 QVOLQESGGLVKPSTLSLTCTVSGGSISSGGNWNWIRQHPGKGLWIGIYYSGNTY 60
Db 20 QVOLQESGGLVKPSTLSLTCTVSGGSISSGGNWNWIRQHPGKGLWIGIYYSGNTY 77
QY 61 YNPGLSKRITISIDTSKQPSLTLSVTAADTAATVYCAR---DDAFDINGQGTMT 116
Db 78 YNPGLSKRITISIDTSKQPSLTLSVTAADTAATVYCAR---DDAFDINGQGTMT 137
QY 117 VSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 176
Db 138 VSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 197
QY 177 QSSGLYSLSSVVTVPSSSLGTITTCNVDPKPSNTKVDKRVSKEYGPPCPAPFELGG 236
Db 198 QSSGLYSLSSVVTVPSSNFGTQITTCNVDPKPSNTKVDKTVRKKCCVECPCPAPP-VAG 256
QY 237 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTKPREEQFN 296
Db 257 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTKPREEQFN 316
QY 297 STYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSREE 356
Db 317 STYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAKGQPREPQVYTLPPSREE 376
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRTVDDKSRW 416
Db 377 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRTVDDKSRW 436
QY 417 QEGNVFSCSMHEALHNNHYTQKSLSLSGK 446
Db 437 QCGNVFSCSMHEALHNNHYTQKSLSLSPGK 466

Db 317 STYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAKGQPREPQVYTLPPSREE 376
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRTVDDKSRW 416
Db 377 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRTVDDKSRW 436
QY 417 QEGNVFSCSMHEALHNNHYTQKSLSLSGK 446
Db 437 QCGNVFSCSMHEALHNNHYTQKSLSLSPGK 466

RESULT 14
US-10-292-088-30
; Sequence 30, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-30

Query Match 88.1%; Score 2096.5; DB 4; Length 466;
Best Local Similarity 88.9%; Pred. No. 2.1e-133;
Matches 400; Conservative 16; Mismatches 27; Indels 7; Gaps 3;

QY 1 QVOLQESGGLVKPSTLSLTCTVSGGSISSGGNWNWIRQHPGKGLWIGIYYSGNTY 60
Db 20 QVOLQESGGLVKPSTLSLTCTVSGGSISSGGNWNWIRQHPGKGLWIGIYYSGNTY 77
QY 61 YNPGLSKRITISIDTSKQPSLTLSVTAADTAATVYCAR---DGGDDAFDIWQGTMT 116
Db 78 YNPGLSKRITISIDTSKQPSLTLSVTAADTAATVYCAR---DGGDDAFDIWQGTMT 137
QY 117 VSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 176
Db 138 VSSASTKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 197
QY 177 QSSGLYSLSSVVTVPSSSLGTITTCNVDPKPSNTKVDKRVSKEYGPPCPAPFELGG 236
Db 198 QSSGLYSLSSVVTVPSSNFGTQITTCNVDPKPSNTKVDKTVRKKCCVECPCPAPP-VAG 256
QY 237 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTKPREEQFN 296
Db 257 PSVFLPPPKPDKTLMISRTPEVTCVVVDVSDPEVFQFNWYVDGVEVHNAKTKPREEQFN 316
QY 297 STYRVVSVLTVLHODWLNKGYCKVSNKGLPSSIEKTIKAKGQPREPQVYTLPPSREE 356
Db 317 STYRVVSVLTVLHODWLNKGYCKVSNKGLPAPIEKTIKAKGQPREPQVYTLPPSREE 376
QY 357 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRTVDDKSRW 416
Db 377 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSEFFLYSLRTVDDKSRW 436
QY 417 QEGNVFSCSMHEALHNNHYTQKSLSLSGK 446
Db 437 QCGNVFSCSMHEALHNNHYTQKSLSLSPGK 466

```
RESULT 15
US-10-818-068-25
; Sequence 25, Application US/10818068
; Publication No. US20050002930A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: METHODS OF PRODUCTION AND USE OF ANTI-INTEGRIN ANTIBODIES FOR THE
; TITLE OF INVENTION: CONTROL OF TISSUE GRANULATION
; FILE REFERENCE: 05882.0186.NPUS01
; CURRENT APPLICATION NUMBER: US/10/818,068
; CURRENT FILING DATE: 2004-04-02
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-818-068-25

Query Match      87.8%; Score 2088.5; DB 5; Length 451;
Best Local Similarity 87.6%; Pred.No. 7.2e-133;
Matches 397; Conservative 20; Mismatches 27; Indels 9; Gaps 2;

Qy      1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYMNIHQHPGKLEWIGYIYSGNTY 60
Db      1 QVQLKESGPGLVAPQSQSLITCTISGFLTDYGVH--WVRQPPGKLEWLVVINS DGSST 58

Qy      61 YNPISLKSRITISIDTSKNQFSLTSSVTAADPAVYYCARDG-----GDDAFDIWGQGT 113
Db      59 YNSALKSRMTIRKDNKSKQVFLIMNSLQTDSDSAMYCARHGTYYGMTTTGDALDYWGQGT 118

Qy      114 MYTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 173
Db      119 SVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 178

Qy      174 AVLQSSGLYSLSVTVTPSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPEF 233
Db      179 AVLQSSGLYSLSVTVTPSSSLGTITYTCNVDPKPSNTKVDKRVESKYGPPCPSPAPEF 238

Qy      234 LGGPSVFLFPPPKPDTLMISRTPETCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE 293
Db      239 LGGPSVFLFPPPKPDTLMISRTPETCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREE 298

Qy      294 QFNSTYRVVSVLTVLIHQDLNKGKEYCKVSNKGLPSSIEKTIISKAKGQPRPQVYTLPPS 353
Db      299 QFNSTYRVVSVLTVLIHQDLNKGKEYCKVSNKGLPSSIEKTIISKAKGQPRPQVYTLPPS 358

Qy      354 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK 413
Db      359 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVDK 418

Qy      414 SRWQEGNVFSCVMHEALHNHYTQKSLSLGLK 446
Db      419 SRWQEGNVFSCVMHEALHNHYTQKSLSLGLK 451
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Search completed: December 17, 2005, 01:29:29
Job time : 148.315 secs

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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:18:45 ; Search time 9.46061 Seconds
(without alignments)
317.590 Million cell updates/sec

Title: US-10-644-277-62
Perfect score: 2379
Sequence: 1 QVQLQESGFLVKPSTLSL.....MHEALHNYTKSLSLGK 446

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.New.*
1: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB_PEP.*
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB_PEP.*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB_PEP.*
4: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB_PEP.*
5: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB_PEP.*
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB_PEP.*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB_PEP.*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2044.5	85.9	476	7	US-11-139-499-12
2	1986.5	83.5	476	7	US-11-139-499-4
3	1970.5	82.8	451	6	US-10-923-327-11
4	1967.5	82.7	451	6	US-10-923-327-7
5	1967.5	82.7	451	6	US-10-923-327-9
6	1928.5	81.1	470	7	US-11-144-248-49
7	1920	80.7	477	7	US-11-000-463-395
8	1917	80.6	473	7	US-11-144-248-50
9	1912.5	80.4	470	7	US-11-144-248-45
10	1910	80.3	452	7	US-11-120-338-14
11	1905	80.1	451	7	US-11-120-338-22
12	1901.5	79.9	470	7	US-11-144-248-46
13	1895	79.7	444	7	US-11-172-320-6
14	1895	79.7	444	7	US-11-173-969-6
15	1895	79.7	452	7	US-11-120-338-15
16	1881	79.1	452	7	US-11-120-338-17
17	1876	78.9	451	7	US-11-120-338-25
18	1863	78.3	450	7	US-11-025-712-12
19	1854.5	78.0	478	7	US-11-139-499-8
20	1853.5	77.9	474	7	US-11-000-463-284
21	1842	77.4	579	7	US-11-174-186-41
22	1743	73.3	327	6	US-10-999-866-38
23	1743	73.3	327	7	US-11-061-821-38
24	1611.5	67.7	335	7	US-11-024-251-35
25	1605.5	67.5	326	6	US-10-999-866-36

26	1605.5	67.5	326	7	US-11-144-248-28	Sequence 28, Appl
27	1605.5	67.5	326	7	US-11-061-821-36	Sequence 36, Appl
28	1596.5	67.1	330	7	US-11-022-289-1	Sequence 1, Appl
29	1596.5	67.1	548	7	US-11-022-289-3	Sequence 3, Appl
30	1596.5	67.1	557	7	US-11-022-289-2	Sequence 2, Appl
31	1596.5	67.1	564	7	US-11-022-289-10	Sequence 10, Appl
32	1594.5	67.0	402	7	US-11-024-251-31	Sequence 31, Appl
33	1590.5	66.9	330	7	US-11-022-289-11	Sequence 11, Appl
34	1590.5	66.9	330	7	US-11-075-351-1	Sequence 15, Appl
35	1590.5	66.9	330	7	US-11-165-141-15	Sequence 1, Appl
36	1590.5	66.9	551	7	US-11-022-289-7	Sequence 7, Appl
37	1590.5	66.9	551	7	US-11-022-289-8	Sequence 8, Appl
38	1590.5	66.9	557	7	US-11-022-289-4	Sequence 4, Appl
39	1590.5	66.9	557	7	US-11-022-289-5	Sequence 5, Appl
40	1590.5	66.9	557	7	US-11-022-289-6	Sequence 6, Appl
41	1580	66.4	339	6	US-10-999-866-35	Sequence 35, Appl
42	1580	66.4	339	7	US-11-061-821-35	Sequence 35, Appl
43	1575	66.2	377	6	US-10-999-866-37	Sequence 37, Appl
44	1575	66.2	377	7	US-11-061-821-37	Sequence 37, Appl
45	1251	52.6	917	7	US-11-144-987-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-11-139-499-12
; Sequence 12, Application US/11139499
; Publication No. US20050260205A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: BRAMS, PETER
; APPLICANT: HEARD, CHERYL
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
; TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
; FILE REFERENCE: 37003-275681
; CURRENT APPLICATION NUMBER: US/11/139,499
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US/09/576,424
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US97/19906
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 08/746,361
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: 08/487,550
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-139-499-12

Query Match 85.9%; Score 2044.5; DB 7; Length 476;
Best Local Similarity 85.6%; Pred. No. 2.1e-116;
Matches 392; Conservative 21; Mismatches 32; Indels 13; Gaps 4;

QY	1	QVQLQESGFLVKPSTLSLTCTVSGGSISSGGYNNWIRQHPGKLEWIGYIY-YSGNT 59	
Db	20	QVQLQESGFLVKPSTLSLTCAVSGSI-SGGYGGWIRQHPGKLEWIGYIYSGNT 78	
QY	60	YNNPSLKSRITISIDTSKNQFSLTSSVTAADTAAYVYCARDG-----GDDAFDIWGQ 111	
Db	79	YNNPSLKSVTISTDTSKNQFSLKNSMTAADTAAYVYCVDRDLFSVVGMYNNWFDVWGP 138	
QY	112	GTWTVSSASTKGPSVFPLAPCSRSESTAAALGCLVKDYFPEPTVTSWNSGALTSGVHT 171	
Db	139	GVLTWTVSSASTKGPSVFPLAPSKSTGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHT 198	
QY	172	FPAVLQSSGLYSLSVVTVPSSSLGTCTVTCNDHKPSNTKVDKRVESK---YGPFPSPSC 228	

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Db 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 258
QY 229 PAPEFLGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKT 288
Db 259 PAPELGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
QY 289 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVY 348
Db 319 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVY 378
QY 349 TLPDSRQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR 408
Db 379 TLPDSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
QY 409 LTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 446
Db 439 LTVDKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPGK 476
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RESULT 2

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US-11-139-499-4
; Sequence 4, Application US/11139499
; Publication No. US200502605A1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: BRAMS, PETER
; APPLICANT: HEARD, CHERYL
; TITLE OF INVENTION: CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
; TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
; FILE REFERENCE: 37003-275681
; CURRENT APPLICATION NUMBER: US/11/139,499
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US/09/576,424
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US97/19906
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 08/746,361
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: 08/487,550
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-139-499-4
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Query Match 83.5%; Score 1986.5; DB 7; Length 476;
Best Local Similarity 83.4%; Pred. No. 6.2e-113;
Matches 382; Conservative 24; Mismatches 39; Indels 13; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLISLTCTVSGGSISSGGYNNWIRQHPGKLEWIGYIYSG-NT 59
Db 20 QVKLQGWGEGLLQPSSETLSRTCVSSGGSI-SGYIYTWIRQTPGKLEWIGHIYNGGATT 78
QY 60 YNPISLKRITISIDTSKNQFSLTLSSVTAADTAVVYCARDGDDA-----FDIWGQ 111
Db 79 NNPISLKRVTLSKDTSKNQFFLNLSVTDATAVYCARGRPRDCTICYGGWVDWVGP 138
QY 112 GTMTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSVGH 171
Db 139 GDLVTVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGH 198
QY 172 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 228
Db 199 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPC 258
QY 229 PAPEFLGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKT 288
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Db 259 PAPELGGSPVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 318
QY 289 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVY 348
Db 319 KPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVY 378
QY 349 TLPDSRQEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSR 408
Db 379 TLPDSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK 438
QY 409 LTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLGLK 446
Db 439 LTVDKSRWQGNVFCFSVMHEALHNHYTQKSLSLSPGK 476

RESULT 3
US-10-923-327-11
; Sequence 11, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 11
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: construct
US-10-923-327-11
```

```
Query Match 82.8%; Score 1970.5; DB 6; Length 451;
Best Local Similarity 83.8%; Pred. No. 5.4e-112;
Matches 379; Conservative 23; Mismatches 43; Indels 7; Gaps 3;

QY 1 QVQLQESGPGLVKPSQTLISLTCTVSGGSISSGGYNNWIRQHPGKLEWIGYIYSGNTY 60
Db 1 EVQLVESGGGLVQPGLSLRLSCAVSGYSITSGYS-WNIRQAPGKLEWVASIKYSGTK 59
QY 61 YNPISLKRITISIDTSKNQFSLTLSSVTAADTAVVYCARDG---GDDAFDIWGGTMTVT 117
Db 60 YNPISLKRITISIDTSKNQFSLTLSSVTAADTAVVYCARDG---GDDAFDIWGGTMTVT 119
QY 118 SSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSVGHFPFPAVLQ 177
Db 120 SSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHFPFPAVLQ 179
QY 178 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPCPAP 234
Db 180 SSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKAEPKSCDKTHTCPPCPAP 239
QY 235 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPREEQ 294
Db 240 GGPSVFLPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 299
QY 295 FNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPOVYTLPPSQ 354
Db 300 YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359
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QY 355 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKS 414
 DB 360 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKS 419

QY 415 RWQEGNVFSCSVMEALHNNHYTKQSLSLGK 446
 DB 420 RWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 451

RESULT 4
 US-10-923-327-7
 ; Sequence 7, Application US/10923327
 ; Publication No. US20050261208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ROBINSON, CYNTHIA B.
 ; APPLICANT: BALL, HOWARD A.
 ; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
 ; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
 ; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
 ; TITLE OF INVENTION: PULMONARY DISEASE
 ; FILE REFERENCE: 30775-723.501
 ; CURRENT APPLICATION NUMBER: US/10/923,327
 ; CURRENT FILING DATE: 2004-08-20
 ; PRIOR APPLICATION NUMBER: PCT/US04/25054
 ; PRIOR FILING DATE: 2004-07-30
 ; PRIOR FILING DATE: 2003-10-29
 ; PRIOR FILING DATE: 2003-10-29
 ; PRIOR FILING DATE: 2003-07-31
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn ver. 3.3
 ; SEQ ID NO 7
 ; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: construct
 US-10-923-327-7

Query Match 82.7%; Score 1967.5; DB 6; Length 451;
 Best Local Similarity 83.6%; Pred. No. 8.1e-112;
 Matches 378; Conservative 24; Mismatches 43; Indels 7; Gaps 3;

QY 1 QVOLQESGGLVQPGGSLRLSCAVSGYSITSYGS-WNWIRQAPGKGLEWASITYDGSN 59
 DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSYGS-WNWIRQAPGKGLEWASITYDGSN 59

QY 61 YNPGLKSRITISIDTSKNQFSLTSSVTAADTAIVYICARDG---GDDAFDIWGGTMTV 117
 DB 60 YNPVSKGRITISRDSDKNTFYLQMSLRRAEDTAIVYICARGSHYFGHWHFAVWGQGLTV 119

QY 118 SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 177
 DB 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 179

QY 178 SGLYSLSSVTVTPSSSLGTTKTYTCNVDHKPSNTKVDKRVESK---YGPCCPCPAPEFL 234
 DB 180 SGLYSLSSVTVTPSSSLGTTKTYTCNVNHKPSNTKVDKRVESKCDKTHTCPPCPAPELL 239

QY 235 GGPSVFLFPKPKDGLMISRTPEVTVVVDVSDQEDPEVQFNWYDGVGVHNAKTKPREEQ 294
 DB 240 GGPSVFLFPKPKDGLMISRTPEVTVVVDVSDHEDPEVKFNWYDGVGVHNAKTKPREEQ 299

QY 295 FNSTYRVVSVLTVLHODWLNKGEYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPPSQ 354
 DB 300 YNSTYRVVSVLTVLHODWLNKGEYCKVSNKGLPAPIEKTISSAKGQPREPQVYTLPPSR 359

QY 355 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKS 414
 DB 360 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKS 419

QY 415 RWQEGNVFSCSVMEALHNNHYTKQSLSLGK 446
 DB 420 RWQGNVFCSCVMHEALHNNHYTKQSLSLSPGK 451

RESULT 5
 US-10-923-327-9
 ; Sequence 9, Application US/10923327
 ; Publication No. US20050261208A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ROBINSON, CYNTHIA B.
 ; APPLICANT: BALL, HOWARD A.
 ; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
 ; TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
 ; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
 ; TITLE OF INVENTION: PULMONARY DISEASE
 ; FILE REFERENCE: 30775-723.501
 ; CURRENT APPLICATION NUMBER: US/10/923,327
 ; CURRENT FILING DATE: 2004-08-20
 ; PRIOR APPLICATION NUMBER: PCT/US04/25054
 ; PRIOR FILING DATE: 2004-07-30
 ; PRIOR FILING DATE: 2003-10-29
 ; PRIOR FILING DATE: 2003-10-29
 ; PRIOR FILING DATE: 2003-07-31
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn ver. 3.3
 ; SEQ ID NO 9
 ; LENGTH: 451
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: construct
 US-10-923-327-9

Query Match 82.7%; Score 1967.5; DB 6; Length 451;
 Best Local Similarity 83.6%; Pred. No. 8.1e-112;
 Matches 378; Conservative 24; Mismatches 43; Indels 7; Gaps 3;

QY 1 QVOLQESGGLVQPGGSLRLSCAVSGYSITSYGS-WNWIRQAPGKGLEWASITYDGSN 59
 DB 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSYGS-WNWIRQAPGKGLEWASITYDGSN 59

QY 61 YNPGLKSRITISIDTSKNQFSLTSSVTAADTAIVYICARDG---GDDAFDIWGGTMTV 117
 DB 60 YNPVSKGRITISRDSDKNTFYLQMSLRRAEDTAIVYICARGSHYFGHWHFAVWGQGLTV 119

QY 118 SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 177
 DB 120 SSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 179

QY 178 SGLYSLSSVTVTPSSSLGTTKTYTCNVDHKPSNTKVDKRVESK---YGPCCPCPAPEFL 234
 DB 180 SGLYSLSSVTVTPSSSLGTTKTYTCNVNHKPSNTKVDKRVESKCDKTHTCPPCPAPELL 239

QY 235 GGPSVFLFPKPKDGLMISRTPEVTVVVDVSDQEDPEVQFNWYDGVGVHNAKTKPREEQ 294
 DB 240 GGPSVFLFPKPKDGLMISRTPEVTVVVDVSDHEDPEVKFNWYDGVGVHNAKTKPREEQ 299

QY 295 FNSTYRVVSVLTVLHODWLNKGEYCKVSNKGLPSSIEKTISSAKGQPREPQVYTLPPSQ 354
 DB 300 YNSTYRVVSVLTVLHODWLNKGEYCKVSNKGLPAPIEKTISSAKGQPREPQVYTLPPSR 359

QY 355 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKS 414
 DB 360 EMTKNQVSLTCLVKGFYPSDIAVEWESNGQPNNTKTPPVLDSDGSPFLYSRLTVDKS 419

```
RESULT 6
US-11-144-248-49
; Sequence 49, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-49

Query Match      81.1%; Score 1928.5; DB 7; Length 470;
Best Local Similarity 81.7%; Pred. No. 1.8e-109;
Matches 371; Conservative 23; Mismatches 49; Indels 11; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYWNIHQHPGKLEWIGYIYSGNTY 60
Db 20 QAQLVESGGGLVKPGGSLRLSCAASGFTFSD--YYMSWIRQAPGKLEWVSYISSGSTR 77
QY 61 -YNPSLKRITISIDTSKNQFSLTSSVTAADTAVYVCARDGGDAF-----DIMGG 112
Db 78 DYADSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYICVRDGVETFTYYVYGMDDVWGQ 137
QY 113 TMVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 172
Db 138 TTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 197
QY 173 PAVLQSSGLYSLSVTVTPSSSLGTQTYTCNVNDHKPSNTKVDKRVESKYPGPCPCPAPE 232
Db 198 PAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVNDHKPSNTKVDKRVKCCVCEPCPAPP 257
QY 233 FLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVVHNAKTKPRE 292
Db 258 -VAGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVVHNAKTKPRE 316
QY 293 EGFNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKQPREPQVYTLPP 352
Db 317 EGFNSTFRVSVSLTVVHODWLNKGEYKCKVSNKGLPAPIEKTISKTKQPREPQVYTLPP 376
QY 353 SOEEMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSRLTVD 412
Db 377 SREEMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 436
QY 413 KSRWQEGNVFSCSVNHEALHNHYTQKSLSLSPGK 446
Db 437 KSRWQEGNVFSCSVNHEALHNHYTQKSLSLSPGK 470

RESULT 7
US-11-000-463-395
; Sequence 395, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenchua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
```

```
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 395
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-395

Query Match      80.7%; Score 1920; DB 7; Length 477;
Best Local Similarity 80.4%; Pred. No. 6e-109;
Matches 370; Conservative 27; Mismatches 47; Indels 16; Gaps 4;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGSISGGNYWNIHQHPGKLEWIGYIYSG-NT 59
Db 20 QVQLVESGGGVQVQPSRLSLSCAASGFTFSNYG--MHVVRQAPGKLEWVAAILWYDGSNK 77
QY 60 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAVYVCARDGG-----DDAFDIW 109
Db 78 YYADSVKGRFTISRDNKNSLYLQNSLRRAEDTAVYICAREGRVRYTIVTIGYFYDIW 137
QY 110 GQGTMTVTSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGV 169
Db 138 GQGTMTVTSSASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGV 197
QY 170 HTFPAVLQSSGLYSLSVTVTPSSSLGTQTYTCNVNDHKPSNTKVDKRVESK---YGPPEP 226
Db 198 HTFPAVLQSSGLYSLSVTVTPSSSLGTQTYTCNVNHNKPSNTKVDKRVESKCDKTHTCP 257
QY 227 SCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSOEDPEVQFNWYVDGVVHNA 286
Db 258 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGVVHNA 317
QY 287 KTKPREEQFNSTYRVSVSLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKQPREPQ 346
Db 318 KTKPREEQFNSTYRVSVSVLTVLHODWLNKGEYKCKVSNKGLPAPIEKTISKAKQPREPQ 377
QY 347 VYTLPPSQEEMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY 406
Db 378 VYTLPPSREEMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLY 437
QY 407 SRLTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLSPGK 446
Db 438 SKLTVDKSRWQEGNVFSCSVNHEALHNHYTQKSLSLSPGK 477

RESULT 8
US-11-144-248-50
; Sequence 50, Application US/11144248
```

```
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 50
LENGTH: 473
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-50

Query Match      80.6%; Score 1917; DB 7; Length 473;
Best Local Similarity 80.7%; Pred. No. 9e-109;
Matches 372; Conservative 22; Mismatches 45; Indels 22; Gaps 5;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNWIHQHPGKLEWIGYIYSGNT- 59
DB 20 QVQLVESGGGLVQPGGSLRLSCAASGFTPSD--YIMSWIRQAPGKLEWYSISSGSI 77
QY 60 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAATVYICAR-----DGDGDA 105
DB 78 YVADSVKGRFTISRDNKNSLYLQMNSLRAEDTAATVYICARVLEWLYYYG---- 133
QY 106 FDIWGQGTMTVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGAL 165
DB 134 MDVWGQGTMTVSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGAL 193
QY 166 TSGVHTPEAVLQSSGLYSLSVTVPSVSSISLGTQYTCNVDPKPSNTKVDKRVESKYGPPC 225
DB 194 TSGVHTPEAVLQSSGLYSLSVTVPSVSSISLGTQYTCNVDPKPSNTKVDKRVESKYGPPC 253
QY 226 PSCPAPEFLGPGSVFLPFPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVGVHN 285
DB 254 PSCPAPE-VAGPSVFLPFPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVGVHN 312
QY 286 AKTKPREEQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREP 345
DB 313 AKTKPREEQNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPAPIEKTIKAKGQPREP 372
QY 346 QVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 405
DB 373 QVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFL 432
QY 406 YSLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK 446
DB 433 YSLTVDKSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK 473

RESULT 9
US-11-144-248-45
Sequence 45, Application US/11144248
Publication No. US20050244408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
```

```
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-45

Query Match      80.4%; Score 1912.5; DB 7; Length 470;
Best Local Similarity 81.3%; Pred. No. 1.7e-108;
Matches 369; Conservative 27; Mismatches 47; Indels 11; Gaps 5;

QY 1 QVQLQESGPGLVKPSQTLSTCTVSGGSISSGGNYNWIHQHPGKLEWIGYIYSGNT 59
DB 20 EVQLLESQGLVQPGGSLRLSCTASGFTFSYA--NMWVRQAPGKLEWVSALSGSGT 77
QY 60 YNPSLKSRITISIDTSKNQFSLTSSVTAADTAATVYICAR-----DWDGAF 112
DB 78 FYADSVKGRFTISRDNSTRTLLQMNLSRAEDTAATVYICARLDGWSDSYIYGMVWGQ 137
QY 113 TWVTYSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTF 172
DB 138 TTVTYSSASTKGPSVFLPAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTF 197
QY 173 PAVLQSSGLYSLSVTVPSVSSISLGTQYTCNVDPKPSNTKVDKRVESKYGPPCPCPAPE 232
DB 198 PAVLQSSGLYSLSVTVPSVSSISLGTQYTCNVDPKPSNTKVDKRVESKYGPPCPCPAPE 257
QY 233 FLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVGVHNKTKPRE 292
DB 258 -VAGPSVFLPFPKPKDTLMISRTPEVTCVVDVSDQEDPEVQFNWYDGVGVHNKTKPRE 316
QY 293 EQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIKAKGQPREQVYTLPP 352
DB 317 EQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPAPIEKTIKAKGQPREQVYTLPP 376
QY 353 SQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVD 412
DB 377 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSRLTVD 436
QY 413 KSRWQEGNVFSCSVMEALHNHYTQKSLSLGLK 446
DB 437 KSRWQEGNVFSCSVMEALHNHYTQKSLSLSPGK 470

RESULT 10
US-11-120-338-14
Sequence 14, Application US/11120338
Publication No. US20050271658A1
GENERAL INFORMATION:
APPLICANT: BRUNETTA, PAUL G.
APPLICANT: GREWAL, IQBAL S.
APPLICANT: WALICKE, PATRICIA A.
TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
FILE REFERENCE: P2079R2
CURRENT APPLICATION NUMBER: US/11/120,338
CURRENT FILING DATE: 2005-05-03
PRIOR APPLICATION NUMBER: US 60/568,460
PRIOR FILING DATE: 2004-05-05
NUMBER OF SEQ ID NOS: 25
SEQ ID NO 14
LENGTH: 452
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
```

US-11-120-338-14

Query Match 80.3%; Score 1910; DB 7; Length 452;
Best Local Similarity 81.1%; Pred. No. 2.3e-108;
Matches 368; Conservative 27; Mismatches 49; Indels 10; Gaps 4;

QY 1 QVLOESGGLVKPQSLTCTVSGGSISSGGNYWNIHQHPGKLEWIGYIY-YSNGT 59
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYN--MHWVRQAPGKLEWVGAIYPGNGDT 58
60 YNPGLSKRITISIDTSKNQFSLTSSVTAADTAVYYCAR----DGGDDAFDIMGQGMV 115
DB 59 SYNQFKGRFTISVDKSKNTLYLQNSLRAEDTAVYYCARVYVYNSYWFYFDVMQGGTLV 118
QY 116 TVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTVSNWNSGALTSVGVHTFP 175
DB 119 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSVGVHTFP 178
QY 176 LOSSGLYSLSVTVTPSSSLGTQYICNVNHKPSNTKVDKRVESK---YGPPCPCPAPE 232
DB 179 LOSSGLYSLSVTVTPSSSLGTQYICNVNHKPSNTKVDKRVESK---YGPPCPCPAPE 238
QY 233 FLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRE 292
DB 239 LLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRE 298
QY 293 EQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPP 352
DB 299 EQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPP 358
QY 353 SOEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 412
DB 359 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 418
QY 413 KSRWQGNVFCSCVMHEALHNHYTQKSLSLGLK 446
DB 419 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 452

RESULT 11

US-11-120-338-22
; Sequence 22, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, IQBAL S.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 22
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized

US-11-120-338-22

Query Match 80.1%; Score 1905; DB 7; Length 451;
Best Local Similarity 81.0%; Pred. No. 4.5e-108;
Matches 367; Conservative 27; Mismatches 49; Indels 10; Gaps 4;

QY 1 QVLOESGGLVKPQSLTCTVSGGSISSGGNYWNIHQHPGKLEWIGYIY-YSNGT 59
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFTSYN--MHWVRQAPGKLEWVGAIYPGNGDT 58
60 YNPGLSKRITISIDTSKNQFSLTSSVTAADTAVYYCAR----DGGDDAFDIMGQGMV 115
DB 59 SYNQFKGRFTISVDKSKNTLYLQNSLRAEDTAVYYCARVYVYNSYWFYFDVMQGGTLV 118

QY 116 TVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTVSNWNSGALTSVGVHTFP 175
DB 119 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSVGVHTFP 178
QY 176 LOSSGLYSLSVTVTPSSSLGTQYICNVNHKPSNTKVDKRVESK---YGPPCPCPAPE 232
DB 179 LOSSGLYSLSVTVTPSSSLGTQYICNVNHKPSNTKVDKRVESK---YGPPCPCPAPE 238
QY 233 FLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRE 292
DB 239 LLGGPSVFLFPKPKDITLMISRTPEVTCVVDVSDQEDPEVQFNWYVDGVEVHNAKTKPRE 298
QY 293 EQFNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPP 352
DB 299 EQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPP 358
QY 353 SOEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 412
DB 359 SREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSRLTVD 418
QY 413 KSRWQGNVFCSCVMHEALHNHYTQKSLSLGL 445
DB 419 KSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 451

RESULT 12

US-11-144-248-46
; Sequence 46, Application US/11144248
; Publication No. US20050244408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Besbe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: AEX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-144-248-46

Query Match 79.9%; Score 1901.5; DB 7; Length 470;
Best Local Similarity 80.8%; Pred. No. 7.6e-108;
Matches 367; Conservative 25; Mismatches 51; Indels 11; Gaps 4;

QY 1 QVLOESGGLVKPQSLTCTVSGGSISSGGNYWNIHQHPGKLEWIGYIYYS-GNT 59
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYA--MSWVRQAPGKLEWVAISGGSGT 77
60 YNPGLSKRITISIDTSKNQFSLTSSVTAADTAVYYCARDGDD-----APDIMGQ 112
DB 78 YYADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKGYSGWYIYVYGMVWGQ 137
QY 113 TMVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTVSNWNSGALTSVGVHTF 172
DB 138 TMVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTVSNWNSGALTSVGVHTF 197
QY 173 PAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHKPSNTKVDKRVESKYGKPPCPCPAPE 232
DB 198 PAVLQSSGLYSLSVTVTPSSSLGTQYICNVNHKPSNTKVDKRVESKCCVCCPCPAPP 257

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:09:23 ; Search time 84,9515 Seconds
(without alignments)
1106.832 Million cell updates/sec

Title: US-10-644-277-64
Perfect score: 1115
Sequence: 1 DQMTQSPSLSASVGRVT.....EVTHQGLSPVTKSFNRGRC 214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1115	100.0	*214	8 ADK52358	Adk52358 Human ant
2	1060	95.1	238	9 ABB45883	Aeb45883 Human mon
3	1051	94.3	236	7 ADD93785	Adg93785 Monoclonal
4	1045	93.7	502	8 ADN97515	Adn97515 Artificia
5	1039	93.2	367	3 AAY55078	Aay55078 Single ch
6	1039	93.2	626	3 AAY55081	Aay55081 Single ch
7	1037	93.0	237	8 ADQ90721	Adq90721 Anti-VEGF
8	1034	92.7	214	7 ADC26154	Adc26154 Parent an
9	1034	92.7	237	5 ABB81107	Abb81107 Protein e
10	1034	92.7	237	5 ABB81107	Abb81107 Anti-VEGF
11	1034	92.7	237	5 ABP51952	Abp51952 Plasmid p
12	1034	92.7	237	8 AD014128	Ado14128 Plasmid p
13	1034	92.7	237	8 AD014131	Ado14131 Plasmid p
14	1034	92.7	237	8 ADQ90703	Adq90703 Anti-VEGF
15	1034	92.7	237	8 ADQ90701	Adq90701 Anti-VEGF
16	1034	92.7	237	8 ADQ90705	Adq90705 Anti-VEGF
17	1034	92.7	237	8 ADQ90709	Adq90709 Anti-VEGF
18	1034	92.7	237	8 ADQ90723	Adq90723 Anti-VEGF
19	1034	92.7	237	8 ADQ90707	Adq90707 Anti-VEGF
20	1034	92.7	260	5 ABP41164	Abp41164 Human ova
21	1034	92.7	650	5 ABP61241	Abp61241 Phage-dis
22	1027	92.1	214	2 AAW34504	Aaw34504 Light cha
23	1027	92.1	214	2 AAW34506	Aaw34506 Light cha
24	1027	92.1	214	2 AAW95615	Aaw95615 Humanized

25	1027	92.1	214	2 AAW30632	Aaw30632 Recombina
26	1027	92.1	214	2 AAY08754	Aay08754 Human ant
27	1027	92.1	214	4 AAB66777	Aab66777 rhuMAB CD
28	1027	92.1	214	5 ABG31889	Abg31889 Humanised
29	1027	92.1	214	8 ADK18342	Adk18342 Amino aci
30	1027	92.1	214	8 ADK18342	Adk18342 Humanised
31	1027	92.1	214	9 AEB27968	Aeb27968 Humanized
32	1027	92.1	233	2 AAR30777	Aar30777 pH52-9.0
33	1027	92.1	237	2 AAW95622	Aaw95622 PS1130 ex
34	1027	92.1	237	2 AAW30634	Aaw30634 Recombina
35	1027	92.1	237	4 AAB66784	Aab66784 Protein e
36	1027	92.1	237	6 ABF72745	Abf72745 Anti-CD18
37	1027	92.1	237	9 AEB27976	Aeb27976 E. coli S
38	1027	92.1	245	2 AAR98943	Aar98943 Humanised
39	1027	92.1	537	3 AAB03664	Aab03664 Anti-CD18
40	1026	92.0	233	2 AAR22754	Aar22754 Reshaped
41	1026	92.0	272	5 AAU97611	Aau97611 Protein #
42	1026	92.0	275	5 AAU97610	Aau97610 Protein e
43	1026	92.0	288	5 AAU97609	Aau97609 Protein e
44	1026	92.0	288	5 AAU97609	Aau97609 Protein e
45	1025.5	92.0	213	8 ADP88495	Adp88495 Humanised

ALIGNMENTS

RESULT 1	
ADK52358	
ID	ADK52358 standard; protein; 214 AA.
XX	XX
AC	ADK52358;
XX	XX
DT	20-MAY-2004 (first entry)
XX	XX
DE	Human anti-MCP-1 variable region light chain #16.
XX	XX
KW	monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW	Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW	Vasotropic; Immunosuppressive; Neuroprotective; Neoplastic;
KW	Inflammatory condition; cancer; arthritis; multiple sclerosis;
KW	anti-MCP-1; heavy chain; light chain.
XX	XX
OS	Homo sapiens.
XX	XX
PN	WQ2004016769-A2.
XX	XX
PD	26-FEB-2004.
XX	XX
PF	19-AUG-2003; 2003WO-US026232.
XX	XX
PR	19-AUG-2002; 2002US-0404802P.
PA	(ABGE-) ABGENIX INC.
XX	XX
PI	Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI	Bhakta S;
XX	XX
DR	WPI; 2004-203794/19.
DR	N-PSDB; ADK52357.
XX	XX
PT	New human monoclonal antibody that binds to monocyte chemo-attractant
PT	protein-1 and is immobilized on an insoluble matrix, useful for
PT	diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT	rheumatoid arthritis or psoriasis.
XX	XX
PS	Claim 2; SEQ ID NO 64; 154pp; English.
XX	XX
CC	The present invention relates to a human monoclonal antibody that binds
CC	to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC	for the preparation of a medicament useful for treating neoplastic or
CC	inflammatory conditions. The neoplastic disease is selected from breast
CC	cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC	stomach cancer, endometrial cancer, kidney cancer, colon cancer,

CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.

XX Sequence 214 AA;

Query Match 100.0%; Score 1115; DB 8; Length 214;
Best Local Similarity 100.0%; Pred. No. 2e-55; Indels 0; Gaps 0;
Matches 214; Conservative 0; Mismatches 0;

QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISNLYNWYQKPKAPKLLIYDASNLETGVP 60
DB |||||
1 DIQMTQSPSSLSASVGRVITTCQASQDISNLYNWYQKPKAPKLLIYDASNLETGVP 60
QY 61 RFSGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSGQGTKLIRKTVAAPSVFIIPP 120
DB |||||
61 RFSGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSGQGTKLIRKTVAAPSVFIIPP 120
QY 121 SPEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180
DB |||||
121 SPEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB |||||
181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 2

ABB45883
ID AEB45883 standard; protein; 238 AA.

AC AEB45883;

DT 06-OCT-2005 (first entry)

DE Human monoclonal anti-MadCAM antibody #24.

KW Monoclonal antibody; mucosal addressin cell adhesion molecule; MadCAM;
KW inflammation; inflammatory bowel disease; Crohn's disease;
KW ulcerative colitis; diverticular disease; gastritis; liver disease;
KW primary biliary cirrhosis; primary sclerosing cholangitis;
KW insulin dependent diabetes; graft versus host disease; antiinflammatory;
KW gastrointestinal-gen.; antidiabetic; hepatotropic; antidiabetic;
KW immunosuppressive; antibody.

OS Homo sapiens.

XX WO2005067620-A2.

XX 28-JUL-2005.

PF 07-JAN-2005; 2005WO-US000370.

PR 09-JAN-2004; 2004US-0535490P.

PA (PFIZ) PFIZER INC.

PA (ABGE-) ABGENIX INC.

PA (PFIZ) PFIZER LTD.

PI Pullen N, Molloy E, Kellermann S, Green LL, Haak-Frendscho M;

DR WPI: 2005-554958/56.

DR N-PSDB; AEB45882.

XX New antibody to Mucosal Adressin Cell Adhesion Molecule, useful for

PT diagnosing and treating an inflammatory disease, e.g. inflammatory bowel

PT disease, ulcerative colitis, gastritis, insulin-dependent diabetes or

PT graft versus host disease.

PS Claim 8; SEQ ID NO 48; 167pp; English.

XX The invention relates to a human monoclonal antibody or its antigen-
CC binding portion that specifically binds to mucosal addressin cell
CC adhesion molecule (MADCAM). The invention also relates to a hybridoma
CC cell line that produces the human monoclonal antibody, a pharmaceutical
CC composition comprising an amount of the monoclonal antibody or its
CC antigen-binding portion and a pharmaceutical carrier, a method of
CC treating inflammatory disease in a subject, an isolated cell line that
CC produces the monoclonal antibody or its antigen-binding portion or the
CC heavy chain or light chain of the antibody or of its portion, an isolated
CC nucleic acid molecule comprising a nucleotide sequence encoding the heavy
CC chain or its antigen-binding portion or the light chain or its antigen-
CC binding portion of an antibody described above, a vector comprising the
CC nucleic acid molecule, where the vector optionally comprises an
CC expression control sequence operably linked to the nucleic acid molecule,
CC a host cell comprising the vector or the nucleic acid molecule above, a
CC method of producing a human monoclonal antibody or its antigen-binding
CC portion that specifically binds MadCAM, a method of isolating an antibody
CC or its antigen-binding portion that specifically binds to MadCAM, a
CC method of treating a subject in need of a human antibody or its antigen-
CC binding portion that specifically binds to MadCAM and inhibits binding to
CC alpha4beta7, a method of inhibiting alpha4beta7 binding to cells
CC expressing human MadCAM, a method of inhibiting MadCAM-mediated leukocyte
CC -endothelial cell adhesion, migration and infiltration into tissues, a
CC method of inhibiting alpha4beta7/MadCAM-dependent cellular adhesion,
CC inhibiting the MadCAM-mediated recruitment of lymphocytes to
CC gastrointestinal lymphoid tissue, a method of diagnosing a disorder
CC characterized by circulating soluble human MadCAM and detecting
CC inflammation in a subject. The antibody, composition and methods are
CC useful for diagnosing and treating inflammatory disease, e.g.
CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
CC diverticular disease, gastritis, liver disease, primary biliary
CC cirrhosis, primary sclerosing cholangitis, insulin dependent diabetes and
CC graft versus host disease. This sequence represents a human monoclonal
XX anti-MadCAM antibody of the invention.

SQ Sequence 238 AA;

Query Match 95.1%; Score 1060; DB 9; Length 238;

Best Local Similarity 95.8%; Pred. No. 2.8e-52;

Matches 205; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISNLYNWYQKPKAPKLLIYDASNLETGVP 60

DB |||||
25 DIQMTQSPSSLSASVGRVITTCQASQDISNLYNWYQKPKAPKLLIYDASNLETGVP 84

QY 61 RFSGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSGQGTKLIRKTVAAPSVFIIPP 120

DB |||||
85 RFSGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSGQGTKLIRKTVAAPSVFIIPP 144

QY 121 SDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180

DB |||||
145 SDEQLKSGTASVVCLLNNFPYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 204

QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

DB |||||
205 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238

RESULT 3

ADD93785

ID ADD93785 standard; protein; 236 AA.

XX ADD93785;

AC ADD93785;

XX 29-JAN-2004 (first entry)

DT Monoclonal antibody 20.13.3 light chain.

DE Monoclonal antibody; antibody; antiasthmatic; antiallergic;

XX antiinflammatory; immunosuppressive; dermatological;

KW gastrointestinal-gen.; antihelminthic; cytostatic; ophthalmological;

KW

bronchodilator; interleukin-5; human; gene therapy.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..22 /note= "Signal peptide"

Protein 23..236 /note= "light chain"

Misc-difference 23..130 /note= "Region specifically described in Claim 2"

Misc-difference 46..119 /note= "Region specifically described in Claim 2"

Region 46..56 /note= "CDR1"

Region 72..78 /note= "CDR2"

Region 111..119 /note= "CDR3"

W02003085089-A2.

16-OCT-2003.

27-MAR-2003; 2003WO-US009260.

29-MAR-2002; 2002US-0369044P.

(SCHE) SCHERING CORP.

(ABGE-) ABGENIX INC.

Greenfeder S, Corvalan J;

WPI; 2003-804302/75.

N-PSDB; ADD93784.

New antibody or its antigen-binding fragment that specifically binds interleukin-5, useful for diagnosing, treating or preventing a condition associated with undesired interleukin-5 activity, e.g. asthma or allergic rhinitis.

Claim 2; Page 26; 75pp; English.

The present sequence is the protein sequence of the light chain of anti-human interleukin-5 (IL-5) human monoclonal antibody (Mab) 20.13.3. To obtain this IgG4 Mab, Xenomice (TM) were immunised with human IL-5. Spleen and/or lymph nodes were then fused with myeloma P3-X63-Ag8.653 or myeloma NSO-bcl2 cells, and hybridomas were screened by ELISA for the presence of human IgG/kappa specific for IL-5. Nucleotides comprising the present sequence, or nucleotides 1-707, 1102-1137, 1256-1585, 1683-2002, 58-709, and 148-381 of it, are claimed and used in methods of the invention. The invention relates to antibodies or their antigen-binding fragments that specifically bind IL-5. Human anti-IL-5 antibodies are provided, including chimeric, bispecific, derivatised, single chain antibodies or portions of fusion proteins, and methods of making anti-IL-5 antibodies, pharmaceutical compositions comprising these antibodies and methods of using the antibodies and compositions for diagnosis and treatment. The invention also provides gene therapy methods using nucleic acids encoding the heavy and/or light chain molecules that comprise the human anti-IL-5 antibodies, and transgenic animals. The antibodies can be used to prevent or inhibit a condition or disorder characterised by undesired IL-5 activity, including asthma, asthma exacerbations, asthma worsening episodes, chronic pneumonia, allergic rhinitis, perennul allergic rhinitis, allergic bronchopulmonary aspergillosis, hyper eosinophilia, Churg-Strauss syndrome, atopic dermatitis, onchocercal dermatitis, episodic angioedema, eosinophilic myalgia syndrome, coeliac disease, eosinophilic gastroenteritis, helminth infections, Hodgkin's disease, nasal polyps, Loeffler's syndrome, urticaria, hypereosinophilic bronchitis, arteritis nodosa, sinusitis, chronic sinusitis, eosinophilic oesophagitis, allergic eosinophilic oesophagitis, or allergic conjunctivitis, by decreasing or inhibiting the infiltration of eosinophils into affected tissue. The antibodies are also useful for preventing or inhibiting an IL-5 mediated allergic response in a subject

or an IL-5 mediated event, such as eosinophil proliferation, maturation, survival, activation, migration into the bloodstream, adhesion to endothelium, infiltration into tissues, pulmonary oedema, bronchoconstriction, airway hyperresponsiveness, pulmonary eosinophilia or neutrophilia, cutaneous eosinophilia, or airway epithelial damage (all claimed).

Query Match 94.3%; Score 1051; DB 7; Length 236;

Best Local Similarity 94.4%; Pred No. 8e-52;

Matches 202; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

1 DIQMTQSPSSLSASVGDRVTITCOASQDISNYLNWYQKPKAPKLLIYDASNLETVGPS 60

23 DIQMTQSPSSLSASVGDRVTITCOASQDIINLNWYQKPKAPKLLIYDASNLETVGPS 82

61 RFGSGSGTDTFTTINSLOPEDIAIYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120

83 RFGSGSGTDTFTTISLQPEDIAIYCOQYDNHPLTFGGGTVKEIRRTVAAPSVFIFPP 142

121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLT 180

143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSLT 202

181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214

203 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 4

ADN97515

ID ADN97515 standard; protein; 502 AA.

XX AC ADN97515;

XX DT 01-JUL-2004 (first entry)

XX DE Artificial protein construction protein #16.

XX KW artificial proprotein; propeptide; protein engineering; antibody.

XX OS Unidentified.

XX PN W02004031362-A2.

XX PD 15-APR-2004.

XX PF 03-OCT-2003; 2003WO-US031420.

XX PR 03-OCT-2002; 2002US-0415940P.

XX PA (LARG-) LARGE SCALE BIOLOGY CORP.

XX PI Reini SJ, Edwards P;

XX DR WPI: 2004-330170/30.

XX N-PSDB; ADN97514.

XX New artificial proprotein comprises three peptide sequences, useful for artificial multimeric protein engineering in eukaryotes.

XX Example 2; SEQ ID NO 88; 244pp; English.

The invention relates to an artificial proprotein comprising three peptide sequences: a first peptide sequence of interest, a propeptide sequence attached to the C-terminus of the first peptide sequence of interest, and a second peptide of interest attached to the C-terminus of the propeptide sequence. The artificial proprotein and polynucleotides are useful for artificial multimeric protein engineering, e.g. antibodies and antibody fragments in eukaryotes. This sequence corresponds to a protein used in the generation of the protein of the invention.

SQ Sequence 502 AA;

Query Match 93.7%; Score 1045; DB 8; Length 502;
Best Local Similarity 93.5%; Pred. No. 3.8e-51;
Matches 200; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQOKPGKAPKLLIYDASNLTGVPS 60
DB 23 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQOKPGKAPKLLIYDASNLTGVPS 82
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120
DB 83 RFGSGYGTDFLTITSSLOPEDFAITYCOQYDNLPLTFGGGKVEIKRTVAAPSVFIFPP 142
QY 121 SDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLTLT 180
DB 143 SDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLTLT 202
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 5
AAV55078
ID AAY55078 standard; protein; 367 AA.
AC AAY55078;
DT 25-FEB-2000 (first entry)
DE Single chain Fv protein sequence shPMI-Kappa.
XX Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretabie functional protein; antigenic protein;
KW protein isolation; diagnosis; ScFv.
OS Synthetic.
XX WO9960113-A1.
XX 25-NOV-1999.
XX 30-APR-1999; 99WO-JP002341.
XX 20-MAY-1998; 98JP-00138652.
PR 01-OCT-1998; 98JP-00279876.
XX (CHUS) CHUGAI SEIYAKU KK.
XX Tsuchiya M, Saito M, Ohtomo T;
PI WPI; 2000-039382/03.
DR N-PSDB; AA240308.
XX
PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein.
PS Example 7; Page 86-89; 120pp; Japanese.
XX This sequence represents a single chain Fv (ScFv) sequence. The invention
CC relates to a method for isolating a gene encoding a membrane-bound
CC protein, comprising introducing a vector into a cell, contacting an
CC antigen with the cell expressing the fused protein encoded by the vector
CC on its surface to select an antigen-binding cell, and isolating the cDNA.
CC The vector contains DNA encoding a secretabie functional protein with
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC of the 3' end of the coding sequence. The method can be used to isolate a
CC membrane-bound protein for diagnosis and study. It can also be used for
CC producing drugs treating abnormal functions of the protein. Such a
CC technique is efficient and selective, which is different from the prior-
CC art transmembrane trap (TMT) method wherein an epitope recognised by an

CC antibody is carried in a fused protein
XX
SQ Sequence 367 AA;

Query Match 93.2%; Score 1039; DB 3; Length 367;
Best Local Similarity 93.9%; Pred. No. 6.2e-51;
Matches 200; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQOKPGKAPKLLIYDASNLTGVPS 60
DB 154 DIQMTQSPSSLSASVGRVTITCRASQDISSYLNWYQOKPGKAPKLLIYTSRLHSGVPS 213
QY 61 RFGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120
DB 214 RFGSGSGTDFTTISSLOPEDIAITYCQQNTLPTFYFGQGTKEIKRTVAAPSVFIFPP 273
QY 121 SDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLTLT 180
DB 274 SDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLTLT 333
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGE 213
DB 334 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGE 366

RESULT 6
AAV55081
ID AAY55081 standard; protein; 626 AA.
AC AAY55081;
DT 25-FEB-2000 (first entry)
DE Single chain Fv protein sequence shPM1-kappa-BvGS3.
XX Gene isolation; membrane-bound protein; fusion protein; drug production;
KW antigen-binding cell; secretabie functional protein; antigenic protein;
KW protein isolation; diagnosis; ScFv.
OS Synthetic.
XX WO9960113-A1.
XX 25-NOV-1999.
XX 30-APR-1999; 99WO-JP002341.
XX 20-MAY-1998; 98JP-00138652.
PR 01-OCT-1998; 98JP-00279876.
XX (CHUS) CHUGAI SEIYAKU KK.
XX Tsuchiya M, Saito M, Ohtomo T;
PI WPI; 2000-039382/03.
DR N-PSDB; AA240316.
XX
PT Efficient and selective isolation of a gene encoding membrane protein
PT with low or no antigenic binding activity, for diagnosis, study of, and
PT production of drugs treating abnormal functions of the protein.
XX Example 7; Page 103-109; 120pp; Japanese.
PS This sequence represents a single chain Fv (ScFv) sequence. The invention
XX relates to a method for isolating a gene encoding a membrane-bound
CC protein, comprising introducing a vector into a cell, contacting an
CC antigen with the cell expressing the fused protein encoded by the vector
CC on its surface to select an antigen-binding cell, and isolating the cDNA.
CC The vector contains DNA encoding a secretabie functional protein with
CC antigenicity and binding affinity, and a cDNA ligated to DNA downstream
CC of the 3' end of the coding sequence. The method can be used to isolate a
CC membrane-bound protein for diagnosis and study. It can also be used for
CC producing drugs treating abnormal functions of the protein. Such a
CC technique is efficient and selective, which is different from the prior-
CC art transmembrane trap (TMT) method wherein an epitope recognised by an

CC technique is efficient and selective, which is different from the prior-
CC art transmembrane trap (TMT) method wherein an epitope recognised by an
CC antibody is carried in a fused protein
XX
SQ Sequence 626 AA;

Query Match 93.2%; Score 1039; DB 3; Length 626;
Best Local Similarity 93.9%; Pred. No. 1e-50; 6; Indels 0; Gaps 0;
Matches 200; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGVS 60
DB 413 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGVS 472

QY 61 RFGSGSGTDFTTINSLOPEDATYTCQYNNLPYSGQGTKEIKRTVAAPSVFIFPP 120
DB 473 RFGSGSGTDFTTINSLOPEDATYTCQYNNLPYSGQGTKEIKRTVAAPSVFIFPP 532

QY 121 SDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
DB 533 SDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 592

QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNNGE 213
DB 593 LSKADYKHKVYACEVTHQGLSSPVTKSFNNGE 625

RESULT 7
ID ADQ90721 standard; protein; 237 AA.
XX ADQ90721;
XX
XX 21-OCT-2004 (first entry)
XX
DE Anti-VEGF antibody light chain protein SEQ ID NO:25.
XX
KW antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cystostatic;
KW antiinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti vascular endothelial cell growth factor antibody; light chain.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX W02004065417-A2.
XX
XX 05-AUG-2004.
XX
XX 23-JAN-2004; 2004WO-US001844.
XX
XX 23-JAN-2003; 2003US-0442484P.
XX
XX (GETH) GENENTECH INC.
XX
XX Simmons L;
XX
XX WPI; 2004-562149/54.
XX
XX N-PSDB; ADQ90720.
XX
XX Producing an antibody or antigen binding fragment in high yield in a cell
XX culture, comprises expressing a variable domain with a modified framework
XX region in a host cell.
XX
XX Example 6; SEQ ID NO 25; 161pp; English.
XX
XX The present invention describes a method for producing an antibody or
XX antigen binding fragment in high yield in a cell culture. The method
XX comprises expressing a variable domain of the antibody or antigen binding
XX fragment comprising a modified framework region (FR) in a host cell, and
XX recovering the antibody or antigen binding fragment variable domain

CC comprising the modified framework from the host cell. The modified PR in
CC the method described above has a substitution of at least one amino acid
CC position with a different amino acid, where the different amino acid is
CC the amino acid found at the corresponding FR position of a human subgroup
CC variable domain consensus sequence that has a hypervariable region 1
CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
CC The antibody or antigen binding fragment variable domain comprises the
CC modified FR that has improved yield in cell culture compared to an
CC unmodified antibody or antigen-binding fragment. The antibody and antigen
CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
CC immunomodulatory activities, and can be used in antibody therapy. The
CC methods and compositions of the present invention are useful for
CC producing antibodies or antigen binding fragments in cell culture, in
CC particular for improving the yield of recombinant antibodies or antigen
CC binding fragments in cell culture. The antibodies of the invention can be
CC used to diagnose, treat, inhibit or prevent e.g. tumours and
CC inflammatory, angiogenic and immunological disorders. The present
CC sequence represents the light chain of an anti-VEGF (vascular endothelial
CC cell growth factor) antibody, which is used in the exemplification of the
XX present invention.
XX
SQ Sequence 237 AA;

Query Match 93.0%; Score 1037; DB 8; Length 237;
Best Local Similarity 92.1%; Pred. No. 5.5e-51;
Matches 197; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGVS 60
DB 24 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGVS 83

QY 61 RFGSGSGTDFTTINSLOPEDATYTCQYNNLPYSGQGTKEIKRTVAAPSVFIFPP 120
DB 84 RFGSGSGTDFTTINSLOPEDATYTCQYNNLPYSGQGTKEIKRTVAAPSVFIFPP 143

QY 121 SDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
DB 144 SDEQLKSGTASVCLLNPFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 203

QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNNGE 214
DB 204 LSKADYKHKVYACEVTHQGLSSPVTKSFNNGE 237

RESULT 8
ADC26154
ID ADC26154 standard; protein; 214 AA.
XX ADC26154;
XX
XX 18-DEC-2003 (first entry)
XX
DE Parent anti-VEGF Y0101 antibody wild-type light chain protein.
XX
XX antibody variant; cytostatic; cancer; parent; anti-VEGF;
XX vascular endothelial growth factor; Y0101; light chain; wild-type.
XX
XX Unidentified.
XX
XX W02003068801-A2.
XX
XX 21-AUG-2003.
XX
XX 11-FEB-2003; 2003WO-US004184.
XX
XX 11-FEB-2002; 2002US-0355895P.
XX
XX 10-SEP-2002; 2002US-0409685P.
XX
XX (GETH) GENENTECH INC.
XX
XX Lowman HB, Marvin JS;
XX

DR WPI: 2003-697521/66.
XX
PT Making an antibody variant of a parent antibody specific to an antigen by
PT identifying a target amino acid residue within the variable domain of the
PT parent antibody and substituting the target residue with a different
PT amino acid residue.
XX
PS Example 1; SEQ ID NO 1; 81pp; English.
XX
CC The invention relates to a novel method for making an antibody variant of
CC a parent antibody specific to an antigen. This is achieved via
CC identifying a target amino acid residue within the variable domain of the
CC parent antibody and substituting the target residue with a different
CC replacement amino acid residue such that the charge complementarity
CC between the antibody and antigen is increased. The antibody variant of
CC the invention demonstrates cytostatic activity whilst the method may be
CC useful for treating cancer. The current sequence is that of the parent
CC anti-VEGF (vascular endothelial growth factor) Y0101 antibody wild-type
CC light chain protein of the invention.
XX
SQ Sequence 214 AA;

Query Match 92.7%; Score 1034; DB 7; Length 214;
Best Local Similarity 91.6%; Pred. No. 7.4e-51;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCOASQDISNYLNWYQKPKAPKLLIYDASNLETGVPS 60
DB 1 DIQLTQSPSSLSASVGDRTVITCSAQDISNYLNWYQKPKAPKLLIYFTSSLHSGVPS 60
QY 61 RFGSGSGDTFTTINSLOPEDIAITYCOEYNNLPYSGQGKLEIKRTVAAPSVFIIPP 120
DB 61 RFGSGSGDTFTLTSSLPEDFATYCCQYSTVPWTFGGTKVEIKRTVAAPSVFIIPP 120
QY 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180
DB 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 9
AAW70703
ID AAW70703 standard; protein; 237 AA.
AC AAW70703;
XX
XX
DT 27-JAN-1999 (first entry)
XX
DE Protein encoded by Fab-display antibody vector phMB4-19-1.6.
XX
XX Murine; humanised antibody; VEGF-induced angiogenesis; tumour;
KW anti-vascular endothelial growth factor antibody; anti-VEGF antibody;
KW retinal disorder; age-related macular degeneration; diabetic retinopathy;
KW rheumatoid arthritis; psoriasis; atherosclerosis; Grave's disease.
XX
OS Synthetic.
XX
XX Key
FN Peptide 1..23
XX /note= "STII signal sequence TIR-1"
XX Protein 24..237
XX /note= "anti-VEGF light chain"
XX
XX WO9845331-A2.
PD 15-OCT-1998.
XX
XX 03-APR-1998; 98WO-US006604.
XX
XX 07-APR-1997; 97US-00833504.
PR 06-AUG-1997; 97US-00908469.
XX
XX (GETH) GENENTECH INC.
XX
XX Baca M, Wells JA, Presta LG, Lowman HB, Chen YM;
PI

DR WPI: 1998-568337/48.
DR N-FSDB; AAV63493.
XX
PT New humanised antibody with affinity for vascular endothelial growth
PT factor - for treatment of tumours, retinal disease and other angiogenic
PT states, also related nucleic acid, vectors and transformed cells.
XX
PS Example 3; Fig 8A-E; 100pp; English.
XX
CC The present sequence is encoded by the Fab-display antibody vector phMB4-
CC 19-1.6, which is used in the course of the invention. The specification
CC describes humanised murine anti-vascular endothelial growth factor (anti-
CC VEGF) antibodies. The humanised antibodies are used to inhibit VEGF-
CC induced angiogenesis, particularly for treating or preventing tumours (of
CC any type) and retinal disorders (e.g. age- related macular degeneration
CC or diabetic retinopathy). They can also be used to treat other conditions
CC that involve angiogenesis, e.g. rheumatoid arthritis, psoriasis,
CC atherosclerosis, Grave's disease, etc
XX
SQ Sequence 237 AA;

Query Match 92.7%; Score 1034; DB 2; Length 237;
Best Local Similarity 91.6%; Pred. No. 8.1e-51;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCOASQDISNYLNWYQKPKAPKLLIYDASNLETGVPS 60
DB 24 DIQLTQSPSSLSASVGDRTVITCSAQDISNYLNWYQKPKAPKLLIYFTSSLHSGVPS 83
QY 61 RFGSGSGDTFTTINSLOPEDIAITYCOEYNNLPYSGQGKLEIKRTVAAPSVFIIPP 120
DB 84 RFGSGSGDTFTLTSSLPEDFATYCCQYSTVPWTFGGTKVEIKRTVAAPSVFIIPP 143
QY 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 180
DB 144 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSLT 203
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 10
ABB81107
ID ABB81107 standard; protein; 237 AA.
XX
XX ABB81107;
XX
XX
DT 05-NOV-2002 (first entry)
XX
DE Anti-VEGF light chain fragment.
XX
XX Immunoglobulin; promoter; cytostatic; antiinflammatory; immunomodulator;
KW neuroprotective; CD11; tissue factor; vascular endothelial growth factor;
KW VEGF.
XX
OS Synthetic.
XX
XX Key
FN Peptide 1..23
XX /note= "STII signal sequence TIR-1"
XX Protein 24..237
XX /note= "anti-VEGF light chain"
XX
XX WO200261090-A2.
XX
XX 08-AUG-2002.
XX
XX 13-DEC-2001; 2001WO-US048691.
XX
XX 14-DEC-2000; 2000US-0256164P.
XX
XX (GETH) GENENTECH INC.

XX Simmons LC, Klimowski L, Reilly DE, Yansura DG;
XX WPI; 2002-619253/66.
XX N-PSDB; ABN86646.
XX New polynucleotide comprising first and second promoter-cistron pairs,
XX useful for diagnosing, treating or preventing diseases associated with
XX abnormal expression and/or activity of antigens such as inflammatory
XX disorders.
XX Disclosure; Fig 21A-C; 104pp; English.
XX The invention provides a polynucleotide, which encodes an immunoglobulin
XX (Ig), comprising a first or second promoter-cistron pair consisting of a
XX first or second promoter and cistron, respectively. The first cistron of
XX the first promoter-cistron pair comprises a first translational
XX initiation region (TIR-L) operably linked to a nucleic acid sequence
XX encoding an Ig light chain and the second cistron of the second promoter-
XX cistron pair comprises a second translational initiation region (TIR-H)
XX operably linked to a nucleic acid sequence encoding an Ig heavy chain.
XX Upon expression of the polynucleotide in a prokaryotic host cell, light
XX and heavy chains are folded and assembled to form a biologically active
XX Ig. The antibody of the invention is useful for diagnosing, treating or
XX preventing diseases or conditions associated with abnormal expression and
XX /or activity of one or more antigen molecules e.g. lymphoid malignancies,
XX inflammatory, angiogenic, immunologic, neuronal, glial, astrocytic,
XX hypothalamic or other glandular disorders. The present sequence
XX represents the amino acid sequence of an anti-vascular endothelial growth
XX factor (VEGF) light chain fragment of the cistron vector pXVG2AP11
XX Sequence 237 AA;
Query Match 92.7%; Score 1034; DB 5; Length 237;
Best Local Similarity 91.6%; Pred. No. 8.1e-51;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
Qy 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 24 DIQLTQSPSSLSASVGDRTVITTCASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 83
Qy 61 RFGSGSGTDFTTINSLOPEDATYTCQSDISNYLNWYQKPGKAPKLLIYDASNLETGVP 120
Db 84 RFGSGSGTDFTTINSLOPEDATYTCQSDISNYLNWYQKPGKAPKLLIYDASNLETGVP 143
Qy 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
Db 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 203
Qy 181 LSKADYEKKHYKVAACEVTHOGLSSPVTKSFNRGEC 214
Db 204 LSKADYEKKHYKVAACEVTHOGLSSPVTKSFNRGEC 237
RESULT 11
ID ABP51952
AC ABP51952 standard; protein; 237 AA.
XX ABP51952;
XX 09-OCT-2002 (first entry)
XX Plasmid pY0317 anti-VEGF Fab amino acid sequence SEQ ID NO:2 #1.
XX Bacterial host; protease; degp; prc; spr; anti-VEGF antibody; antibody;
XX humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;
XX anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;
XX anti-CD11a; Fab; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab'; Fab';
XX Mus sp.
XX Escherichia coli.
XX Synthetic.
XX

XX FH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT Protein 24..237
XX /label= anti-VEGF_Fab
XX WO200248376-A2.
XX 20-JUN-2002.
XX 07-DEC-2001; 2001WO-US047581.
XX 14-DEC-2000; 2000US-02561622p.
XX (GETH) GENENTECH INC.
XX Chen CY;
XX WPI; 2002-583522/62.
XX N-PSDB; ABQ73919.
XX Novel Escherichia coli strain useful for producing polypeptide, deficient
XX in degp and prc encoding protease, and harboring mutant spr gene, product
XX of gene suppresses growth phenotypes of strains harboring prc mutants.
XX Example 1; Fig 1A-C; 63pp; English.
XX The present invention describes an Escherichia coli strain (I) deficient
XX in chromosomal degp and prc encoding protease Degp and Prc, respectively,
XX and harbouring a mutant spr gene, the product of mutant spr gene
XX suppresses growth phenotypes exhibited by strains harbouring prc mutants.
XX (I) is useful for producing a polypeptide, by culturing (I) comprising
XX nucleic acid encoding the polypeptide, which is heterologous to the
XX strain, such that the nucleic acid is expressed, and recovering the
XX heterologous polypeptide from the strain. The heterologous polypeptide is
XX proteolytically sensitive. Culturing of (I) is performed in a fermentor
XX under conditions of high- or low-cell density fermentation. The
XX polypeptide is recovered from the periplasm or culture medium of the
XX strain. The polypeptide is an antibody (humanised or full-length
XX antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular
XX endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,
XX anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an
XX antibody fragment having a light chain (kappa light chain). The antibody
XX fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18
XX Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper
XX fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-
XX tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-
XX -CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18
XX Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence
XX represents an anti-VEGF Fab amino acid sequence from the present
XX invention
XX Sequence 237 AA;
Query Match 92.7%; Score 1034; DB 5; Length 237;
Best Local Similarity 91.6%; Pred. No. 8.1e-51;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
Qy 1 DIOMTQSPSSLSASVGDRTVITTCASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 24 DIQLTQSPSSLSASVGDRTVITTCASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 83
Qy 61 RFGSGSGTDFTTINSLOPEDATYTCQSDISNYLNWYQKPGKAPKLLIYDASNLETGVP 120
Db 84 RFGSGSGTDFTTINSLOPEDATYTCQSDISNYLNWYQKPGKAPKLLIYDASNLETGVP 143
Qy 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
Db 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 203
Qy 181 LSKADYEKKHYKVAACEVTHOGLSSPVTKSFNRGEC 214
Db 204 LSKADYEKKHYKVAACEVTHOGLSSPVTKSFNRGEC 237

RESULT 12
ADO14128
ID ADO14128 standard; protein; 237 AA.
XX
AC ADO14128;
XX
DT 12-AUG-2004 (first entry)
XX
DE Plasmid pxVG2AP11 expression cassette light chain protein SEQ ID NO:8.
XX
KW antibody; variant heavy chain hinge region; immunoconjugate; cytostatic;
KW immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
KW expression cassette; plasmid pxVG2AP11; anti-VEGF light chain.
XX
OS Synthetic.
XX
PN WO2004042017-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034610.
XX
PR 31-OCT-2002; 2002US-0422952P.
XX
PA (GETH) GENENTECH INC.
XX
PI Reilly D, Yansura DG;
XX
DR WPI; 2004-390607/36.
DR N-PSDB; ADO14127.
XX
PT New antibody comprising a variant heavy chain hinge region incapable of
PT inter-heavy chain disulfide linkage, useful for treating, preventing,
PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
PT immune disorder.
XX
PS Example 1; SEQ ID NO 8; 124pp; English.
XX
CC The present invention describes an antibody comprising a variant heavy
CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also
CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;
CC (2) an immunoconjugate comprising the antibody conjugated with a
CC heterologous moiety; (3) a composition comprising the antibody or
CC immunoconjugate, and carrier; (4) an article of manufacture comprising
CC the composition in a container; (5) a polynucleotide encoding the
CC antibody or immunoconjugate, or a variant immunoglobulin heavy chain
CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant
CC vector for expressing the antibody or immunoconjugate; (7) a host cell
CC comprising the recombinant vector; (8) expressing in a host cell an
CC antibody of interest in which at least one inter-heavy chain disulfide
CC linkage is eliminated, and recovering the antibody from the host cell;
CC (9) an aglycosylated antibody produced by the method; and (10) treating,
CC preventing, diagnosing, delaying or preventing a disease in a subject.
CC The antibody has cytostatic and immunosuppressive activities, and can be
CC used in immunotherapy. The antibody, immunoconjugate and methods are
CC useful for treating, preventing, diagnosing, delaying or preventing a
CC disease, e.g. tumour, cancer or immune disorder. The present sequence
CC represents the anti-VEGF light chain from the expression cassette of
CC plasmid pxVG2AP11, which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 237 AA;
Query Match 92.7%; Score 1034; DB 8; Length 237;
Best Local Similarity 91.6%; Pred. No. 8.1e-51;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRVTITCSASQDINSYLNYYQKPKAPKLLIYDASNLTGVP 60
DB 24 DIQLTQSPSSLSASVGDRVTITCSASQDINSYLNYYQKPKAPKLVLYFTSSLSHGVP 83

QY 61 RFGSGSGTDFTFITNSLQPEDIATYYCOEYNNLPYSPFGQGTKEIKRTVAAPSFI 120
DB 84 RFGSGSGTDFTLTISSLOPEDFATYYCQQYSTVPTWTFGQGTKEIKRTVAAPSFI 143
QY 121 SDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKSTYLSSTLT 180
DB 144 SDEQLKSGTASVWCLNNFYPREAKVQWKVDNALQSGNSQSVTEQDSKSTYLSSTLT 203
QY 181 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 237
RESULT 13
ADO14131
ID ADO14131 standard; protein; 237 AA.
XX
AC ADO14131;
XX
DT 12-AUG-2004 (first entry)
XX
DE Plasmid pxVG11VNERK expression cassette light chain protein SEQ ID NO:11.
XX
KW antibody; variant heavy chain hinge region; immunoconjugate; cytostatic;
KW immunosuppressive; immunotherapy; tumour; cancer; immune disorder;
KW expression cassette; plasmid pxVG11VNERK; anti-VEGF light chain.
XX
OS Synthetic.
XX
PN WO2004042017-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034610.
XX
PR 31-OCT-2002; 2002US-0422952P.
XX
PA (GETH) GENENTECH INC.
XX
PI Reilly D, Yansura DG;
XX
DR WPI; 2004-390607/36.
DR N-PSDB; ADO14130.
XX
PT New antibody comprising a variant heavy chain hinge region incapable of
PT inter-heavy chain disulfide linkage, useful for treating, preventing,
PT diagnosing, delaying or preventing a disease, e.g. tumor, cancer or
PT immune disorder.
XX
PS Example 1; SEQ ID NO 11; 124pp; English.
XX
CC The present invention describes an antibody comprising a variant heavy
CC chain hinge region incapable of inter-heavy chain disulfide linkage. Also
CC described: (1) an antibody lacking inter-heavy chain disulfide linkage;
CC (2) an immunoconjugate comprising the antibody conjugated with a
CC heterologous moiety; (3) a composition comprising the antibody or
CC immunoconjugate, and carrier; (4) an article of manufacture comprising
CC the composition in a container; (5) a polynucleotide encoding the
CC antibody or immunoconjugate, or a variant immunoglobulin heavy chain
CC incapable of inter-heavy chain disulfide linkage; (6) a recombinant
CC vector for expressing the antibody or immunoconjugate; (7) a host cell
CC comprising the recombinant vector; (8) expressing in a host cell an
CC antibody of interest in which at least one inter-heavy chain disulfide
CC linkage is eliminated, and recovering the antibody from the host cell;
CC (9) an aglycosylated antibody produced by the method; and (10) treating,
CC preventing, diagnosing, delaying or preventing a disease in a subject.
CC The antibody has cytostatic and immunosuppressive activities, and can be
CC used in immunotherapy. The antibody, immunoconjugate and methods are
CC useful for treating, preventing, diagnosing, delaying or preventing a
CC disease, e.g. tumour, cancer or immune disorder. The present sequence
CC represents the anti-VEGF light chain from the expression cassette of
CC plasmid pxVG11VNERK, which is used in the exemplification of the present
CC invention.

XX Sequence 237 AA;
SQ
Query Match 92.7%; Score 1034; DB 8; Length 237;
Best Local Similarity 91.6%; Pred. No. 8.1e-51;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 24 DIQLTQSPSSLSASVGDRTITTCASQDISNYLNWYQKPGKAPKLVLYFTSSLSHGVPS 83
QY 61 RFGSGSGTDFTTINSLQPEDIATYYCOEYNNLPYFQGTGKLEIKRTVAAPSFIPIPP 120
DB 84 RFGSGSGTDFLTITSSLPEDFAIYYCOQYSTVPWTFQGTGKVEIKRTVAAPSFIPIPP 143
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSSLT 180
DB 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSSLT 203
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 237
RESULT 14
ADQ90703
ID ADQ90703 standard; protein; 237 AA.
XX
AC ADQ90703;
XX
XX
XX 21-OCT-2004 (first entry)
DE Anti-VEGF antibody Y0317 light chain protein SEQ ID NO:7.
XX antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cytostatic;
KW antinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti vascular endothelial cell growth factor antibody; light chain.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX PN WO2004065417-A2.
XX
XX PD 05-AUG-2004.
XX
XX PF 23-JAN-2004; 2004WO-US001844.
XX
XX PR 23-JAN-2003; 2003US-0442484P.
XX (GETH) GENENTECH INC.
XX Simmons L;
XX
XX PI WPI; 2004-562149/54.
XX
XX DR N-PSDB; ADQ90702.
XX
XX PT Producing an antibody or antigen binding fragment in high yield in a cell
PT culture, comprises expressing a variable domain with a modified framework
PT region in a host cell.
XX
XX PS Example 2; SEQ ID NO 7; 161pp; English.
XX
XX CC The present invention describes a method for producing an antibody or
CC antigen binding fragment in high yield in a cell culture. The method
CC comprises expressing a variable domain of the antibody or antigen binding
CC fragment comprising a modified framework region (FR) in a host cell, and
CC recovering the antibody or antigen binding fragment variable domain
CC comprising the modified framework from the host cell. The modified FR in
CC the method described above has a substitution of at least one amino acid
CC position with a different amino acid, where the different amino acid is

CC the amino acid found at the corresponding FR position of a human subgroup
CC variable domain consensus sequence that has a hypervariable region 1
CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
CC The antibody or antigen binding fragment variable domain comprises the
CC modified FR that has improved yield in cell culture compared to an
CC unmodified antibody or antigen-binding fragment. The antibody and antigen
CC binding fragment have cytostatic, antinflammatory, antiangiogenic and
CC immunomodulatory activities, and can be used in antibody therapy. The
CC methods and compositions of the present invention are useful for
CC producing antibodies or antigen binding fragments in cell culture, in
CC particular for improving the yield of recombinant antibodies or antigen
CC binding fragments in cell culture. The antibodies of the invention can be
CC used to diagnose, treat, inhibit or prevent e.g. tumours and
CC inflammatory, angiogenic and immunological disorders. The present
CC sequence represents the light chain of an anti-VEGF (vascular endothelial
CC cell growth factor) antibody, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 237 AA;

Query Match 92.7%; Score 1034; DB 8; Length 237;
Best Local Similarity 91.6%; Pred. No. 8.1e-51;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 24 DIQLTQSPSSLSASVGDRTITTCASQDISNYLNWYQKPGKAPKLVLYFTSSLSHGVPS 83
QY 61 RFGSGSGTDFTTINSLQPEDIATYYCOEYNNLPYFQGTGKLEIKRTVAAPSFIPIPP 120
DB 84 RFGSGSGTDFLTITSSLPEDFAIYYCOQYSTVPWTFQGTGKVEIKRTVAAPSFIPIPP 143
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSSLT 180
DB 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSSLT 203
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 15
ADQ90701
ID ADQ90701 standard; protein; 237 AA.
XX
AC ADQ90701;
XX
XX 21-OCT-2004 (first entry)
DE Anti-VEGF antibody VNERK light chain protein SEQ ID NO:5.
XX
XX antibody; antigen binding fragment; cell culture; variable domain;
KW modified framework region; hypervariable region; cytostatic;
KW antinflammatory; antiangiogenic; immunomodulatory; antibody therapy;
KW tumour; inflammatory disorder; angiogenic disorder;
KW immunological disorder; anti-VEGF antibody;
KW anti vascular endothelial cell growth factor antibody; light chain.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX PN WO2004065417-A2.
XX
XX PD 05-AUG-2004.
XX
XX PF 23-JAN-2004; 2004WO-US001844.
XX
XX PR 23-JAN-2003; 2003US-0442484P.
XX (GETH) GENENTECH INC.
XX
XX PI Simmons L;

XX WPI: 2004-562149/54.
DR N-PSDB; ADQ90700.
XX
PT Producing an antibody or antigen binding fragment in high yield in a cell
PT culture, comprises expressing a variable domain with a modified framework
PT region in a host cell.
XX
PS Example 2; SEQ ID NO 5; 161pp; English.
XX
CC The present invention describes a method for producing an antibody or
CC antigen binding fragment in high yield in a cell culture. The method
CC comprises expressing a variable domain of the antibody or antigen binding
CC fragment comprising a modified framework region (FR) in a host cell, and
CC recovering the antibody or antigen binding fragment variable domain
CC comprising the modified framework from the host cell. The modified FR in
CC the method described above has a substitution of at least one amino acid
CC position with a different amino acid, where the different amino acid is
CC the amino acid found at the corresponding FR position of a human subgroup
CC variable domain consensus sequence that has a hypervariable region 1
CC (HVR1) and/or HVR2 amino acid sequence with the most sequence identity
CC with a corresponding HVR1 and/or HVR2 sequence of the variable domain.
CC The antibody or antigen binding fragment variable domain comprises the
CC modified FR that has improved yield in cell culture compared to an
CC unmodified antibody or antigen-binding fragment. The antibody and antigen
CC binding fragment have cytostatic, antiinflammatory, antiangiogenic and
CC immunomodulatory activities, and can be used in antibody therapy. The
CC methods and compositions of the present invention are useful for
CC producing antibodies or antigen binding fragments in cell culture, in
CC particular for improving the yield of recombinant antibodies or antigen
CC binding fragments in cell culture. The antibodies of the invention can be
CC used to diagnose, treat, inhibit or prevent e.g. tumours and
CC inflammatory, angiogenic and immunological disorders. The present
CC sequence represents the light chain of an anti-VEGF (vascular endothelial
CC cell growth factor) antibody, which is used in the exemplification of the
CC present invention.
XX
SQ Sequence 237 AA;

Query Match 92.7%; Score 1034; DB 8; Length 237;
Best Local Similarity 91.6%; Pred. No. 8.1e-51;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRVTITCQASQDISNYLNWYQKPKGKAPKLLIYDASNLETGYPS 60
DB 24 DIQLTQSPSSLSASVGDRVTITCSASQDISNYLNWYQKPKGKAPKLLIYFTSSLHSGVPS 83
QY 61 RFGSGSGTDFTTINSLQPEDIATYYCOEYNNLPYFQGGTKLEIKRTVAAPSVFIFPP 120
DB 84 RFGSGSGTDFTLTISSLPEDFAIYYCQQYSTVPWTFGGTKVEIKRTVAAPSVFIFPP 143
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 180
DB 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 203
QY 181 LSKADYEKKHYVACEVTHQGLSSPVTKSFNRGEC 214
DB 204 LSKADYEKKHYVACEVTHQGLSSPVTKSFNRGEC 237

Search completed: December 17, 2005, 01:18:33
Job time : 86.9515 secs

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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:10:58 ; Search time 16,2121 Seconds
(without alignments)
1270.061 Million cell updates/sec

Title: US-10-644-277-64
Perfect score: 1115
Sequence: 1 DIQMTQSPSSLSASVGDRTV.....EVTHQGLSPVTKSFNRGEC 214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	943.5	84.6	215	2 JE0242	Ig kappa chain NIG
2	913.5	81.9	215	2 JE0244	Ig kappa chain NIG
3	897.5	80.5	215	2 JE0243	Ig kappa chain NIG
4	882.5	79.1	215	2 A23746	Ig kappa chain V-I
5	868	77.8	216	2 JE0241	Ig kappa chain Am3
6	745	66.8	230	2 S33161	Ig kappa chain - s
7	742	66.5	234	2 S14237	Ig kappa chain pre
8	741	66.5	240	2 S06084	Ig kappa chain pre
9	721	64.7	234	2 S01320	Ig kappa chain V r
10	716	64.2	218	2 S68241	Ig kappa chain V r
11	714	64.0	218	2 JC5810	monoclonal antibody
12	712	63.9	220	2 A31790	Ig kappa chain V r
13	708.5	63.5	225	2 S37484	Ig kappa chain - m
14	696	62.4	214	2 S68212	Ig kappa chain (Ma
15	688.5	61.7	219	2 S38865	Ig kappa chain - m
16	683.5	61.3	235	2 S25058	Ig kappa chain - m
17	683	61.3	210	2 A56169	Ig kappa chain V r
18	682.5	61.2	217	2 S42772	Ig kappa chain - m
19	681.5	61.1	219	2 PC4203	Ig kappa chain (mo
20	678.5	60.9	219	2 S52038	Ig kappa chain - m
21	670.5	60.1	219	2 S16112	Ig kappa chain V r
22	661.5	59.3	225	2 JL0029	Ig kappa chain pre
23	602	54.0	178	2 P70219	Ig kappa chain V-C
24	601.5	53.9	135	2 S52059	JC-kappa protein -
25	571.5	51.3	229	2 A20969	Ig kappa chain pre
26	551	49.4	139	2 S40365	Ig kappa chain - h
27	548	49.1	106	1 K3HU	Ig kappa chain C r
28	546.5	49.0	238	2 A49633	Ig lambda-like cha
29	516.5	46.3	197	2 S29593	Ig kappa chain (WM

Ig kappa chain V-J
Ig kappa chain C r
Ig kappa chain V-I
Ig kappa chain C r
Ig kappa chain V r
Ig kappa chain V-I
Ig kappa chain V-I
Ig kappa chain (BR
Ig kappa chain pre
Ig kappa chain V-I
Ig kappa chain V-J
Ig kappa chain V-I
Ig kappa chain V r
Ig kappa chain pre
Ig kappa chain V-I
Ig kappa chain V-I

ALIGNMENTS

RESULT 1

JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappatype light chains with AL amyloidosis: Mult
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
A:Cross-references: UNIPARC:UPI0000176983
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <1MW>

Query Match 84.6%; Score 943.5; DB 2; Length 215;
Best Local Similarity 82.8%; Pred. No. 1.2e-55;
Matches 178; Conservative 18; Mismatches 18; Indels 1; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDIS-NYLNWYQKPGKAPKLLIYDASNLFTGVP 59
Db 1 EIVLTQSPGTLISLSPGERATLSCRASQSVSNVYQKPGQAPSLIYDASSRATGIP 60
QY 60 SRPFGSGSGTDFFTTINSIQPEDIATYYCOEYNNLPYFTGQTKLEIKRTVAAPSVFIIP 119
Db 61 DRPFGSGSGTDFITLTISGLEPEDFAVYQCQYDRPPTFGQTKVEIKRTVAAPSVFIIP 120
QY 120 PSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSSSTL 179
Db 121 PSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSLSSSTL 180
QY 180 TLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 TLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

RESULT 2

JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T.
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (Vk) identified in cases of AL amyloidosis
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
A:Cross-references: UNIPARC:UPI0000176982


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A:Molecule type: mRNA
A:Residues: 1-234 <DEL>
A:Cross-references: UNIPARC:UPI00000115DDA; EMBL:X13187; NID:951784; PIDN:CAA31579.1; PID
A>Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-234/Product: Ig kappa chain #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match      64.7%; Score 721; DB 2; Length 234;
Best Local Similarity 62.6%; Pred. No. 6,7e-41;
Matches 134; Conservative 33; Mismatches 47; Indels 0; Gaps 0;

Qy 1 DIQMTQSPSSLSASVGRVITTCASQDSITSNLYNWYQOKPGKAPKLIYDASNLETGVP 60
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 21 DIQMTQSPASLSVSVGESVITTCRASENIYSLNLTWYQOKGSPQLLYVATKLVLDGVP 80
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 61 RFGSGSGGTDTFTINSLPEDIATYYCQEYNLPSYFGQGTKLEIKRTVAAPSVFIFPP 120
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db a1 RFGSGSGGTQVSLKTNLSQSEDFGYSYCHFWDPPTFTFGSGTKLEMKRAADAAPTVSIFPP 140
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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QY 121 SDEQLKSGTASVVCVCLNNFYPREAKVQKVDNALQSGNSQBSVTVTQDSKDSSTYSLSLSTLT 180
Db 141 SSEEQTSGGASVVCFLNNFYPKDINVKWKIDGSRQGVLSWTDQDSKDSSTYSLSLSTLT 200
QY 181 LSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 214
Db 201 LTKDEYERHNSYTCEATHKTSPIVKSFNRRNEC 234

RESULT 10
S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N:Alternate names: immunoglobulin light chain
C:Species: Mus musculus (house mouse)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68241; S68214
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
submitted to the EMBL Data Library, March 1994
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin
A:Reference number: S68241
A:Accession: S68241
A:Molecule type: mRNA
A:Residues: 1-218 <TAK>
A:Cross-references: UNIPARC:UPI000011B263; EMBL:D29670; NID:9473962; PIDN:BAA06141.1; PI
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68214
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'NI', 3-212 <TAW>
A:Cross-references: UNIPARC:UPI0000176980; EMBL:D29670
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 64.2%; Score 716; DB 2; Length 218;
Best Local Similarity 60.6%; Pred. No. 1.3e-40;
Matches 132; Conservative 37; Mismatches 45; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISN----YLNWYQOKPGKAPKLLIYDASNLET 56
Db 1 ELVLTQSPASLAVSLGQRATISCRASKSVASGYIYMHYQOKPGQPPKLLISLATNLES 60
QY 57 GVPSPFSGSGSGTDFTFTINSIQPEDIAITYYCOEYNNLPYSPFGQGTKLEIKRTVAAPSVF 116
Db 61 GVPARFSGSGSGTDFTLNHPVEEDVATYYCQHSRELPLTFGAGTKLELRADAAPTYS 120
QY 117 IPPPSDEQLKSGTASVVCVCLNNFYPREAKVQKVDNALQSGNSQBSVTVTQDSKDSSTYSL 176
Db 121 IPPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQGVLSWTDQDSKDSSTYSL 180
QY 177 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 STLTUTKDEYERHNSYTCEATHKTSPIVKSFNRRNEC 218

RESULT 11
JC5810
monoclonal antibody 13-1 light chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C:Accession: JC5810
R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277; PMID:9398605
A:Accession: JC5810
A:Molecule type: protein
A:Residues: 1-218 <AKA>
A:Cross-references: UNIPARC:UPI0000176988
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porp

C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 64.0%; Score 714; DB 2; Length 218;
Best Local Similarity 61.0%; Pred. No. 1.8e-40;
Matches 133; Conservative 35; Mismatches 46; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVITTCQASQDISN----YLNWYQOKPGKAPKLLIYDASNLET 56
Db 1 NIVLTQSPASLAVSLGQRATISCRASKSVASGYIYMHYQOKPGQPPKLLISLATNLES 60
QY 57 GVPSPFSGSGSGTDFTFTINSIQPEDIAITYYCOEYNNLPYSPFGQGTKLEIKRTVAAPSVF 116
Db 61 GVPARFSGSGSGTDFTLNHPVEEDVATYYCQHSRELPLTFGAGTKLELRADAAPTYS 120
QY 117 IPPPSDEQLKSGTASVVCVCLNNFYPREAKVQKVDNALQSGNSQBSVTVTQDSKDSSTYSL 176
Db 121 IPPPSDEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQGVLSWTDQDSKDSSTYSL 180
QY 177 STLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 STLTUTKDEYERHNSYTCEATHKTSPIVKSFNRRNEC 218

RESULT 12
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an anti
A:Reference number: A92886; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: UNIPARC:UPI0000114E12; GB:M23626; GB:J04061; NID:9533234; PIDN:AAA391
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 63.9%; Score 712; DB 2; Length 220;
Best Local Similarity 61.1%; Pred. No. 2.5e-40;
Matches 135; Conservative 34; Mismatches 44; Indels 8; Gaps 3;

QY 1 DIQMTQSPSSLSASVGRVITTCQASQDI-----SNYLNWYQOKPGKAPKLLIYDASN 54
Db 1 DIVMTQSPSLTVTAGEKVTMSTSSQSLFNSGKQKYLTYWYQKPGQPPKVLIVWASTR 60
QY 55 ETGVPSRPSGSGSGTDFTFTINSIQPEDIAITYYCO-EYNNLPYSPFGQGTKLEIKRTVAAP 113
Db 61 ESGVPDRFTSGSGSGTDFTLTISVQAEDLAVYYCQDYSN-PLTFGGGTKLELRADAAP 119
QY 114 SVETFPSPDEQLKSGTASVVCVCLNNFYPREAKVQKVDNALQSGNSQBSVTVTQDSKDS 173
Db 120 TVSIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQGVLSWTDQDSKDS 179
QY 174 SLSTLTLSKADYEKKHKYACEVTHQGLSSPVTKSFNRGEC 214
Db 180 SMSSTLTUTKDEYERHNSYTCEATHKTSPIVKSFNRRNEC 220

RESULT 13
S37484
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37484

A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: UNIPARC:UPI0000116118; EMBL:X70424; NID:G406254; PIDN:CAA49869.1; PII
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 63.5%; Score 708.5; DB 2; Length 225;
Best Local Similarity 63.1%; Pred. No. 4.3e-40;
Matches 135; Conservative 32; Mismatches 44; Indels 3; Gaps 2;

QY 2 IQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPKAPKLLIYDASNLETGVPGR 61
DB 14 IVMTQPKFLLSAGDRVITTCASQSVNDVAWYQKQSPKLLIYVASSRYTGVDP 73

QY 62 FSGSGGTDTFTTINSLOPEDIATYCYQBYNNLPYSFGOGTKLEIKRTVAAPSVFI 120
DB 74 FTGSGVGTDTFTTISTVQAEADLAVYFCQDYSS--YTFGGGTGLEIKRADAAPT 131

QY 121 SDQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDYSLSTLT 180
DB 132 SSQQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSLSTLT 191

QY 181 LSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 214
DB 192 LTKDEYERHNSYTCEATHTKSTSPIVKSFNRNEC 225

RESULT 14
S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
R:Accession: S68212
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
PEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68212
A>Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-214 <TAK>
A:Cross-references: UNIPARC:UPI000017697E; EMBL:D29668
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 62.4%; Score 696; DB 2; Length 214;
Best Local Similarity 60.7%; Pred. No. 2.7e-39;
Matches 130; Conservative 35; Mismatches 43; Indels 6; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDI-----SNYLNWYQKPKAPKLLIYDASN 54
DB 1 DIVMTQSPSSLSASVGDRTVITTCQASQDI-----SNYLNWYQKPKAPKLLIYDASN 60

QY 55 ETGVPSRFSGSGGTDTFTTINSLOPEDIATYCYQBYNNLPYSFGOGTKLEIKRTVAAPS 114
DB 61 ESGVPSRFSGSGGTDTFTTINSLOPEDIATYCYQBYNNLPYSFGOGTKLEIKRTVAAPS 120

QY 115 VFIPPPDEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDYSL 174
DB 121 VSIFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSL 180

QY 175 LSSTLTLSKADYEKKHYACEVTHOGLSSPVTKS 208
DB 181 MSSTLTLTQDEYERHNSYTCEATHTKSTSPIVKS 214

RESULT 15
S38865
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S38865
R:Klipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Accession: S38865
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <KIP>
A:Cross-references: UNIPARC:UPI000011653B; EMBL:Z27396; NID:G416538; PIDN:CAA81787.1; PII
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 61.7%; Score 688.5; DB 2; Length 219;
Best Local Similarity 58.0%; Pred. No. 8.7e-39;
Matches 127; Conservative 38; Mismatches 49; Indels 5; Gaps 1;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDI-----SNYLNWYQKPKAPKLLIYDASN 55
DB 1 ELVMTQSPPLSUSVSGDQASISCRSSQSLVHTNGTYLHWYLOKPLGLSPKLLIYVSNRF 60

QY 56 TGVPSRFSGSGGTDTFTTINSLOPEDIATYCYQBYNNLPYSFGOGTKLEIKRTVAAPSV 115
DB 61 SGVPSRFSGSGGTDTFTTINSLOPEDIATYCYQBYNNLPYSFGOGTKLEIKRTVAAPSV 120

QY 116 FIFPPSDEQLKSGTASVVCLLNNFYPRKQVQKVDNALQSGNSQESVTEQDSKDYSL 175
DB 121 SIFPPSDEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYSL 180

QY 176 LSSTLTLSKADYEKKHYACEVTHOGLSSPVTKSFNRGEC 214
DB 181 SSSLTTLTKDEYERHNSYTCEATHTKSTSPIVKSFNRGEC 219

Search completed: December 17, 2005, 01:24:34
Job time : 17.2121 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:10:08 ; Search time 97,9212 Seconds
(without alignments)
1541.883 Million cell updates/sec

Title: US-10-644-277-64
Perfect score: 1115
Sequence: 1 DQMTQSPSLASVGRVT.....EVTHQGLSPVTKSFNRGEC 214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1012	90.8	236	Q7Z3Y4_HUMAN	Q7Z3Y4 homo sapien
2	1004	90.0	236	Q502W4_HUMAN	Q502W4 homo sapien
3	1003	90.0	236	Q6GXX8_HUMAN	Q6GXX8 homo sapien
4	1003	90.0	236	Q6GMW1_HUMAN	Q6GMW1 homo sapien
5	1001	89.8	236	Q6GMX0_HUMAN	Q6GMX0 homo sapien
6	992	89.0	236	Q6PIH4_HUMAN	Q6PIH4 homo sapien
7	992	89.0	236	Q6PIH7_HUMAN	Q6PIH7 homo sapien
8	986	88.4	236	Q6GMX9_HUMAN	Q6GMX9 homo sapien
9	985	88.3	236	Q6PIT5_HUMAN	Q6PIT5 homo sapien
10	984	88.3	234	Q5EPE6_HUMAN	Q5EPE6 homo sapien
11	974	87.4	234	Q7Z473_HUMAN	Q7Z473 homo sapien
12	935.5	81.9	235	Q6GMW0_HUMAN	Q6GMW0 homo sapien
13	914	82.0	236	Q6PII8_HUMAN	Q6PII8 homo sapien
14	905.5	81.2	235	Q6PJF2_HUMAN	Q6PJF2 homo sapien
15	901.5	80.9	235	Q6GMV9_HUMAN	Q6GMV9 homo sapien
16	900	80.7	236	Q6P5S8_HUMAN	Q6P5S8 homo sapien
17	872.5	78.4	240	Q6PIH6_HUMAN	Q6PIH6 homo sapien
18	872.5	78.3	239	Q8TC00_HUMAN	Q8TC00 homo sapien
19	871	78.1	234	Q56919_HUMAN	Q56919 homo sapien
20	868.5	77.9	239	Q8NEK0_HUMAN	Q8NEK0 homo sapien
21	849.5	76.2	239	Q6P491_HUMAN	Q6P491 homo sapien
22	770	69.1	234	Q4KM66_RAT	Q4KM66 rattus norv
23	750	67.3	189	Q56917_HUMAN	Q56917 homo sapien
24	742	66.5	236	Q7TS98_MOUSE	Q7TS98 mus musculu
25	735	65.9	234	Q5M838_RAT	Q5M838 rattus norv
26	725	65.0	240	Q52L64_MOUSE	Q52L64 mus musculu
27	723	64.8	238	Q58EU4_MOUSE	Q58EU4 mus musculu
28	716	64.2	238	Q66J87_MOUSE	Q66J87 mus musculu
29	715	64.1	236	Q52L95_MOUSE	Q52L95 mus musculu
30	687.5	61.7	235	Q58EV6_MOUSE	Q58EV6 mus musculu
31	682.5	61.2	219	Q65ZC0_MOUSE	Q65ZC0 mus musculu

32	682.5	61.2	237	2	Q569Y8_MOUSE	Q569Y8 mus musculu
33	674.5	60.5	235	2	Q5XFY8_MOUSE	Q5XFY8 mus musculu
34	670.5	60.1	239	2	Q58EU8_MOUSE	Q58EU8 mus musculu
35	653.5	58.6	234	2	Q5XKG4_MOUSE	Q5XKG4 mus musculu
36	631	56.6	241	2	Q63ZX4_MOUSE	Q63ZX4 mus musculu
37	599	53.7	120	2	Q6P5R5_HUMAN	Q6P5R5 homo sapien
38	555.5	49.8	243	2	Q6NTU5_XENLA	Q6NTU5 xenopus lae
39	549	49.2	237	2	Q7SZ36_XENLA	Q7SZ36 homo sapien
40	548	49.1	106	1	KAC_HUMAN	KAC homo sapien
41	518.5	46.5	239	2	Q5HZC6_XENTR	Q5HZC6 xenopus tro
42	510	45.7	108	1	KVIB_HUMAN	KVIB homo sapien
43	503	45.1	108	1	KVIO_HUMAN	KVIO homo sapien
44	501	44.9	108	1	KVIA_HUMAN	KVIA homo sapien
45	495	44.4	108	1	KVIP_HUMAN	KVIP homo sapien

ALIGNMENTS

RESULT 1
Q7Z3Y4_HUMAN
ID Q7Z3Y4_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q7Z3Y4;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC005332; AAH05332.1; -; mRNA.
HSP; P01834; IHEZ.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein; Immunoglobulin domain.

SQ SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;

Query Match 90.8%; Score 1012; DB 2; Length 236;
Best Local Similarity 90.7%; Pred. No. 1.8e-74;
Matches 194; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRDVTITCOASODISNVLNNYQOKPGKAPKLLIYDASNLETGVPS 60
DB 23 DIQMTQSPSSLSASVGRDVTITCRASQDISNVLNNYQOKPGKAPKLLIYDASNLETGVPS 82

QY 61 RFGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYFSGQGTKEIKRTVAAPSFIIPP 120
DB 83 KFGSGSGTDFLTITISLOPEDFAITYCOQYKSPVTFQGTKEIKRTVAAPSFIIPP 142

QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 202

QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 2

Q502W4 HUMAN
ID Q502W4_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC095489; AAH95489.1; -, mRNA.
DR SMR; Q502W4; 23-236.
DR Ensemble; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query Match 90.0%; Score 1004; DB 2; Length 236;
Best Local Similarity 90.2%; Pred. No. 8e-74;
Matches 193; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRDVTITCOASODISNVLNNYQOKPGKAPKLLIYDASNLETGVPS 60
DB 23 DIQMTQSPSSLSASVGRDVTITCRASQDISNVLNNYQOKPGKAPKLLIYDASNLETGVPS 82

QY 61 RFGSGSGTDFTTINSLOPEDIAITYCOEYNNLPYFSGQGTKEIKRTVAAPSFIIPP 120
DB 83 RFGSGSGTDFLTITISLOPEDFAITYCLQNSVPTFGQGTKEIKRTVAAPSFIIPP 142

QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 202

QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 3

Q6GMX8 HUMAN
ID Q6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

RA SCHMERCH A., SCHERH J.E., JONES S.J.M., MALLA M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human

```
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH3775.1; -; mRNA.
DR SMR; Q6GMX0; 23-236.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7B92BF8F CRC64;

Query Match 89.8%; Score 1001; DB 2; Length 236;
Best Local Similarity 89.3%; Pred. No. 1.4e-73;
Matches 191; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPKAPKLLIYDASNLGTGVP 60
DB 23 DIQMTQSPSSLSASVGRVTITCRASQNNYLNWYQLKPGKAPNLLIYAASSLSQ 82

OY 61 RFGSGSGTDFTTINSIQPEDIAIYCYQENNLPSYFGQGTKEIKRTVAAPSFI 120
DB 83 RFGSGSGTDFTLTISRLRPDDFATYCYQSYNIPLTFGGTNVIRKRTVAAPSFI 142

OY 121 SDEQLKSGTASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
DB 143 SDEQLKSGTASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 202

OY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 6
OQPIH4 HUMAN
ID O6PIH4 HUMAN PRELIMINARY; PRT; 236 AA.
AC O6PIH4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034146; AAH34146.1; -; mRNA.
DR HSSP; P01607; 1AR2.
DR SMR; O6PIH4; 23-236.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25871 MW; BE01A28CD06BEE26 CRC64;

Query Match 89.0%; Score 992; DB 2; Length 236;
Best Local Similarity 89.3%; Pred. No. 7.6e-73;
Matches 191; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

OY 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPKAPKLLIYDASNLGTGVP 60
DB 23 DIQMTQSPSTLSASVGRVTIACASQWISDMLAWYQKPKAPKLLIYDASRLS 82

OY 61 RFGSGSGTDFTTINSIQPEDIAIYCYQENNLPSYFGQGTKEIKRTVAAPSFI 120
DB 83 RFGSGSGTDFSLTISGLQPDFFATYCYQSYNSPQFGQGTKEIKRTVAAPSFI 142

OY 121 SDEQLKSGTASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 180
DB 143 SDEQLKSGTASVVLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYSL 202

OY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 7
OQPIH7 HUMAN
ID O6PIH7 HUMAN PRELIMINARY; PRT; 236 AA.
AC O6PIH7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
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DE	IGKC protein.	
GN	Name=IGKC;	
OS	Homo sapiens (Human)	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;	
OC	Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Primary B-Cells;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.,	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE.	
RC	TISSUE=Primary B-Cells;	
RX	NIH MGC Project;	
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC034141; AAH34141.1; -; mRNA.	
DR	HSSP; P01607; 1A2.	
DR	SMR; Q6PIH7; 23-236.	
DR	Ensembl; ENSG00000163245; Homo sapiens.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003597; Ig cl.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig v.	
DR	Pfam; PF07654; Cl-set; 1.	
DR	SMART; SM00407; IGc1; 1.	
DR	SMART; SM00406; IGv; 1.	
DR	PROSITE; PS00835; IG LIKE; 2.	
DR	PROSITE; PS00290; IG_MHC; UNKNOWN 1.	
SQ	SEQUENCE 236 AA; 25603 MW; 8BC561106861213P CRC64;	
	Query Match 89.0%; Score 992; DB 2; Length 236;	
	Best Local Similarity 89.3%; Pred. No. 7.6e-73;	
	Matches 191; Conservative 11; Mismatches 12; Indels 0; Gaps 0;	
Qy	1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLEGTGPS 60	
Db	23 DIQLTQSPFLSASVGRVTITCRASQGISSYLAWYQKPGKAPNLLIYAASLTQSGVPS 82	
Qy	61 RFGSGSGDTFTTINSLOPEDATYTCQVNNLPYSFGOGTKLEIKRTVAAPSVFIIPP 120	
Db	83 RFGSGSGDTFTTINSLOPEDATYTCQVNNLPYSFGOGTKLEIKRTVAAPSVFIIPP 142	
Qy	121 SDQLKSGTASVVCLLNNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDSSTLSSTLT 180	
Db	143 SDQLKSGTASVVCLLNNFPYPRKQVQKVDNALQSGNSQESVTEQDSKDSSTLSSTLT 202	
Qy	181 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 214	
Db	203 LSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 236	
RESULT 8		
ID	Q6GMX9 HUMAN PRELIMINARY; PRT; 236 AA.	
AC	Q6GMX9;	
DT	05-JUL-2004 (TrEMBLrel. 27, Created)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)	

RESULT 9

QSPITS_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q6PIT5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029444; AAH29444.1; -; mRNA.
DR HSSP; P01607; 1A92.
DR SMR; Q6PIT5; 26-236.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEE351 CRC64;
Query Match 88.3%; Score 985; DB 2; Length 236;
Best Local Similarity 88.7%; Pred. No. 2.8e-72;
Matches 189; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
QY 2 IQMTQSPSSLSASVGDRTVITCOASQDISNVLNMYQQKPGKAPKLLIYDASNLETGVPSR 61
DB 24 IQLTQSPSSLSASVGERVTITCRASQGISALLAWYQKPGKPKLLIYDASTMESGVPSR 83
QY 62 FSGSGSGTDFTTINSIQLQPEDIATYYCQYNNLPYSFGQYKLEIKRTVAAPSVFIFPPS 121
DB 84 FSGSGSGTHFTLTISLQPEDFATYCCQFKSYPRFGQYKLEIKRTVAAPSVFIFPPS 143
QY 122 DEQLKSGTASVVLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSLSSLTLL 181

RESULT 10

QSEF56_HUMAN PRELIMINARY; PRT; 234 AA.
AC QSEF56;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Anti-Rhd monoclonal T125 kappa light chain precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RT "Sequencing determination of the recombinant human anti-Rhd monoclonal
antibody T125.";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY894991; AAW82027.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF07686; V-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 20 Potential.
FT CHAIN 21 234 anti-Rhd monoclonal T125 kappa light
chain.
FT SEQUENCE 234 AA; 25698 MW; 866DCD1E4FD7D5EA CRC64;
Query Match 88.3%; Score 984; DB 2; Length 234;
Best Local Similarity 88.7%; Pred. No. 3.4e-72;
Matches 189; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 2 IQMTQSPSSLSASVGDRTVITCOASQDISNVLNMYQQKPGKAPKLLIYDASNLETGVPSR 61
DB 22 IRMTQSPSSFSASTGDRVTITCRASQDIRNVAVYQKSGKAPKFLIYASTLQSGVPSR 81
QY 62 FSGSGSGTDFTTINSIQLQPEDIATYYCQYNNLPYSFGQYKLEIKRTVAAPSVFIFPPS 121
DB 82 FSGSGSGTDFTLTINSIQLQSEDFATYYCQYNNSPPTFGQYKLEIKRTVAAPSVFIFPPS 141
QY 122 DEQLKSGTASVVLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSLSSLTLL 181
DB 142 DEQLKSGTASVVLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSLSSLTLL 201
QY 182 SKADYKHKVYACVETHQGLSSPVTKSFNRGEC 214
DB 202 SKADYKHKVYACVETHQGLSSPVTKSFNRGEC 234
RESULT 11
Q7Z473_HUMAN PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE	IGKC protein.
GN	Name=IGKC;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo.
NCBI_TaxID=9606;	
[1]	
TX	NUCLEOTIDE SEQUENCE.
RC	TISSUE=Lung;
RX	MDLNE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Stenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Uadin T.B., Tohiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA	Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
RL	[Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).]
RP	(2)
RC	TISSUE=Lung;
RG	NIH MGC Project;
RL	Submitted (AUG-2003) to the ENBL/GenBank/DBJ databases.
DR	ENBL; BC056256; AAH56256.1; -; mRNA.
DR	HSSP; P01834; IHEZ.
DR	SMR; Q72473; 22-234.
DR	Ensembl; ENSG00000163245; Homo sapiens.
DR	InterPro; IPRO07110; Ig-like.
DR	InterPro; IPRO03597; Ig cl.
DR	InterPro; IPRO03006; Ig MHC.
DR	InterPro; IPRO03596; Ig v.
DR	Pfam; PF07654; Cl-set; 1.
DR	SMART; SM00406; IGv; 1.
DR	PROSITE; PS0835; IG_LIKE; 2.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	Immunoglobulin domain.
SEQ	SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
Query Match	87.4%; Score 974; DB 2; Length 234;
Best Local Similarity	87.3%; Pred. No. 2.2e-71;
Matches 186; Conservative 12; Mismatches 15; Indels 0; Gaps 0;	
Qy	2 IQMTQSPPSSLSASVGDVRVTITCOASQDISINLYNQKPKGAPKLIIYDASNLETGVPSR 61
Db	22 IRMTQSPSSFASGTGDRVTITCRASQISGLSYLAWSYQQKPGAPQLLIYAATSLQSGVPSR 81
Qy	62 PSGSGSGTDFTTINSLOPEDIAITYCOEYNLLPYSCFGQTKLEIKRTVAAPSFIPIPPS 121
Db	82 PSGSASGTDFTLSISICLSQSEDFATVYCQOYYTPWTFCGGTKVEIKRTVAAPSFIPIPPS 141
Qy	122 DEQLKSQTASVVCLLNPNFYPREAKVQWKVDNALQSGNSQESVTEODSKDSYISLSSTLT 181
Db	142 DEQLKSQTASVVCLLNPNFYPREAKVQWKVDNALQSGNSQESVTEODSKDSYISLSSTLT 201
Qy	182 SKADYEKKHVACEVTHOGLSSPVTKSFNRGEC 214
Db	202 SKADYEKKHVACEVTHOGLSSPVTKSFNRGEC 234

RESULT 12

QY 180 TLKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 214
 Db 201 TLKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 13

OS PII18 HUMAN
 ID Q6PJF2 HUMAN PRELIMINARY; PRT; 236 AA.
 AC Q6PJF2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

TX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Udwin T.B., Toshituyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

NUCLEOTIDE SEQUENCE.

RP TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC032451; AAH32451.1; -; mRNA.
 DR HSP; P01837; 1KCU.
 DR SMR; Q6PJF2; 21-236.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match 82.0%; Score 914; DB 2; Length 236;

Best Local Similarity 81.7%; Pred. No. 1.8e-66;

Matches 174; Conservative 19; Mismatches 18; Indels 2; Gaps 2;

QY 4 MTQSPSSLSASVGRVITTCASQDI-SNYLNWYQKPGKAPKLLIYDASNLETGVPSRF 62

Db 24 LTQSPGTLSPGERATLSCRSQSLSSYLAWYQKPGQAPRLIIYGVSSRATGIPDRF 83

QY 63 SGSGSGDTFTTINSLOPEDIATYYCOEY-NNLPYSFGQGTKLRIKRTVAAPSVFIFPPS 121
 Db 84 SGSGSGDTFTTISRLEPEDFAVYCCQYGTSTRITFGQGTRLDIKRTVAAPSVFIFPPS 143
 QY 122 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALGSGNSQESVTEQDSKDSYSLSTLTL 181
 Db 144 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALGSGNSQESVTEQDSKDSYSLSTLTL 203

QY 182 SKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 214

Db 204 SKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 14

OS PII18 HUMAN
 ID Q6PJF2 HUMAN PRELIMINARY; PRT; 235 AA.
 AC Q6PJF2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

TX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M.J., Udwin T.B., Toshituyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

NUCLEOTIDE SEQUENCE.

RP TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016380; AAH16380.1; -; mRNA.
 DR HSP; P01837; 1KCU.
 DR SMR; Q6PJF2; 21-235.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 81.2%; Score 905.5; DB 2; Length 235;

RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH73793.1; -, mRNA.
DR SMR; Q6GMV9; 21-235.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.

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Job time : 98.9212 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:13:49 ; Search time 21.4 Seconds
(without alignments)
826.757 Million cell updates/sec

Title: US-10-644-277-64
Perfect score: 1115
Sequence: 1 DIQMTQSSLSASVGRVT.....EVTHQGLSPVTKSFNRGEC 214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents AA.*
- 1: /cgn2_6/prodata/1/iaa/5 COMB.pep.*
 - 2: /cgn2_6/prodata/1/iaa/6 COMB.pep.*
 - 3: /cgn2_6/prodata/1/iaa/H COMB.pep.*
 - 4: /cgn2_6/prodata/1/iaa/PCUTUS COMB.pep.*
 - 5: /cgn2_6/prodata/1/iaa/RE COMB.pep.*
 - 6: /cgn2_6/prodata/1/iaa/baCkfilea1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1034	92.7	237	2	US-08-908-469-100
2	1034	92.7	491	2	US-10-011-125A-2
3	1032	92.6	214	1	US-07-934-373C-39
4	1032	92.6	214	2	US-08-437-642B-39
5	1032	92.6	214	4	PCT-US93-07832-39
6	1027	92.1	214	1	US-07-934-373C-40
7	1027	92.1	214	1	US-08-788-800-11
8	1027	92.1	214	2	US-08-437-642B-40
9	1027	92.1	214	2	US-09-037-309-2
10	1027	92.1	214	2	US-09-097-171A-2
11	1027	92.1	214	2	US-09-460-587-2
12	1027	92.1	214	2	US-09-940-166A-2
13	1027	92.1	214	4	PCT-US93-07832-40
14	1027	92.1	233	1	US-07-934-373C-25
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16	1027	92.1	233	2	US-08-146-206C-25
17	1027	92.1	233	2	US-09-705-686-25
18	1027	92.1	233	2	US-09-705-392A-25
19	1027	92.1	233	2	US-09-705-398-25
20	1027	92.1	233	4	PCT-US93-07832-25
21	1027	92.1	237	2	US-09-037-309-6
22	1027	92.1	237	2	US-09-097-171A-10
23	1027	92.1	237	2	US-09-422-712B-2
24	1027	92.1	237	2	US-09-607-756-2
25	1027	92.1	237	2	US-09-460-587-6
26	1027	92.1	237	2	US-09-940-166A-6
27	1025	91.9	233	2	US-08-030-175-43

28	1020	91.5	214	2	US-09-472-087-71	Sequence 71, Appl
29	1016	91.1	218	4	PCT-US96-13152-2	Sequence 2, Appl1
30	1014	90.9	214	1	US-08-458-516-12	Sequence 12, Appl
31	1013	90.9	212	2	US-10-011-125A-5	Sequence 5, Appl1
32	1011	90.7	236	2	US-09-859-053-30	Sequence 30, Appl
33	1010	90.6	234	2	US-09-800-729-150	Sequence 150, Appl
34	1006	90.2	218	1	US-08-887-352B-13	Sequence 13, Appl
35	1006	90.2	218	2	US-08-466-151-9	Sequence 9, Appl1
36	1006	90.2	218	2	US-09-109-207C-13	Sequence 13, Appl
37	1006	90.2	218	2	US-09-296-005-13	Sequence 13, Appl
38	1006	90.2	218	2	US-08-466-163B-9	Sequence 9, Appl1
39	1006	90.2	218	2	US-09-920-171-13	Sequence 13, Appl
40	1006	90.2	218	2	US-09-802-096-9	Sequence 9, Appl1
41	1006	90.2	218	2	US-09-802-077-9	Sequence 9, Appl1
42	1006	90.2	218	2	US-09-716-028-13	Sequence 13, Appl
43	1006	90.2	218	2	US-10-113-996-13	Sequence 13, Appl
44	1006	90.2	218	2	US-09-925-179-9	Sequence 9, Appl1
45	1004.5	90.1	235	2	US-09-910-059-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-08-908-469-100
; Sequence 100, Application US/08908469
; Patent No. 6884879
; GENERAL INFORMATION:
; APPLICANT: Baca, Manuel
; Wells, James A.
; Presta, Leonard G.
; Lowman, Henry B.
; Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/908,469
FILING DATE: 21-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/833,504
FILING DATE: 07-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-08-908-469-100

Query Match 92.7%; Score 1034; DB 2; Length 237;
Best Local Similarity 91.6%; Pred. No. 1.4e-78;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

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QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNNWYQKPGKAPKLLIYDASNLETGVPS 60
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QY 61 RFGSGSGGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKEIKRTVAAPSVEFIIPP 120
Db 84 RFGSGSGGTDYTLTISLQPEDFAITYCQYSTVPWTFQGTKEIKRTVAAPSVEFIIPP 143
QY 121 SDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 144 SDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 203
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNREGC 214
Db 204 LSKADYERKHVYACEVTHQGLSSPVTKSFNREGC 237
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RESULT 2

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US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2
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Query Match 92.7%; Score 1034; DB 2; Length 491;
Best Local Similarity 91.6%; Pred. No. 3.3e-78;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 24 DIQLTQSPSSLSASVGDRTVITTCASQDISNYLNNWYQKPGKAPKLLIYFTSSLSHSGVPS 83
QY 61 RFGSGSGGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKEIKRTVAAPSVEFIIPP 120
Db 84 RFGSGSGGTDYTLTISLQPEDFAITYCQYSTVPWTFQGTKEIKRTVAAPSVEFIIPP 143
QY 121 SDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 144 SDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 203
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RESULT 3

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US-07-934-373C-39
; Sequence 39, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
```

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; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-39

Query Match 92.6%; Score 1032; DB 1; Length 214;
Best Local Similarity 92.5%; Pred. No. 1.8e-78;
Matches 198; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNNWYQKPGKAPKLLIYDASNLETGVPS 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNYLNNWYQKPGKAPKLLIYFTSSLSHSGVPS 60
QY 61 RFGSGSGGTDFTTINSLOPEDIAITYCOEYNNLPYSFGQGTKEIKRTVAAPSVEFIIPP 120
Db 61 RFGSGSGGTDYTLTISLQPEDFAITYCQCGNTLPTFTGGQGTKEIKRTVAAPSVEFIIPP 120
QY 121 SDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 121 SDEQLKSGTASVVCLLNNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNREGC 214
Db 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNREGC 214

RESULT 4
US-08-437-642B-39
; Sequence 39, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 39:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-39

Query Match          92.6%; Score 1032; DB 2; Length 214;
Best Local Similarity 92.5%; Pred. No. 1.8e-78;
Matches 198; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYVTSLESGVPS 60
QY 61 RFGSGSGTDFTTINSLOPEDATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIAPP 120
DB 61 RFGSGSGTDYTLTISSLQPEDFATYYCQGNLTPPTFGQGTKEIKRTVAAPSVFIAPP 120
QY 121 SDQLKSGTASVCLNNFYPRKAVQWVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 180
DB 121 SDEQLKSGTASVCLNNFYPRKAVQWVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 180
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 5
PCT-US93-07832-39
US-07-934-373C-40
Sequence 39, Application PC/TUS9307832
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEFAX: 910/371-7168
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-39

Query Match          92.6%; Score 1032; DB 4; Length 214;
Best Local Similarity 92.5%; Pred. No. 1.8e-78;
Matches 198; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITCRASQDINNYLNWYQKPGKAPKLLIYVTSLESGVPS 60
QY 61 RFGSGSGTDFTTINSLOPEDATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIAPP 120
DB 61 RFGSGSGTDYTLTISSLQPEDFATYYCQGNLTPPTFGQGTKEIKRTVAAPSVFIAPP 120
QY 121 SDEQLKSGTASVCLNNFYPRKAVQWVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 180
DB 121 SDEQLKSGTASVCLNNFYPRKAVQWVDNALQSGNSQESVTEQDSKDSSTYSLSSTLT 180
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 6
US-07-934-373C-40
Sequence 40, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-40

Query Match 92.1%; Score 1027; DB 1; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNLYQKPGKAPKLLIYTTSTLHSGVPS 60
QY 61 RFGSGSGTDTFTTINSIQPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120
Db 61 RFGSGSGTDTYLTITSSIQPEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPP 120
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 7
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
```

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; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-11

Query Match 92.1%; Score 1027; DB 1; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDINSYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNLYQKPGKAPKLLIYTTSTLHSGVPS 60
QY 61 RFGSGSGTDTFTTINSIQPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120
Db 61 RFGSGSGTDTYLTITSSIQPEDFATYYCQGNLTLPPTFGQGTKEIKRTVAAPSVFIFPP 120
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 8
US-08-437-642B-40
; Sequence 40, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
```


INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-40

Query Match 92.1%; Score 1027; DB 2; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

1 DIQMTQSPSSLSASVGDRVTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
1 DIQMTQSPSSLSASVGDRVTITCRASQDINNLYNWKQKPGKAPKLLIYVTSYTHSGVPS 60
61 RFGSGSGTDTFTTINSLOPEDIAITYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIPT 120
61 RFGSGSGTDTFTTINSLOPEDIAITYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIPT 120
121 SDEQLKSGTASVVCLLNFPYKQVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
121 SDEQLKSGTASVVCLLNFPYKQVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 10
US-09-097-171A-2
Sequence 2, Application US/09097171A
Patent No. 6171586
GENERAL INFORMATION:
APPLICANT: Lam, Xanthe M.
APPLICANT: Oeswein, James Q.
APPLICANT: Ongpipattanakul, Boonsri
APPLICANT: Shahrokh, Zahra
APPLICANT: Wang, Sharon X.
APPLICANT: Weissburg, Robert P.
APPLICANT: Wong, Rita L.
TITLE OF INVENTION: Antibody Formulation
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,171A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874897
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1089R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-171A-2

Query Match 92.1%; Score 1027; DB 2; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

1 DIQMTQSPSSLSASVGDRVTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
1 DIQMTQSPSSLSASVGDRVTITCRASQDINNLYNWKQKPGKAPKLLIYVTSYTHSGVPS 60

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-40

Query Match 92.1%; Score 1027; DB 2; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

1 DIQMTQSPSSLSASVGDRVTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
1 DIQMTQSPSSLSASVGDRVTITCRASQDINNLYNWKQKPGKAPKLLIYVTSYTHSGVPS 60
61 RFGSGSGTDTFTTINSLOPEDIAITYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIPT 120
61 RFGSGSGTDTFTTINSLOPEDIAITYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIPT 120
121 SDEQLKSGTASVVCLLNFPYKQVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
121 SDEQLKSGTASVVCLLNFPYKQVQKVDNALQSGNSQESVTEQDSKDSYSLSTLT 180
181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 9
US-09-097-309-2
Sequence 2, Application US/09097309
Patent No. 6121428
GENERAL INFORMATION:
APPLICANT: Blank, Gregory S.
APPLICANT: Narindray, Daljit S.
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Protein Recovery
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,309
FILING DATE: 12-Jun-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050951
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Schwartz, Timothy R.
REGISTRATION NUMBER: 32171
REFERENCE/DOCKET NUMBER: P1105R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-7467
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-097-309-2

Query Match 92.1%; Score 1027; DB 2; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;

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QY 61 RFSGSGTDTFTTINSLOPEDIATYCOEYNNLPYSFGQGTKLBIKRTVAAPSFIIPP 120
Db 61 RFSGSGGTDYTLTISSLOPEFATYCOQGNLPTFTFGQTKVEIKRTVAAPSFIIPP 120

QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180

QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 11
US-09-460-587-2
; Sequence 2, Application US/09460587
; Patent No. 6322997
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,587
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/097,309
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-460-587-2

Query Match 92.1%; Score 1027; DB 2; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNLYNWYQKPGKAPKLLIYDASNLETGVP 60
Db 1 DIQMTQSPSSLSASVGRVTITTCRASQDINNLYNWYQKPGKAPKLLIYDASNLETGVP 60

QY 61 RFSGSGTDTFTTINSLOPEDIATYCOEYNNLPYSFGQGTKLBIKRTVAAPSFIIPP 120
Db 61 RFSGSGGTDYTLTISSLOPEFATYCOQGNLPTFTFGQTKVEIKRTVAAPSFIIPP 120

QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180

QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 13
PCT-US93-07832-40
; Sequence 40, Application PC/TUS9307832
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QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 12
US-09-940-166A-2
; Sequence 2, Application US/09940166A
; Patent No. 6716598
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/940.166A
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/097,309
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-940-166A-2

Query Match 92.1%; Score 1027; DB 2; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNLYNWYQKPGKAPKLLIYDASNLETGVP 60
Db 1 DIQMTQSPSSLSASVGRVTITTCRASQDINNLYNWYQKPGKAPKLLIYDASNLETGVP 60

QY 61 RFSGSGTDTFTTINSLOPEDIATYCOEYNNLPYSFGQGTKLBIKRTVAAPSFIIPP 120
Db 61 RFSGSGGTDYTLTISSLOPEFATYCOQGNLPTFTFGQTKVEIKRTVAAPSFIIPP 120

QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
Db 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180

QY 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214

RESULT 13
PCT-US93-07832-40
; Sequence 40, Application PC/TUS9307832
```

GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
PRIOR APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 709P2PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-07832-40
Query Match 92.1%; Score 1027; DB 4; Length 214;
Best Local Similarity 92.1%; Pred. No. 4.7e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPKAPKLLIYDASNLETGVP 60
Db 1 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNWYQKPKAPKLLIYTTSTLHSGVPS 60
Qy 61 RFGSGSGTDFTTINSLOPEDATYYCQYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120
Db 61 RFGSGSGTDYLTITSLQPEDFATYYCQGNLTPPTFGQGTKEIKRTVAAPSVFIFPP 120
Qy 121 SDEQLKSGTASVCLLNFPYFREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSSTLT 180
Db 121 SDEQLKSGTASVCLLNFPYFREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSSTLT 180
Qy 181 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214
Db 181 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214
RESULT 14
US-07-934-373C-25
Sequence 25, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants

NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-AUG-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-25
Query Match 92.1%; Score 1027; DB 1; Length 233;
Best Local Similarity 92.1%; Pred. No. 5.2e-78;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
Qy 1 DIQMTQSPSSLSASVGRVTITCOASQDISNYLNWYQKPKAPKLLIYDASNLETGVP 60
Db 20 DIQMTQSPSSLSASVGRVTITCRASQDINNLYNWYQKPKAPKLLIYTTSTLHSGVPS 79
Qy 61 RFGSGSGTDFTTINSLOPEDATYYCQYNNLPYSFGQGTKEIKRTVAAPSVFIFPP 120
Db 80 RFGSGSGTDYLTITSLQPEDFATYYCQGNLTPPTFGQGTKEIKRTVAAPSVFIFPP 139
Qy 121 SDEQLKSGTASVCLLNFPYFREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSSTLT 180
Db 140 SDEQLKSGTASVCLLNFPYFREAKVQKVDNALQSGNSQESVTEQDSKDSSTLSSTLT 199
Qy 181 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 214
Db 200 LSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 233
RESULT 15
US-08-437-642B-25
Sequence 25, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

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OM protein - protein search, using sw model

Run on: December 17, 2005, 01:14:05 ; Search time 70.6849 Seconds
(without alignments)
1264.988 Million cell updates/sec

Title: US-10-644-277-64
Perfect score: 1115
Sequence: 1 DIQMTQSPSSLSASVGDVRT.....EVTHQGLSPVTKSFNRGEC 214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main:*
1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pgp:*
2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pgp:*
3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pgp:*
4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pgp:*
5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pgp:*
6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pgp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1115	100.0	214	5	US-10-644-277-64
2	1060	95.1	238	6	US-11-031-485-48
3	1051	94.3	236	4	US-10-401-344-4
4	1045	93.7	502	4	US-10-679-820-88
5	1045	93.7	502	6	US-11-132-143-88
6	1043	93.5	236	6	US-11-131-648-20
7	1043	93.5	236	6	US-11-131-648-49
8	1037	93.0	667	5	US-10-764-428-25
9	1034	92.7	214	4	US-10-364-953-1
10	1034	92.7	237	3	US-09-056-1608-100
11	1034	92.7	237	4	US-10-020-786-10
12	1034	92.7	237	4	US-10-234-671-100
13	1034	92.7	237	5	US-10-697-995-8
14	1034	92.7	237	5	US-10-697-995-11
15	1034	92.7	237	5	US-10-974-591-100
16	1034	92.7	237	6	US-11-071-291-10
17	1034	92.7	260	4	US-10-264-049-2296
18	1034	92.7	491	4	US-10-011-125-2
19	1034	92.7	667	5	US-10-764-428-7
20	1034	92.7	667	5	US-10-764-428-13
21	1034	92.7	670	5	US-10-764-428-5
22	1034	92.7	670	5	US-10-764-428-9
23	1034	92.7	670	5	US-10-764-428-11
24	1034	92.7	670	5	US-10-764-428-27
25	1034	92.7	670	5	US-10-764-428-2
26	1027	92.1	214	3	US-09-940-166A-2
27	1027	92.1	214	4	US-09-811-384-11
					US-10-404-286-11

28	1027	92.1	214	4	US-10-762-967-2	Sequence 2, Appli
29	1027	92.1	214	5	US-10-745-775-17	Sequence 17, Appli
30	1027	92.1	214	6	US-11-077-717-2	Sequence 2, Appli
31	1027	92.1	233	5	US-10-835-641-25	Sequence 25, Appli
32	1027	92.1	237	3	US-09-940-166A-6	Sequence 6, Appli
33	1027	92.1	237	4	US-10-762-967-6	Sequence 1, Appli
34	1027	92.1	237	4	US-10-762-967-1	Sequence 6, Appli
35	1027	92.1	237	5	US-10-754-212-2	Sequence 2, Appli
36	1027	92.1	237	6	US-11-077-717-10	Sequence 10, Appli
37	1027	92.1	245	3	US-09-797-941A-6	Sequence 6, Appli
38	1027	92.1	245	5	US-10-965-585-6	Sequence 4, Appli
39	1026	92.0	259	3	US-09-979-948C-4	Sequence 6, Appli
40	1026	92.0	259	3	US-09-979-948C-6	Sequence 6, Appli
41	1025	91.9	213	4	US-10-379-392-135	Sequence 135, App
42	1023	91.7	213	4	US-10-379-392-153	Sequence 153, App
43	1023	91.7	233	4	US-10-404-724-68	Sequence 68, Appli
44	1022	91.7	212	4	US-10-320-231A-77	Sequence 77, Appli
45	1022	91.7	212	5	US-10-867-506-77	Sequence 77, Appli

ALIGNMENTS

RESULT 1
US-10-644-277-64
; Sequence 64, Application US/10644277
; Publication No. US20050058639A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean M.
; APPLICANT: Haak-Frendach, Mary
; APPLICANT: Foord, Orit
; APPLICANT: Liang, Meina L.
; APPLICANT: Ahluwalia, Kiran
; APPLICANT: Bhakta, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
; FILE REFERENCE: ABGENIX.091A
; CURRENT APPLICATION NUMBER: US/10/644,277
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homosapien
US-10-644-277-64

Query Match	100.0%	Score 1115;	DB 5;	Length 214;
Best Local Similarity	100.0%	Pred. No. 1.1e-57;		
Matches 214;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	DIQMTQSPSSLSASVGDVRTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS	60	
Db	1	DIQMTQSPSSLSASVGDVRTITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS	60	
QY	61	RFGSGSGDFTFTINSLOPEDIATYVCOEYNNLPYSFGGTTKLEIKRTVAAPSVFIAPP	120	
Db	61	RFGSGSGDFTFTINSLOPEDIATYVCOEYNNLPYSFGGTTKLEIKRTVAAPSVFIAPP	120	
QY	121	SDQLKSGTASVVCLNNFVPREKQVQKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT	180	
Db	121	SDQLKSGTASVVCLNNFVPREKQVQKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT	180	
QY	181	LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	214	
Db	181	LSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC	214	

RESULT 2
US-11-031-485-48
; Sequence 48, Application US/11031485

Publication No. US20050232917A1
GENERAL INFORMATION:
APPLICANT: PULLEN, NICHOLAS
APPLICANT: MOLLOY, ELIZABETH
APPLICANT: KELLERMANN, SIRID-AIMEE
APPLICANT: GREEN, LARRY L.
APPLICANT: HAAK-FRENDSCHO, MARY
TITLE OF INVENTION: ANTIBODIES TO MadCAM
FILE REFERENCE: ABX-PF6
CURRENT APPLICATION NUMBER: US/11/031,485
CURRENT FILING DATE: 2005-01-07
PRIOR APPLICATION NUMBER: 60/535,490
PRIOR FILING DATE: 2004-01-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin ver. 3.3
SEQ ID NO 48
LENGTH: 238
TYPE: PRT
ORGANISM: Homo sapiens
US-11-031-485-48

Query Match 95.1%; Score 1060; DB 6; Length 238;
Best Local Similarity 95.8%; Pred. No. 1.9e-54;
Matches 205; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
DB 25 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 84
QY 61 RFGSGSGTDFTTINSLOPEDIAITYYCOEYNNLPYSGQGTKEIKRTVAAPSFIIPP 120
DB 85 RFGSGSGTDFTTISSLOPEDIAITYYCOHSDNLSITFGQGTREIKRTVAAPSFIIPP 144
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180
DB 145 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 204
QY 181 LSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 214
DB 205 LSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 238

RESULT 3
US-10-401-344-4
Sequence 4, Application US/10401344
Publication No. US20030194404A1
GENERAL INFORMATION:
APPLICANT: Schering Corporation and Abgenix, Inc.
APPLICANT: Corvalan, Jose
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COME
FILE REFERENCE: LI01564W
CURRENT APPLICATION NUMBER: US/10/401,344
CURRENT FILING DATE: 2003-03-27
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: Signal Peptide
LOCATION: (1)..(22)
OTHER INFORMATION:
US-10-401-344-4

Query Match 94.3%; Score 1051; DB 4; Length 236;
Best Local Similarity 94.4%; Pred. No. 6.3e-54;
Matches 202; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60

DB 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 82
QY 61 RFGSGSGTDFTTINSLOPEDIAITYYCOEYNNLPYSGQGTKEIKRTVAAPSFIIPP 120
DB 83 RFGSGSGTDFTTISSLOPEDIAITYYCOQYDNHPLTFGGGTKEIKRTVAAPSFIIPP 142
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 202
QY 181 LSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 236

RESULT 4
US-10-679-620-88
Sequence 88, Application US/10679620
Publication No. US20040110930A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology
APPLICANT: Reinel, Stephen J.
APPLICANT: Edwards, Patricia C.
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
FILE REFERENCE: 34150-004A
CURRENT APPLICATION NUMBER: US/10/679,620
CURRENT FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.2
SEQ ID NO 88
LENGTH: 502
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hufab H2, see Example 2
NAME/KEY: misc feature
LOCATION: (232)..(232)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-679-620-88

Query Match 93.7%; Score 1045; DB 4; Length 502;
Best Local Similarity 93.5%; Pred. No. 2.7e-53;
Matches 200; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 82
QY 61 RFGSGSGTDFTTINSLOPEDIAITYYCOEYNNLPYSGQGTKEIKRTVAAPSFIIPP 120
DB 83 RFGSGSGTDFTTISSLOPEDIAITYYCOQYDNHPLTFGGGTKEIKRTVAAPSFIIPP 142
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 180
DB 143 SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYSLSLT 202
QY 181 LSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYKHKYVACEVTHQGLSSPVTKSFNRGEC 236

RESULT 5
US-11-132-143-88
Sequence 88, Application US/11132143
Publication No. US20050207977A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology
APPLICANT: Reinel, Stephen J.
APPLICANT: Edwards, Patricia C.
TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING

```
FILE REFERENCE: 34150-004A
CURRENT APPLICATION NUMBER: US/11/132,143
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: US/10/679,620
PRIOR FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.2
SEQ ID NO 88
LENGTH: 502
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hufab H2 , see Example 2
FEATURE:
NAME/KEY: misc feature
LOCATION: (232)..(232)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-132-143-88

Query Match
Best Local Similarity 93.7%; Score 1045; DB 6; Length 502;
Matches 200; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 82
QY 61 RFGSGSGTDFTTINSLOPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIAPP 120
DB 83 RFGSGSGTDFTTINSLOPEDIATYYCOQYDNLPTFGGKVEIKRTVAAPSVFIAPP 142
QY 121 SDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
DB 143 SDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 202
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 6
US-11-131-648-20
Sequence 20, Application US/11/131648
Publication No. US20050221400A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Jakobovits, Aya
APPLICANT: Xiao-Chi, Jia
APPLICANT: Morrison, Robert Kendall
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Shao, Hui
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
FILE REFERENCE: 51158-20088.20
CURRENT FILING DATE: 2005-05-17
CURRENT APPLICATION NUMBER: US/11/131,648
PRIOR FILING DATE: 2004-10-05
PRIOR APPLICATION NUMBER: 60/616,381
PRIOR FILING DATE: 2004-10-12
PRIOR APPLICATION NUMBER: 60/617,881
PRIOR FILING DATE: 2004-10-12
PRIOR APPLICATION NUMBER: 60/621,310
PRIOR FILING DATE: 2004-10-21
PRIOR APPLICATION NUMBER: 60/633,077
PRIOR FILING DATE: 2004-12-02
PRIOR APPLICATION NUMBER: 10/857,484
PRIOR FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 60/475,064
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-11-131-648-49

Query Match
Best Local Similarity 93.5%; Score 1043; DB 6; Length 236;
Matches 199; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 82
QY 61 RFGSGSGTDFTTINSLOPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIAPP 120
DB 203 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
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FILE REFERENCE: 34150-004A
CURRENT APPLICATION NUMBER: US/11/132,143
CURRENT FILING DATE: 2005-05-17
PRIOR APPLICATION NUMBER: US/10/679,620
PRIOR FILING DATE: 2003-10-03
PRIOR APPLICATION NUMBER: 60/415,940
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.2
SEQ ID NO 88
LENGTH: 502
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hufab H2 , see Example 2
FEATURE:
NAME/KEY: misc feature
LOCATION: (232)..(232)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-132-143-88

Query Match
Best Local Similarity 93.7%; Score 1045; DB 6; Length 502;
Matches 200; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 82
QY 61 RFGSGSGTDFTTINSLOPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIAPP 120
DB 83 RFGSGSGTDFTTINSLOPEDIATYYCOQYDNLPTFGGKVEIKRTVAAPSVFIAPP 142
QY 121 SDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 180
DB 143 SDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSYLSSTLT 202
QY 181 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 6
US-11-131-648-20
Sequence 20, Application US/11/131648
Publication No. US20050221400A1
GENERAL INFORMATION:
APPLICANT: Gudas, Jean
APPLICANT: Jakobovits, Aya
APPLICANT: Xiao-Chi, Jia
APPLICANT: Morrison, Robert Kendall
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Shao, Hui
APPLICANT: Challita-Eid, Pia M.
APPLICANT: Raitano, Arthur B.
TITLE OF INVENTION: ANTIBODIES AND RELATED MOLECULES THAT BIND TO PSCA PROTEINS
FILE REFERENCE: 51158-20088.20
CURRENT FILING DATE: 2005-05-17
CURRENT APPLICATION NUMBER: US/11/131,648
PRIOR FILING DATE: 2004-10-05
PRIOR APPLICATION NUMBER: 60/616,381
PRIOR FILING DATE: 2004-10-12
PRIOR APPLICATION NUMBER: 60/617,881
PRIOR FILING DATE: 2004-10-12
PRIOR APPLICATION NUMBER: 60/621,310
PRIOR FILING DATE: 2004-10-21
PRIOR APPLICATION NUMBER: 60/633,077
PRIOR FILING DATE: 2004-12-02
PRIOR APPLICATION NUMBER: 10/857,484
PRIOR FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 60/475,064
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 49
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-11-131-648-49

Query Match
Best Local Similarity 93.5%; Score 1043; DB 6; Length 236;
Matches 199; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 60
DB 23 DIQMTQSPSSLSASVGDRTVITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETVGPS 82
QY 61 RFGSGSGTDFTTINSLOPEDIATYYCOEYNNLPYSFGQGTKEIKRTVAAPSVFIAPP 120
DB 203 LSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
```


Publication No. US20030190317A1
GENERAL INFORMATION:
APPLICANT: Baca, Manuel
Wells, James A.
Presta, Leonard G.
Lowman, Henry B.
Chen, Yvonne M.
TITLE OF INVENTION: ANTI-VEGF ANTIBODIES
NUMBER OF SEQUENCES: 131
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/234,671
FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/056160
FILING DATE: 06-APR-1998
APPLICATION NUMBER: 60/126446
FILING DATE: 07-APR-1997
APPLICATION NUMBER: 60/054856
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: Cui, Steven X.
REGISTRATION NUMBER: 44,637
REFERENCE/DOCKET NUMBER: P1093R2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-234-671-100

Query Match 92.7%; Score 1034; DB 4; Length 237;
Best Local Similarity 91.6%; Pred. No. 6.2e-53;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 24 DIQLTQSPSSLSASVGDRTVITCSAQDISNYLNWYQKPGKAPKLLIYFTSLHSGVPS 83
QY 61 RFGSGSGDTFTTINSLOPEDATYTCQYNNLPYSFGQGTKEIKRTVAAPSVFIIPP 120
DB 84 RFGSGSGDTFTLTISLQPEDFATYCCQYSTVPWTFGGTKVEIKRTVAAPSVFIIPP 143
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYLSSTLT 180
DB 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYLSSTLT 203
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 13
US-10-697-995-8
Sequence 8, Application US/10697995
Publication No. US20050048572A1
GENERAL INFORMATION:

TYPE: Amino Acid
TOPOLOGY: Linear
US-09-056-1608-100
Query Match 92.7%; Score 1034; DB 3; Length 237;
Best Local Similarity 91.6%; Pred. No. 6.2e-53;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 24 DIQLTQSPSSLSASVGDRTVITCSAQDISNYLNWYQKPGKAPKLLIYFTSLHSGVPS 83
QY 61 RFGSGSGDTFTTINSLOPEDATYTCQYNNLPYSFGQGTKEIKRTVAAPSVFIIPP 120
DB 84 RFGSGSGDTFTLTISLQPEDFATYCCQYSTVPWTFGGTKVEIKRTVAAPSVFIIPP 143
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYLSSTLT 180
DB 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYLSSTLT 203
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237
RESULT 11
US-10-020-786-10
Sequence 10, Application US/10020786
Publication No. US20030073164A1
GENERAL INFORMATION:
APPLICANT: Simons, Laura C.
APPLICANT: Klimowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 10
LENGTH: 237
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: anti-VEGF light chain
US-10-020-786-10

Query Match 92.7%; Score 1034; DB 4; Length 237;
Best Local Similarity 91.6%; Pred. No. 6.2e-53;
Matches 196; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITCOASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 24 DIQLTQSPSSLSASVGDRTVITCSAQDISNYLNWYQKPGKAPKLLIYFTSLHSGVPS 83
QY 61 RFGSGSGDTFTTINSLOPEDATYTCQYNNLPYSFGQGTKEIKRTVAAPSVFIIPP 120
DB 84 RFGSGSGDTFTLTISLQPEDFATYCCQYSTVPWTFGGTKVEIKRTVAAPSVFIIPP 143
QY 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYLSSTLT 180
DB 144 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSTYLSSTLT 203
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 204 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 237

RESULT 12
US-10-234-671-100
Sequence 100, Application US/10234671

Qy	181	L	S	K	A	D	E	K	H	K	V	A	C	E	V	T	H	Q	G	L	S	S	P	T	K	S	F	N	R	G	E	C	214
Db	204	L	S	K	A	D	E	K	H	K	V	A	C	E	V	T	H	Q	G	L	S	S	P	T	K	S	F	N	R	G	E	C	237

Search completed: December 17, 2005, 01:29:31
Job time : 72.6849 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model
Run on: December 17, 2005, 01:18:45 ; Search time 4.53939 Seconds
(without alignments)
317.590 Million cell updates/sec

Title: US-10-644-277-64
Perfect score: 1115
Sequence: 1 DQMTQSPSSLSASVGRVT.....EVTHQGLSPVTKFNRGRC 214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters: 51470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*
1: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US08 NEW PUB pep.*
5: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB pep.*
7: /cgn2_6/ptodata/1/pubpaa/US11 NEW PUB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US60 NEW PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1027	92.1	214	7	US-11-025-712-11 Sequence 11, Appl
2	1010	90.6	236	7	US-11-144-248-48 Sequence 48, Appl
3	1006	90.2	218	7	US-11-084-554-11 Sequence 11, Appl
4	1003	90.0	218	6	US-10-923-327-12 Sequence 12, Appl
5	1003	90.0	218	6	US-10-923-327-17 Sequence 17, Appl
6	1002	89.9	236	7	US-11-144-248-52 Sequence 52, Appl
7	1001	89.8	218	6	US-10-923-327-8 Sequence 8, Appl
8	1001	89.8	218	6	US-10-923-327-10 Sequence 10, Appl
9	1001	89.8	363	7	US-11-000-463-335 Sequence 335, App
10	998	89.5	218	6	US-10-923-327-6 Sequence 6, Appl
11	997	89.4	367	7	US-11-000-463-899 Sequence 899, App
12	993	89.1	236	7	US-11-144-248-47 Sequence 47, Appl
13	989	88.7	214	7	US-11-094-625-9 Sequence 9, Appl
14	987	88.5	236	7	US-11-144-248-51 Sequence 51, Appl
15	985.5	88.4	213	7	US-11-120-338-13 Sequence 13, Appl
16	984.5	88.3	213	7	US-11-120-338-16 Sequence 16, Appl
17	957	85.8	237	7	US-11-054-669-109 Sequence 109, App
18	949	85.1	214	7	US-11-173-564-1 Sequence 1, Appl
19	932.5	83.6	384	7	US-11-000-463-804 Sequence 804, App
20	932.5	83.6	384	7	US-11-000-463-805 Sequence 805, App
21	932.5	83.6	384	7	US-11-000-463-806 Sequence 806, App
22	932.5	83.6	384	7	US-11-000-463-807 Sequence 807, App
23	919.5	82.5	213	7	US-11-172-320-4 Sequence 4, Appl
24	919.5	82.5	213	7	US-11-173-969-4 Sequence 4, Appl
25	909.5	81.6	213	7	US-11-173-969-8 Sequence 8, Appl

26	909.5	81.6	213	7	US-11-173-969-8	Sequence 8, Appl
27	895.5	80.3	213	7	US-11-174-186-42	Sequence 42, Appl
28	858.5	77.0	239	7	US-11-139-499-6	Sequence 6, Appl
29	622.5	55.8	307	7	US-11-000-463-332	Sequence 332, App
30	622.5	55.8	312	7	US-11-000-463-334	Sequence 334, App
31	592	53.1	136	7	US-11-144-248-2	Sequence 2, Appl
32	572.5	51.3	411	7	US-11-075-351-47	Sequence 47, Appl
33	569.5	51.1	374	7	US-11-075-351-42	Sequence 42, Appl
34	558	50.0	366	7	US-11-075-351-38	Sequence 38, Appl
35	554	49.7	110	7	US-11-024-251-27	Sequence 27, Appl
36	553	49.6	107	6	US-10-999-866-40	Sequence 40, Appl
37	553	49.6	107	7	US-11-025-712-5	Sequence 5, Appl
38	553	49.6	107	7	US-11-075-351-61	Sequence 61, Appl
39	548	49.1	106	7	US-11-061-821-40	Sequence 40, Appl
40	548	49.1	106	7	US-11-144-248-26	Sequence 26, Appl
41	548	49.1	106	7	US-11-024-251-29	Sequence 29, Appl
42	548	49.1	106	7	US-11-165-141-17	Sequence 17, Appl
43	498	44.7	108	7	US-11-120-338-3	Sequence 3, Appl
44	498	44.7	110	6	US-10-648-816-1	Sequence 1, Appl
45	495	44.4	110	6	US-10-648-816-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-11-025-712-11
; Sequence 11, Application US/11025712
; Publication No. US20050255108A1
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; Thomas, G. Roger
; Gross, Cordell E.

TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/025,712
FILING DATE: 28-Dec-2004
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/404,286
FILING DATE: 31-Mar-2003
APPLICATION NUMBER: 09/811384
FILING DATE: 20-DEC-2000
APPLICATION NUMBER: 09/251652
FILING DATE: 17-FEB-2000
APPLICATION NUMBER: 08/788800
FILING DATE: 22-JAN-1997
APPLICATION NUMBER: 60/093038
FILING DATE: 23-JAN-1996

ATTORNEY/AGENT INFORMATION:
NAME: Evans, David W.
REGISTRATION NUMBER: NONE
REFERENCE/DOCKET NUMBER: P1729C2
TELEPHONE: 650/225-1739
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
TYPE: Amino Acid

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;
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-025-712-11

Query Match      92.1%; Score 1027; DB 7; Length 214;
Best Local Similarity 92.1%; Pred. No. 2.1e-48;
Matches 197; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 1 DIQMTQSPSSLSASVGRVTITTCRASQDINNVLNNWYQKPGKAPKLLIYTTSTLHSGVPS 60
QY 61 RSGSGSGDTFTTINSLOPEDIAITYCOEYNNLPYSFCQGTKEIKRTVAAPSVFIIPP 120
DB 61 RFGSGSGDTFTLTISLQPEFATYCCQGNLPTFTGGTKVEIKRTVAAPSVFIIPP 120
QY 121 SDEQLKSGTASVVCLLNNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLSLT 180
DB 121 SDEQLKSGTASVVCLLNNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLSLT 180
QY 181 LSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 214
DB 181 LSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 214
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RESULT 2
US-11-144-248-48
; Sequence 48, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-48
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Query Match      90.6%; Score 1010; DB 7; Length 236;
Best Local Similarity 90.7%; Pred. No. 1.7e-47;
Matches 194; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDISNYLNWYQKPGKAPKLLIYDASNLETGVPS 60
DB 23 DIQMTQSPSSLSASVGRVTITTCRASQGIKNDLWYQKPGKAPKRLIYAASSLQSGVPS 82
QY 61 RSGSGSGDTFTTINSLOPEDIAITYCOEYNNLPYSFCQGTKEIKRTVAAPSVFIIPP 120
DB 83 RFGSGSGDTFTLTISLQPEFATYCCLOHNSPYTFTGGTKVEIKRTVAAPSVFIIPP 142
QY 121 SDEQLKSGTASVVCLLNNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLSLT 180
DB 143 SDEQLKSGTASVVCLLNNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLSLT 202
QY 181 LSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 214
DB 203 LSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 236
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RESULT 3
US-11-084-554-11
; Sequence 11, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Strid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korvetz, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-11
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Query Match      90.2%; Score 1006; DB 7; Length 218;
Best Local Similarity 89.0%; Pred. No. 2.6e-47;
Matches 194; Conservative 11; Mismatches 9; Indels 4; Gaps 1;

QY 1 DIQMTQSPSSLSASVGRVTITTCQASQDI-----SNYLNWYQKPGKAPKLLIYDASNLET 56
DB 1 DIQMTQSPSSLSASVGRVTITTCRASQSDVDGSDSYNNWYQKPGKAPKLLIYAASYLES 60
QY 57 GVPFRFSGSGSGDTFTTINSLOPEDIAITYCYQEYNNLPYSFGQGTKEIKRTVAAPSVF 116
DB 61 GVPFRFSGSGSGDTFTLTISLQPEDEATYCCQSHEDPYTFTGGTKVEIKRTVAAPSVF 120
QY 117 IFPPSDEQLKSGTASVVCLLNNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 176
DB 121 IFPPSDEQLKSGTASVVCLLNNFPYPRKAVQWKVDNALQSGNSQESVTEQDSKDSYLS 180
QY 177 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 214
DB 181 STLTLSKADYKHKVYACEVTHQGLSPVTKSFNRGEC 218
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RESULT 4
US-10-923-327-12
; Sequence 12, Application US/10923327
; Publication No. US20050261208A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, CYNTHIA B.
; APPLICANT: BALL, HOWARD A.
; TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
; FILE REFERENCE: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
; TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
; TITLE OF INVENTION: PULMONARY DISEASE
; FILE REFERENCE: 30775-723.501
; CURRENT APPLICATION NUMBER: US/10/923,327
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: PCT/US04/25054
; PRIOR FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 10/698,073
; PRIOR FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/492,231
; PRIOR FILING DATE: 2003-07-31
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: construct
US-10-923-327-12

Query Match 90.0%; Score 1003; DB 6; Length 218;
Best Local Similarity 89.0%; Pred. No. 3.8e-47;
Matches 194; Conservative 11; Mismatches 9; Indels 4; Gaps 1;
QY 1 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNVYQKPGKAPKLLIYDASNLET 56
DB 1 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNVYQKPGKAPKLLIYDASNLET 60
QY 57 GVPSSRFGSGSGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 116
DB 61 GVPSSRFGSGSGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 120
QY 117 IFPPSDEQLKSGTASVVCLLNPNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 176
DB 121 IFPPSDEQLKSGTASVVCLLNPNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 180
QY 177 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 5

US-10-923-327-17
Sequence 17, Application US/10923327
Publication No. US20050261208A1
GENERAL INFORMATION:
APPLICANT: ROBINSON, CYNTHIA B.
APPLICANT: BALL, HOWARD A.
TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
TITLE OF INVENTION: PULMONARY DISEASE
FILE REFERENCE: 30775-723.501
CURRENT APPLICATION NUMBER: US/10/923,327
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: PCT/US04/25054
PRIOR FILING DATE: 2004-07-30
PRIOR APPLICATION NUMBER: 10/698,073
PRIOR FILING DATE: 2003-10-29
PRIOR APPLICATION NUMBER: 60/492,231
PRIOR FILING DATE: 2003-07-31
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patent In Ver. 3.3
SEQ ID NO 17
LENGTH: 218
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: construct
US-10-923-327-17

Query Match 90.0%; Score 1003; DB 6; Length 218;
Best Local Similarity 89.0%; Pred. No. 3.8e-47;
Matches 194; Conservative 11; Mismatches 9; Indels 4; Gaps 1;
QY 1 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNVYQKPGKAPKLLIYDASNLET 56
DB 1 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNVYQKPGKAPKLLIYDASNLET 60
QY 57 GVPSSRFGSGSGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 116
DB 61 GVPSSRFGSGSGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 120
QY 117 IFPPSDEQLKSGTASVVCLLNPNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 176
DB 121 IFPPSDEQLKSGTASVVCLLNPNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 180
QY 177 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

Db 181 STLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 218

RESULT 6

US-11-144-248-52
Sequence 52, Application US/11144248
Publication No. US2005024408A1
GENERAL INFORMATION:
APPLICANT: Cohen, Bruce D.
APPLICANT: Beebe, Jean
APPLICANT: Miller, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Corvalan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/11/144,248
CURRENT FILING DATE: 2005-06-02
PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 52
LENGTH: 236
TYPE: PRT
ORGANISM: Homo sapiens
US-11-144-248-52

Query Match 89.9%; Score 1002; DB 7; Length 236;
Best Local Similarity 89.7%; Pred. No. 4.5e-47;
Matches 192; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNVYQKPGKAPKLLIYDASNLETGVP 60
DB 23 DIQMTQSPSSLSASVGRVTITTCASQDI-----SNLYNNVYQKPGKAPKLLIYDASNLETGVP 82
QY 61 RFGSGSGSGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 120
DB 83 RFGSGSGSGDTFTTINSLOPEDATYVCOYNNLPYSFGQGTKEIKRTVAAPSVP 142
QY 121 SDEQLKSGTASVVCLLNPNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 180
DB 143 SDEQLKSGTASVVCLLNPNFYPREAKVQWVDNALQSGNSQESVTEQDSKDYSL 202
QY 181 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214
DB 203 LSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 7

US-10-923-327-8
Sequence 8, Application US/10923327
Publication No. US20050261208A1
GENERAL INFORMATION:
APPLICANT: ROBINSON, CYNTHIA B.
APPLICANT: BALL, HOWARD A.
TITLE OF INVENTION: COMBINATION OF DEHYDROEPIANDROSTERONE OR
TITLE OF INVENTION: DEHYDROEPIANDROSTERONE-SULFATE WITH AN ANTI-IGE
TITLE OF INVENTION: ANTIBODY FOR TREATMENT OF ASTHMA OR CHRONIC OBSTRUCTIVE
TITLE OF INVENTION: PULMONARY DISEASE
FILE REFERENCE: 30775-723.501
CURRENT APPLICATION NUMBER: US/10/923,327
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: PCT/US04/25054
PRIOR FILING DATE: 2004-07-30
PRIOR APPLICATION NUMBER: 10/698,073
PRIOR FILING DATE: 2003-10-29
PRIOR APPLICATION NUMBER: 60/492,231
PRIOR FILING DATE: 2003-07-31
NUMBER OF SEQ ID NOS: 19

QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQGINRDLMGYQKPGKAPKRLIYAASRLHRGVPS 82
QY 61 RFGSGSGTDFTTINSLOPEDIAITYYCOEYNNLPYSFGQGTGKLEIKRTVAAPSFIIPP 120
Db 83 RFGSGSGTDFTTINSLOPEDIAITYYCLQHSYPCSFQGTGKLEIKRTVAAPSFIIPP 142
QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
Db 143 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 202
QY 181 LSKADYERKHVYACEVTHQGLSSPVTGSFNRGEC 214
Db 203 LSKADYERKHVYACEVTHQGLSSPVTGSFNRGEC 236

RESULT 13
US-11-094-625-9
; Sequence 9, Application US/11094625
; Publication No. US20050260711A1
; GENERAL INFORMATION:
; APPLICANT: Datta, Deepshikha
; APPLICANT: Goddard, William A.
; APPLICANT: Tirrell, David
; APPLICANT: Peng, Joyce Yaochun
; TITLE OF INVENTION: MODULATING PH-SENSITIVE BINDING USING
; FILE OF INVENTION: NON-NATURAL AMINO ACIDS
; CURRENT APPLICATION NUMBER: CTCH-P01-031
; CURRENT FILING DATE: 2005-03-30
; PRIOR APPLICATION NUMBER: US/11/094,625
; PRIOR FILING DATE: 2005-03-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-094-625-9

Query Match 88.7%; Score 989; DB 7; Length 214;
Best Local Similarity 89.3%; Pred. No. 2e-46;
Matches 191; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASQDWTAVAWYQKPGKAPKLLIYASFLYSGVPS 60
QY 61 RFGSGSGTDFTTINSLOPEDIAITYYCOEYNNLPYSFGQGTGKLEIKRTVAAPSFIIPP 120
Db 61 RFGSGSGTDFTTINSLOPEDIAITYYCOQHYTPTTFGQGTGKLEIKRTVAAPSFIIPP 120
QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
Db 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
QY 181 LSKADYERKHVYACEVTHQGLSSPVTGSFNRGEC 214
Db 181 LSKADYERKHVYACEVTHQGLSSPVTGSFNRGEC 214

RESULT 14
US-11-144-248-51
; Sequence 51, Application US/11144248
; Publication No. US2005024408A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael

; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ASX-PP2
; CURRENT APPLICATION NUMBER: US/11/144,248
; CURRENT FILING DATE: 2005-06-02
; PRIOR APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 51
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-144-248-51

Query Match 88.5%; Score 987; DB 7; Length 236;
Best Local Similarity 88.8%; Pred. No. 2.8e-46;
Matches 190; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 23 DIQMTQSPSSLSASVGDRTVITTCRASQDIRDLQWYQKPGKAPKRLIYAASRLQSGVPS 82
QY 61 RFGSGSGTDFTTINSLOPEDIAITYYCOEYNNLPYSFGQGTGKLEIKRTVAAPSFIIPP 120
Db 83 RFGSGSGTDFTTINSLOPEDIAITYYCLQHNPTPTFGQGTGKLEIKRTVAAPSFIIPP 142
QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180
Db 143 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 202
QY 181 LSKADYERKHVYACEVTHQGLSSPVTGSFNRGEC 214
Db 203 LSKADYERKHVYACEVTHQGLSSPVTGSFNRGEC 236

RESULT 15
US-11-120-338-13
; Sequence 13, Application US/11120338
; Publication No. US20050271658A1
; GENERAL INFORMATION:
; APPLICANT: BRUNETTA, PAUL G.
; APPLICANT: GREWAL, PATRICIA A.
; APPLICANT: WALICKE, PATRICIA A.
; TITLE OF INVENTION: PREVENTING AUTOIMMUNE DISEASE
; FILE REFERENCE: P2079R2
; CURRENT APPLICATION NUMBER: US/11/120,338
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: US 60/568,460
; PRIOR FILING DATE: 2004-05-05
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 13
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-120-338-13

Query Match 88.4%; Score 985.5; DB 7; Length 213;
Best Local Similarity 89.3%; Pred. No. 3.1e-46;
Matches 191; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
QY 1 DIQMTQSPSSLSASVGDRTVITTCRASQDISNYLNWYQKPGKAPKLLIYDASNLETGVP 60
Db 1 DIQMTQSPSSLSASVGDRTVITTCRASSVS-YMHWYQKPGKAPKPLIYAPSNLASGVP 59
QY 61 RFGSGSGTDFTTINSLOPEDIAITYYCOEYNNLPYSFGQGTGKLEIKRTVAAPSFIIPP 120
Db 60 RFGSGSGTDFTTINSLOPEDIAITYYCOQWSPPTFGQGTGKLEIKRTVAAPSFIIPP 119
QY 121 SDEQLKSGTASVVCLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDYSLSLT 180

Db 120 SDEQLSGTASVVCLLNFFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYLSSTLT 179
Qy 181 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 214
Db 180 LSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 213

Search completed: December 17, 2005, 01:29:50
Job time : 5.53939 secs

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GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: February 6, 2006, 14:23:38 ; Search time 251 Seconds
 (without alignments)
 44.974 Million cell updates/sec

Title: US-10-644-277-149_COPY_20_35

Perfect score: 73

Sequence: 1 ISVQRLASYRRITSSK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : UniProt_05.80.*

1: uniprot_eprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	99	1	CCL2_HUMAN
2	73	100.0	99	1	CCL2_MACFA
3	73	100.0	99	1	CCL2_MACMU
4	73	100.0	99	1	CCL2_PONPY
5	73	100.0	99	2	Q6XVW5_MACNE
6	73	100.0	99	2	Q7IME7_MACMU
7	68	83.2	101	1	CCL2_CANFA
8	64	87.7	74	1	MCBP_BOVIN
9	64	87.7	97	2	Q9TTS6_BOVIN
10	64	87.7	99	1	CCL2_PIG
11	61	83.6	99	1	MCFA_BOVIN
12	60	82.2	100	1	CCL1_HORSE
13	59	80.8	99	1	CCL2_HORSE
14	57	78.1	97	2	Q9Z318_CAVPO
15	56	76.7	97	1	CCL11_HUMAN
16	56	76.7	97	2	Q619T4_HUMAN
17	56	76.7	125	1	CCL2_RABIT
18	54	74.0	99	2	OS16F8_CANFA
19	52	71.2	96	1	CCL11_CAVPO
20	52	71.2	104	1	CCL12_MOUSE
21	52	71.2	104	2	Q5SVB4_MOUSE
22	52	71.2	109	2	Q8G5F3_MACNE
23	51	69.9	81	2	Q9TTO2_HORSE
24	50	68.5	97	1	CCL11_MACMU
25	50	68.5	97	2	Q8HXZ5_MACMU
26	50	68.5	106	2	Q9Z292_9RODE
27	50	68.5	150	2	Q8CGM5_SIGHI
28	49	67.1	65	2	Q7TMS1_MOUSE
29	49	67.1	99	2	Q5KSU7_CANFA
30	49	67.1	148	1	CCL2_MOUSE
31	49	67.1	148	2	Q5SVU3_MOUSE

32	48	65.8	99	2	Q8MKC8_HORSE
33	47	64.4	99	1	CCL7_HUMAN
34	47	64.4	99	2	Q569J6_HUMAN
35	47	64.4	109	2	Q7Z7Q8_HUMAN
36	46	63.0	44	2	Q9BG83_PONPY
37	46	63.0	99	2	Q865F4_MACNE
38	46	63.0	99	2	Q8HYQ0_MACMU
39	46	63.0	148	1	CCL2_RAT
40	46	63.0	148	2	Q549R5_RAT
41	45	61.6	97	1	CCL7_MOUSE
42	45	61.6	97	2	Q5SVU0_MOUSE
43	45	61.6	97	2	Q4PIY1_92ZZZ
44	44	60.3	99	1	CCL8_CANFA
45	44	60.3	99	1	CCL8_HUMAN
46	44	60.3	253	2	Q621J4_CABER
47	44	60.3	271	2	Q5XPM8_ERWAM
48	43	58.9	421	2	Q8D3D7_WIGBR
49	43	58.9	447	2	Q4Q1I5_LEIMA
50	42	57.5	60	1	YRHL_AZOVI
51	42	57.5	97	1	CCL7_RAT
52	42	57.5	298	2	Q9D3J9_MOUSE
53	42	57.5	301	2	Q9HAI6_HUMAN
54	42	57.5	305	2	Q5CQI7_CRYPV
55	42	57.5	306	2	Q5CL59_CRYHO
56	42	57.5	377	1	FLAE_VIBAN
57	42	57.5	399	2	Q8P9C4_XANCP
58	42	57.5	401	2	Q4UHH3_XANCP
59	42	57.5	436	2	Q41WF4_AZOVI
60	42	57.5	526	2	Q707N2_HUMAN
61	42	57.5	625	2	Q7Z441_HUMAN
62	42	57.5	1477	2	Q6A8J4_PROAC
63	41	56.2	75	2	Q5WEZ4_BACSK
64	41	56.2	120	1	CCL2_CAVPO
65	41	56.2	339	1	ENG_C_PSEAE
66	41	56.2	422	2	Q5GZN6_XANOR
67	41	56.2	550	2	Q9S4M6_ECOLI
68	41	56.2	588	2	Q6L984_HUMAN
69	41	56.2	859	2	Q6L985_HUMAN
70	41	56.2	919	1	SNCAP_HUMAN
71	41	56.2	919	2	Q6L986_HUMAN
72	41	56.2	919	2	Q9HC59_HUMAN
73	41	56.2	973	2	Q57XV4_9TRYP
74	41	56.2	1199	1	MEF_SXNV3
75	40	54.8	191	2	Q8JFJ3_9HEPC
76	40	54.8	327	2	Q8KMM6_LEGPN
77	40	54.8	337	2	Q6SGS9_9BACT
78	40	54.8	361	2	Q8KMN0_LEGPN
79	40	54.8	399	2	Q8PL31_XANAC
80	40	54.8	440	2	Q5JCA4_9LILI
81	40	54.8	451	2	Q5JCA3_9LILI
82	40	54.8	475	2	Q48824_LEGPN
83	40	54.8	475	2	Q7ATT9_LEGPN
84	40	54.8	475	2	Q8KID5_LEGLO
85	40	54.8	475	2	Q8KMM8_LEGPN
86	40	54.8	475	2	Q5WX06_LEGPL
87	40	54.8	475	2	Q5X5M6_LEGPA
88	40	54.8	475	2	Q5ZVVO_LEGPH
89	40	54.8	476	2	Q8KMM7_LEGPN
90	40	54.8	489	2	Q8KMR7_LEGBO
91	40	54.8	491	2	Q8KMM9_LEGPN
92	40	54.8	492	2	Q9FAE7_9BURK
93	40	54.8	492	2	Q9FAE8_9BURK
94	40	54.8	493	2	Q8KMN1_LEGPN
95	40	54.8	1132	2	Q5BFT4_EMENI
96	40	54.8	1148	2	Q86A16_DICTDI
97	39.5	54.1	98	1	CCL13_CANFA
98	39	53.4	62	2	Q95690_HUMAN
99	39	53.4	118	2	Q5LOV3_GEOKA
100	39	53.4	125	2	Q6MPQ1_BDEBA
101	39	53.4	132	2	Q5L3T7_GEOKA
102	39	53.4	150	2	Q5ZNT9_9VIRU
103	39	53.4	181	2	Q4UK19_RICPE
104	39	53.4	329	2	Q7VHR6_HELHP

Q8mkc8	equus cabal
P80098	homo sapien
Q569j6	homo sapien
Q7z7q8	homo sapien
Q9bg83	pongo pygma
Q865f4	macaca neme
Q8hyq0	macaca mula
P14844	rattus norv
Q549r5	rattus norv
Q03366	mus musculus
Q5svu0	mus musculus
Q4piy1	unidentifie
Q68av9	canis famil
P80075	homo sapien
Q621j4	caenorhabdi
Q5xpm8	erwinia amy
Q8d3d7	wiggleswort
Q4q1i5	leishmania
Q44557	azotobacter
Q9qxy8	rattus norv
Q9d3j9	mus musculus
Q9hai6	homo sapien
Q5cqi7	cryptospori
Q5cl59	cryptospori
Q56570	vibrio angu
Q8p9c4	xanthomonas
Q4uuH3	xanthomonas
Q41wf4	azotobacter
Q707n2	homo sapien
Q7z441	homo sapien
Q6a8j4	propionibac
Q5wez4	bacillus cl
Q08782	cavia porce
Q9nul3	pseudomonas
Q5gzn6	xanthomonas
Q9s4m6	escherichia
Q61984	homo sapien
Q61985	homo sapien
Q9yeh5	homo sapien
Q61986	homo sapien
Q9hc59	homo sapien
Q57xv4	trypanosoma
Q5750	synecocyst
Q8jPJ3	hepatitis c
Q8kmm6	legionella
Q6sgs9	uncultured
Q8knn0	legionella
Q8pl31	xanthomonas
Q5jca4	monotagma p
Q5jca3	monotagma s
Q48824	legionella
Q7att9	legionella
Q8kid5	legionella
Q8kmm8	legionella
Q5wx06	legionella
Q5x5m6	legionella
Q5zvvo	legionella
Q8kmm7	legionella
Q8kmm9	legionella
Q9fae7	acidovorax
Q9fae8	acidovorax
Q8knn1	legionella
Q5bft4	aspergillus
Q86a16	dictyosteli
Q89y88	canis famil
Q95690	homo sapien
Q510y3	geobacillus
Q6mpq1	bdellovibri
Q5l3t7	geobacillus
Q5znt9	cotesia con
Q4uk19	rickettsia
Q7vhr6	helicobacte

105	39	53.4	365	1	ENGC_METMA	Q8ptz6 methanosarc	178	37	50.7	379	2	Q58FG3_VIBHA	Q58fg3 vibrio harv
106	39	53.4	377	1	FLAF_VIBPA	Q87081 vibrio para	179	37	50.7	399	2	Q842C5_ECOLI	Q842c5 escherichia
107	39	53.4	377	2	Q5E3R6_VIBF1	Q5e3n6 vibrio fisc	180	37	50.7	408	2	Q51PJ3_MAGGR	Q51pj3 magnaporthe
108	39	53.4	377	2	Q8R4Q1_VIBF1	Q8r4q1 vibrio fisc	181	37	50.7	408	2	Q70LL6_ECOLI	Q70ll6 escherichia
109	39	53.4	377	2	Q8DB99_VIBVU	Q8db99 vibrio vuln	182	37	50.7	420	2	Q6VMU1_ECOLI	Q6vmu1 escherichia
110	39	53.4	377	2	Q7MIM3_VIBVU	Q7mim3 vibrio vuln	183	37	50.7	420	2	Q9L9M3_ECOLI	Q9l9m3 escherichia
111	39	53.4	398	1	YFHE_SCHPO	Q42851 schizosacch	184	37	50.7	420	2	Q842D5_ECOLI	Q842d5 escherichia
112	39	53.4	558	2	Q6AHD0_LEIXX	Q6ahd0 leifsonia x	185	37	50.7	426	2	Q6VMV1_ECOLI	Q6vmv1 escherichia
113	39	53.4	765	2	Q4TLJ5_TETNG	Q4tlj5 tetradon n	186	37	50.7	426	2	Q6VMV4_ECOLI	Q6vmv4 escherichia
114	39	53.4	893	2	Q9X1G2_THEMA	Q9x1g2 thermotoga	187	37	50.7	426	2	Q9L9M1_ECOLI	Q9l9m1 escherichia
115	39	53.4	1020	2	Q55L67_CRYNE	Q55l67 cryptococcus	188	37	50.7	426	2	Q842B2_ECOLI	Q842b2 escherichia
116	39	53.4	1020	2	Q5KAB4_CRYNE	Q5kab4 cryptococcus	189	37	50.7	428	2	Q93ES3_ECOLI	Q93es3 escherichia
117	39	53.4	1652	2	Q5NAA4_ORYSA	Q5naa4 oryza sativ	190	37	50.7	428	2	Q842B8_ECOLI	Q842b8 escherichia
118	38	52.1	99	1	CCL8_PIG	P49873 sus scrofa	191	37	50.7	432	2	Q842B4_ECOLI	Q842b4 escherichia
119	38	52.1	125	2	Q5ANF7_CANAL	Q5anf7 candida alb	192	37	50.7	436	2	Q6VMV2_ECOLI	Q6vmv2 escherichia
120	38	52.1	178	2	Q89ZJ1_BACTN	Q89zj1 bacteroides	193	37	50.7	436	2	Q9S0T9_ECOLI	Q9s0t9 escherichia
121	38	52.1	216	2	Q5AS19_EMENI	Q5asl9 aspergillus	194	37	50.7	440	2	Q842A7_ECOLI	Q842a7 escherichia
122	38	52.1	241	2	Q6BQC9_DEBHA	Q6bcq9 debaryomyce	195	37	50.7	442	2	Q6VMT9_ECOLI	Q6vmt9 escherichia
123	38	52.1	242	2	Q9PF23_XYLFA	Q9pf23 xyella fas	196	37	50.7	442	2	Q9FZP0_ARATH	Q9fzp0 arabidopsis
124	38	52.1	244	2	Q87AK3_XYLFT	Q87ak3 xyella fas	197	37	50.7	443	2	Q842C0_ECOLI	Q842c0 escherichia
125	38	52.1	282	2	Q7NRA4_CHRVO	Q7nra4 chromobacte	198	37	50.7	447	2	Q6VMU8_ECOLI	Q6vmu8 escherichia
126	38	52.1	304	2	Q8EHX7_SHEON	Q8ehx7 shewanella	199	37	50.7	447	2	Q6VMU5_ECOLI	Q6vmu5 escherichia
127	38	52.1	306	2	Q5P1X4_AZOSE	Q5plx4 azoarcus sp	200	37	50.7	447	2	Q842A8_ECOLI	Q842a8 escherichia
128	38	52.1	311	2	Q62942_RAT	Q62942 rattus norv	201	37	50.7	447	2	Q842B5_ECOLI	Q842b5 escherichia
129	38	52.1	402	2	Q4KCK5_PSEF5	Q4kck5 pseudomonas	202	37	50.7	460	2	Q72KY4_THET2	Q72ky4 thermus the
130	38	52.1	422	2	Q7QJG3_ANOGA	Q7qjg3 anopheles g	203	37	50.7	461	2	Q842C6_ECOLI	Q842c6 escherichia
131	38	52.1	430	2	Q5L5U8_CHLAB	Q5l5u8 chlamydia	204	37	50.7	474	1	FLA_LEGMI	P53606 legionella
132	38	52.1	479	2	Q52080_PSEPU	Q52080 pseudomonas	205	37	50.7	475	2	Q7TQ3_BRARE	Q7t3q3 brachydanio
133	38	52.1	486	2	Q68384_PSEPU	Q68384 pseudomonas	206	37	50.7	497	1	FLIC_ECOLI	P04949 escherichia
134	38	52.1	505	2	Q8XPW2_RALSO	Q8xpw2 ralstonia s	207	37	50.7	501	2	Q9L9M0_ECOLI	Q9l9m0 escherichia
135	38	52.1	535	2	Q5L4M6_ORYSA	Q5l4m6 oryza sativ	208	37	50.7	508	2	Q9S4M1_ECOLI	Q9s4m1 escherichia
136	38	52.1	628	2	Q51E04_ENTHI	Q5led4 entamoeba h	209	37	50.7	517	2	Q9S4M0_ECOLI	Q9s4m0 escherichia
137	38	52.1	732	2	Q50UJ5_ENTHI	Q50uuj5 entamoeba h	210	37	50.7	521	2	Q9XCS3_ECOLI	Q9xcs3 escherichia
138	38	52.1	754	2	Q7F9F8_ORYSA	Q7f9f8 oryza sativ	211	37	50.7	521	2	Q9XCS4_ECOLI	Q9xcs4 escherichia
139	38	52.1	818	2	Q86XFP_HUMAN	Q86xpf0 homo sapien	212	37	50.7	523	2	Q93ES2_ECOLI	Q93es2 escherichia
140	38	52.1	857	2	Q6AJ08_DESPS	Q6ajg8 desulfotale	213	37	50.7	545	2	Q842B7_ECOLI	Q842b7 escherichia
141	38	52.1	888	1	GOGA2_MOUSE	Q92lm4 mus musculu	214	37	50.7	545	2	Q70LL8_ECOLI	Q70ll8 escherichia
142	38	52.1	890	2	Q7UWJ7_RHOBA	Q7uwj7 rhodopirell	215	37	50.7	548	2	Q842D7_ECOLI	Q842d7 escherichia
143	38	52.1	1022	2	Q5DTH1_MOUSE	Q5dth1 mus musculu	216	37	50.7	549	2	Q53969_SHIDY	Q53969 shigella dy
144	38	52.1	1187	2	Q7XN13_ORYSA	Q7xnl3 oryza sativ	217	37	50.7	550	1	FLIC_SHIFL	Q98860 shigella fl
145	38	52.1	1574	2	Q8GU62_ORYSA	Q8gu62 oryza sativ	218	37	50.7	550	2	Q9L9M2_ECOLI	Q9l9m2 escherichia
146	38	52.1	3320	2	Q8CFU1_YARLI	Q8cfll1 yarrowia li	219	37	50.7	550	2	Q842D3_ECOLI	Q842d3 escherichia
147	37.5	51.4	146	1	LCRR_YERPE	P69959 yersinia pe	220	37	50.7	554	2	Q9KJA0_ECOLI	Q9kja0 escherichia
148	37.5	51.4	146	1	LCRR_YERPE	P69959 yersinia pe	221	37	50.7	554	2	Q842D0_ECOLI	Q842d0 escherichia
149	37.5	51.4	146	1	LCRR_YERPS	P99960 yersinia ps	222	37	50.7	555	2	Q842B9_ECOLI	Q842b9 escherichia
150	37	50.7	73	2	Q5G9J9_TUPGB	Q5g9j9 tupatia glis	223	37	50.7	555	2	Q842B9_ECOLI	Q842b9 escherichia
151	37	50.7	99	1	CCL8_BOVIN	Q9141 bos taurus	224	37	50.7	556	2	Q9S4M3_ECOLI	Q9s4m3 escherichia
152	37	50.7	147	2	Q8BN49_MOUSE	Q8bn49 mus musculu	225	37	50.7	556	2	Q6VMU0_ECOLI	Q6vmu0 escherichia
153	37	50.7	169	2	Q70518_MOUSE	Q70616 mus musculu	226	37	50.7	557	2	Q842C4_ECOLI	Q842c4 escherichia
154	37	50.7	171	2	Q70616_MOUSE	Q70616 mus musculu	227	37	50.7	557	2	Q842C4_ECOLI	Q842c4 escherichia
155	37	50.7	171	2	Q70619_MOUSE	Q70619 mus musculu	228	37	50.7	559	2	Q9S4M2_ECOLI	Q9s4m2 escherichia
156	37	50.7	178	2	Q52AY2_MAGGR	Q52ay2 magnaporthe	229	37	50.7	560	2	Q9S4M5_ECOLI	Q9s4m5 escherichia
157	37	50.7	194	2	Q62061_CABEL	Q62061 caenorhabdi	230	37	50.7	561	2	Q842B6_ECOLI	Q842b6 escherichia
158	37	50.7	197	2	Q82Z13_ENTFA	Q82z13 enterococcu	231	37	50.7	562	2	Q842D2_ECOLI	Q842d2 escherichia
159	37	50.7	214	2	Q7YYU0_CRYPV	Q7yyu0 cryptospori	232	37	50.7	564	2	Q93ES1_ECOLI	Q93es1 escherichia
160	37	50.7	214	2	Q5CWM1_CRYPV	Q5cwm1 cryptospori	233	37	50.7	564	2	Q842A9_ECOLI	Q842a9 escherichia
161	37	50.7	214	2	Q5CFP9_CRYHO	Q5cf90 cryptospori	234	37	50.7	564	2	Q9S0T3_ECOLI	Q9s0t3 escherichia
162	37	50.7	216	2	Q4J416_AZOVI	Q4j416 azotobacter	235	37	50.7	565	2	Q9S4M4_ECOLI	Q9s4m4 escherichia
163	37	50.7	274	2	Q66XA2_9BACT	Q66xa2 endosymbion	236	37	50.7	565	2	Q47226_ECOLI	Q47226 shigella bo
164	37	50.7	274	2	Q66XC2_9BACT	Q66xc2 endosymbion	237	37	50.7	568	2	Q53789_SHIBO	Q53789 shigella bo
165	37	50.7	281	2	Q32FD6_9GAMM	Q32fd6 endosymbion	238	37	50.7	568	2	Q9S0T5_ECOLI	Q9s0t5 escherichia
166	37	50.7	295	2	Q4KEW7_PSEF5	Q4kem7 pseudomonas	239	37	50.7	568	2	Q842B1_ECOLI	Q842b1 escherichia
167	37	50.7	305	2	Q8ATN3_RAT	Q8ayn3 rattus norv	240	37	50.7	568	2	Q9AL29_ECOLI	Q9al29 escherichia
168	37	50.7	348	2	Q5Z3D3_NOCFA	Q5z3d3 nocardia fa	241	37	50.7	570	2	Q9S0T4_ECOLI	Q9s0t4 escherichia
169	37	50.7	349	2	Q5QS22_ECOLI	Q5qs22 escherichia	242	37	50.7	570	2	Q842C1_ECOLI	Q842c1 escherichia
170	37	50.7	349	2	Q5QS23_ECOLI	Q5qs23 escherichia	243	37	50.7	572	2	Q842B0_ECOLI	Q842b0 escherichia
171	37	50.7	349	2	Q70UUV_ECOLI	Q70uu9 escherichia	244	37	50.7	573	2	Q4RQ66_TETNG	Q4rq66 tetraodon n
172	37	50.7	349	2	Q83XMS_ECOLI	Q83xms escherichia	245	37	50.7	576	2	Q842C8_ECOLI	Q842c8 escherichia
173	37	50.7	349	2	Q9S0U0_ECOLI	Q9s0u0 escherichia	246	37	50.7	579	1	YGT6_YEAST	P53099 saccharomyc
174	37	50.7	360	2	Q6BV22_DEBHA	Q6bv22 debaryomyce	247	37	50.7	579	2	Q874L4_SACPS	Q874l4 saccharomyc
175	37	50.7	374	2	Q9ZSH6_ARATH	Q9zsh6 arabidopsis	248	37	50.7	579	2	Q842C2_ECOLI	Q842c2 escherichia
176	37	50.7	378	1	FLAA_VIBCH	Q9kq60 vibrio chol	249	37	50.7	584	2	Q06352_ECOLI	Q06352 escherichia
177	37	50.7	379	1	FLAA_VIBCH	Q030858 vibrio chol	250	37	50.7				

251	37	50.7	585	2	P71246	escherichia	324	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
252	37	50.7	585	2	Q9K2X8	escherichia	325	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
253	37	50.7	585	2	Q9L736	escherichia	326	36	49.3	191	2	Q8BBL9	9HEPC	Q8BBL9	hepatitis c
254	37	50.7	585	2	Q9S0T8	escherichia	327	36	49.3	191	2	Q8BBL1	9HEPC	Q8BBL1	hepatitis c
255	37	50.7	585	2	Q7AD06	ECO57	328	36	49.3	191	2	Q8BBL2	9HEPC	Q8BBL2	hepatitis c
256	37	50.7	585	2	Q9K2Y6	ECOLI	329	36	49.3	191	2	Q8BBL3	9HEPC	Q8BBL3	hepatitis c
257	37	50.7	585	2	Q7DB10	ECO57	330	36	49.3	191	2	Q8BBL4	9HEPC	Q8BBL4	hepatitis c
258	37	50.7	588	2	Q9S0T6	escherichia	331	36	49.3	191	2	Q8BBL5	9HEPC	Q8BBL5	hepatitis c
259	37	50.7	585	2	Q6K351	escherichia	332	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
260	37	50.7	585	2	Q6K353	escherichia	333	36	49.3	191	2	Q8BBL7	9HEPC	Q8BBL7	hepatitis c
261	37	50.7	585	2	Q6VMU7	ECOLI	334	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
262	37	50.7	585	2	Q6VMU0	escherichia	335	36	49.3	191	2	Q8BBL9	9HEPC	Q8BBL9	hepatitis c
263	37	50.7	585	2	Q9S0T7	ECOLI	336	36	49.3	191	2	Q8BBL1	9HEPC	Q8BBL1	hepatitis c
264	37	50.7	585	2	Q9S0U1	escherichia	337	36	49.3	191	2	Q8BBL2	9HEPC	Q8BBL2	hepatitis c
265	37	50.7	585	2	Q8FGM2	ECOL6	338	36	49.3	191	2	Q8BBL3	9HEPC	Q8BBL3	hepatitis c
266	37	50.7	605	2	Q9S0T2	ECOLI	339	36	49.3	191	2	Q8BBL4	9HEPC	Q8BBL4	hepatitis c
267	37	50.7	610	2	Q9T6U4	USEUD	340	36	49.3	191	2	Q8BBL5	9HEPC	Q8BBL5	hepatitis c
268	37	50.7	610	2	Q6VMU3	ECOLI	341	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
269	37	50.7	613	2	Q842C9	escherichia	342	36	49.3	191	2	Q8BBL7	9HEPC	Q8BBL7	hepatitis c
270	37	50.7	670	2	Q85825	escherichia	343	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
271	37	50.7	681	2	Q7ZTU7	BRARE	344	36	49.3	191	2	Q8BBL9	9HEPC	Q8BBL9	hepatitis c
272	37	50.7	725	2	Q5SM00	CRYNE	345	36	49.3	191	2	Q8BBL1	9HEPC	Q8BBL1	hepatitis c
273	37	50.7	725	2	Q5K8R8	CRYNE	346	36	49.3	191	2	Q8BBL2	9HEPC	Q8BBL2	hepatitis c
274	37	50.7	730	2	Q4UQL0	XANCP	347	36	49.3	191	2	Q8BBL3	9HEPC	Q8BBL3	hepatitis c
275	37	50.7	730	2	Q8PCU0	XANCP	348	36	49.3	191	2	Q8BBL4	9HEPC	Q8BBL4	hepatitis c
276	37	50.7	730	2	Q840Y3	ARATH	349	36	49.3	191	2	Q8BBL5	9HEPC	Q8BBL5	hepatitis c
277	37	50.7	786	2	Q67Y76	ARATH	350	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
278	37	50.7	788	2	Q57XU7	TRYYP	351	36	49.3	191	2	Q8BBL7	9HEPC	Q8BBL7	hepatitis c
279	37	50.7	809	2	Q7QRF3	GIALA	352	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
280	37	50.7	809	2	Q9X8B0	STRCO	353	36	49.3	191	2	Q8BBL9	9HEPC	Q8BBL9	hepatitis c
281	37	50.7	880	2	Q51VF6	MAGGR	354	36	49.3	191	2	Q8BBL1	9HEPC	Q8BBL1	hepatitis c
282	37	50.7	897	2	Q4HZ42	GIBZE	355	36	49.3	191	2	Q8BBL2	9HEPC	Q8BBL2	hepatitis c
283	37	50.7	1119	2	Q9LK04	ARATH	356	36	49.3	191	2	Q8BBL3	9HEPC	Q8BBL3	hepatitis c
284	37	50.7	1175	2	Q9ZPF3	ARATH	357	36	49.3	191	2	Q8BBL4	9HEPC	Q8BBL4	hepatitis c
285	37	50.7	1198	2	Q9C6N9	ARATH	358	36	49.3	191	2	Q8BBL5	9HEPC	Q8BBL5	hepatitis c
286	37	50.7	1265	2	Q5AAU3	CANAL	359	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
287	37	50.7	1285	2	Q9ZR01	ARATH	360	36	49.3	191	2	Q8BBL7	9HEPC	Q8BBL7	hepatitis c
288	37	50.7	1305	2	Q9ZU21	ARATH	361	36	49.3	191	2	Q8BBL8	9HEPC	Q8BBL8	hepatitis c
289	37	50.7	1312	2	Q9M0W7	ARATH	362	36	49.3	191	2	Q8BBL9	9HEPC	Q8BBL9	hepatitis c
290	37	50.7	1314	2	Q9M194	ARATH	363	36	49.3	191	2	Q8BBL1	9HEPC	Q8BBL1	hepatitis c
291	37	50.7	1444	2	Q9LTC8	ARATH	364	36	49.3	191	2	Q8BBL2	9HEPC	Q8BBL2	hepatitis c
292	37	50.7	1444	2	Q9SFY0	ARATH	365	36	49.3	191	2	Q8BBL3	9HEPC	Q8BBL3	hepatitis c
293	37	50.7	1472	2	Q9SL11	ARATH	366	36	49.3	191	2	Q8BBL4	9HEPC	Q8BBL4	hepatitis c
294	37	50.7	1473	2	Q9SBT9	NEUCR	367	36	49.3	191	2	Q8BBL5	9HEPC	Q8BBL5	hepatitis c
295	37	50.7	1756	2	Q80975	ARATH	368	36	49.3	191	2	Q8BBL6	9HEPC	Q8BBL6	hepatitis c
296	37	50.7	1821	2	Q64E21	TENMO	369	36	49.3	217	1	ATL2K	ARATH	Q8BBL7	hepatitis c
297	36.5	50.0	261	2	Q9KWS4	PSESP	370	36	49.3	223	1	QOS11	ARATH	Q8BBL8	hepatitis c
298	36	49.3	65	2	Q9ZTN3	PETHY	371	36	49.3	228	2	Q4WJ00	ASPFU	Q8BBL9	hepatitis c
299	36	49.3	74	2	Q5LD25	BACFN	372	36	49.3	252	2	Q832P5	ENTFA	Q8BBL1	hepatitis c
300	36	49.3	113	1	LCCI	LEUGE	373	36	49.3	266	2	Q5CPG2	CRYPV	Q8BBL2	hepatitis c
301	36	49.3	113	1	MESI	LEUME	374	36	49.3	269	1	CALB2	CHICK	Q8BBL3	hepatitis c
302	36	49.3	113	2	Q6LD90	LEUCA	375	36	49.3	295	2	Q23376	ARATH	Q8BBL4	hepatitis c
303	36	49.3	113	2	Q791W0	LEUME	376	36	49.3	295	2	Q4LYQ3	9BURK	Q8BBL5	hepatitis c
304	36	49.3	156	2	Q49945	SOLTU	377	36	49.3	326	2	Q9RBR1	9PROT	Q8BBL6	hepatitis c
305	36	49.3	158	2	Q8BBL5	9HEPC	378	36	49.3	326	2	Q8UW4	9HEPC	Q8BBL7	hepatitis c
306	36	49.3	170	2	Q917Q1	9HEPC	379	36	49.3	331	2	Q6SYW1	PASMU	Q8BBL8	hepatitis c
307	36	49.3	170	2	Q917S1	9HEPC	380	36	49.3	331	2	Q9VT05	DROME	Q8BBL9	hepatitis c
308	36	49.3	171	2	Q8QR70	9HEPC	381	36	49.3	335	2	Q5JC79	9LILI	Q8BBL1	hepatitis c
309	36	49.3	180	2	Q5MMF5	9HEPC	382	36	49.3	336	2	Q8PP26	XANAC	Q8BBL2	hepatitis c
310	36	49.3	183	2	Q5L230	PICTO	383	36	49.3	343	2	Q7N812	PHOLI	Q8BBL3	hepatitis c
311	36	49.3	183	2	Q6A2A4	RABIN	384	36	49.3	345	2	Q83918	TREPA	Q8BBL4	hepatitis c
312	36	49.3	183	2	Q4QPF5	HAB18	385	36	49.3	386	2	Q5QLS4	ORYSA	Q8BBL5	hepatitis c
313	36	49.3	185	2	Q7VMK6	HABDU	386	36	49.3	387	2	Q86265	PSEAE	Q8BBL6	hepatitis c
314	36	49.3	186	2	Q91YP7	9HEPC	387	36	49.3	387	2	Q86266	PSEAE	Q8BBL7	hepatitis c
315	36	49.3	188	2	Q7VBV7	PROMA	388	36	49.3	387	2	Q83TF1	PSEAE	Q8BBL8	hepatitis c
316	36	49.3	189	2	Q8BBL5	9HEPC	389	36	49.3	387	2	Q83WT8	PSEAE	Q8BBL9	hepatitis c
317	36	49.3	190	2	Q8BBL1	9HEPC	390	36	49.3	393	1	FLICA	PSEAE	Q8BBL1	hepatitis c
318	36	49.3	191	2	Q8BBL6	9HEPC	391	36	49.3	393	2	Q683B3	PSEFL	Q8BBL2	hepatitis c
319	36	49.3	191	2	Q8BBL7	9HEPC	392	36	49.3	394	2	Q53ZR9	PSEAE	Q8BBL3	hepatitis c
320	36	49.3	191	2	Q8BBL8	9HEPC	393	36	49.3	394	2	Q53ZS1	PSEAE	Q8BBL4	hepatitis c
321	36	49.3	191	2	Q8BBL9	9HEPC	394	36	49.3	394	2	Q5TJ08	DICLA	Q8BBL5	hepatitis c
322	36	49.3	191	2	Q8BBL1	9HEPC	395	36	49.3	413	2	Q7NZQ6	CHRCO	Q8BBL6	hepatitis c
323	36	49.3	191	2	Q8BBL2	9HEPC	396	36	49.3	430	2	Q822X8	CHLCV	Q8BBL7	hepatitis c

397	Q5JC78_9LILI	2	439	49.3	36	Q5jc78 thalia geni	470	35	47.9	65	1	CSRA_SHEON	Q8eb3 shewanella
398	Q9HZC7_PSEAE	2	455	49.3	36	Q9hzc7 pseudomonas	471	35	47.9	83	2	Q8CQ6_PSEPK	Q8ec6 pseudomonas
399	Q73UZ0_MYCPA	2	457	49.3	36	Q73uz0 mycobacteri	472	35	47.9	93	2	Q7WCE6_BORPA	Q7wce6 bordetella
400	MS3L1_HUMAN	1	521	49.3	36	Q85V2 homo sapien	473	35	47.9	94	2	Q8W2U6_ORYSA	Q8w2u6 oryza sativ
401	QSR6Y9_PONPY	1	521	49.3	36	Q8r6y9 pongo pygma	474	35	47.9	105	2	Q5F4U5_CABEL	Q5f4u5 caenorhabdi
402	LNT_CAUCR	3	530	49.3	36	Q8acl6 caulobacter	475	35	47.9	111	2	Q95X71_CABEL	Q95x71 caenorhabdi
403	Q8ZTW4_PYRAE	2	546	49.3	36	Q8ztw4 pyrobaculum	476	35	47.9	118	2	Q8G5F8_BIFLO	Q8g5f8 bifidobacte
404	Q9T6S7_AMBTC	2	547	49.3	36	Q9t6s7 amborella t	477	35	47.9	120	2	Q7RLY6_PLAYO	Q7rly6 plasmodium
405	Q8GHN2_PSERE	2	552	49.3	36	Q8ghn2 pseudomonas	478	35	47.9	137	2	Q9KGI4_BACHD	Q9kgi4 bacillus ha
406	Q4P982_USTMA	2	575	49.3	36	Q4p982 ustilago ma	479	35	47.9	141	2	Q5TRP2_ANOGA	Q5trp2 anopheles g
407	Q4W903_ASPFU	2	580	49.3	36	Q4w903 aspergillus	480	35	47.9	152	2	Q6CST0_KLULA	Q6cst0 kluyveromyc
408	Q4QD44_LEIMA	2	599	49.3	36	Q4qd44 leishmania	481	35	47.9	156	2	Q6N179_RHOPA	Q6n179 rhodospseudo
409	Q5WP98_BUBBU	2	606	49.3	36	Q5wp98 bubalus bub	482	35	47.9	158	2	Q3G6G6_STAAU	Q3g6g6 staphylococ
410	Q5ZQP4_BUBBU	2	606	49.3	36	Q5zqp4 bubalus bub	483	35	47.9	163	2	Q9SY46_ARATH	Q9sy46 arabidopsis
411	Q68GD0_BUBBU	2	606	49.3	36	Q68gd0 bubalus bub	484	35	47.9	171	2	Q98BB8_RHILO	Q98bb8 rhizobium l
412	Q8AKB8_DESPS	2	607	49.3	36	Q8akb8 desulfotale	485	35	47.9	176	2	Q9JY2_MOUSE	Q9jy2 mus musculu
413	Q5A8N5_CANAL	2	622	49.3	36	Q5a8n5 candida alb	486	35	47.9	177	2	Q56D00_DUNSA	Q56d00 dunaliella
414	Q61CN2_CAEBR	2	626	49.3	36	Q61cn2 caenorhabdi	487	35	47.9	178	2	Q7WSB3_RICJA	Q7wsb3 rickettsia
415	Q6CC93_YARLII	2	658	49.3	36	Q6cc93 yarrowia li	488	35	47.9	178	2	Q7WSB8_RICSI	Q7wsb8 rickettsia
416	Q9BE94_WACFA	2	705	49.3	36	Q9be94 macaca fasc	489	35	47.9	178	2	Q7WSB9_RICAK	Q7wsb9 rickettsia
417	Q9H961_HUMAN	2	762	49.3	36	Q9h961 homo sapien	490	35	47.9	178	2	Q7WSC0_RICCN	Q7wsc0 rickettsia
418	Q8BY85_DEBHA	2	779	49.3	36	Q8by85 debaryomyc	491	35	47.9	179	2	Q4RIS8_TETNG	Q4ris8 tetraodon n
419	Q6AMS9_DESPS	2	782	49.3	36	Q6ams9 desulfotale	492	35	47.9	197	2	Q8HY68_MACPL	Q8hy68 macropus fu
420	Q7W542_BORPA	2	786	49.3	36	Q7w542 bordetella	493	35	47.9	205	2	Q4I200_LYCPE	Q4i200 lycopersico
421	Q7WCM4_BORBR	2	786	49.3	36	Q7wcm4 bordetella	494	35	47.9	206	2	Q6Y7S0_9VIRU	Q6y7s0 staphylococ
422	Q7VW05_BORPE	2	789	49.3	36	Q7vw05 bordetella	495	35	47.9	206	2	Q4ZAI9_9CAUD	Q4zai9 bacterioph
423	SVFB_RICPR	1	815	49.3	36	Q8zdb4 rickettsia	496	35	47.9	209	1	HIS7_ANASP	Q5068 anabaena sp
424	SVFB_RICCN	1	818	49.3	36	Q8zdb4 rickettsia	497	35	47.9	216	2	Q6P079_PELPU	Q6p079 pelvicachro
425	Q7PBUI_RICSI	2	818	49.3	36	Q7pbui rickettsia	498	35	47.9	219	2	Q9VG22_DROME	Q9vg22 drosophila
426	Q4ULS4_RICPE	2	829	49.3	36	Q4uls4 rickettsia	499	35	47.9	242	2	Q4K171_PSEFS	Q4k171 pseudomonas
427	Q6ZNL0_HUMAN	2	829	49.3	36	Q6znl0 homo sapien	500	35	47.9	242	2	Q8KG32_CHLTE	Q8kg32 chlorobium
428	Q9LE38_ARATH	2	844	49.3	36	Q9le38 arabidopsis	501	35	47.9	253	2	Q4SFC7_TETNG	Q4sfc7 tetraodon n
429	Q92500_FUGRU	2	851	49.3	36	Q92500 fugu rubrip	502	35	47.9	256	2	Q9K7R4_BACHD	Q9k7r4 bacillus ha
430	Q853J1_9CAUD	2	874	49.3	36	Q853j1 mycobacteri	503	35	47.9	259	2	Q9AKF8_RICRI	Q9akf8 rickettsia
431	Q6CKK3_KLULA	2	931	49.3	36	Q6ckk3 kluyveromyc	504	35	47.9	259	2	Q9AKL2_RICMO	Q9akl2 rickettsia
432	Q4S40_BACFR	2	970	49.3	36	Q4s40 bacteroides	505	35	47.9	263	2	Q6DCX9_XENLA	Q6dcx9 xenopus lae
433	Q4K7J4_PSEFS	2	974	49.3	36	Q4k7j4 pseudomonas	506	35	47.9	268	2	Q8W151_9MAGN	Q8w151 ciassampelos
434	Q6R703_HUMAN	2	979	49.3	36	Q6r703 homo sapien	507	35	47.9	271	2	Q7MA67_WOLSU	Q7ma67 wolinnella s
435	Q4FS95_9GAMM	2	1001	49.3	36	Q4fs95 psychobact	508	35	47.9	272	2	Q8ECA6_SHEON	Q8eca6 shewanella
436	MKL2_MOUSE	1	1080	49.3	36	P59759 mus musculu	509	35	47.9	273	2	Q8ECA5_SHEON	Q8eca5 shewanella
437	Q5DTK3_MOUSE	2	1080	49.3	36	Q5dtk3 mus musculu	510	35	47.9	275	2	Q82UA3_NITBU	Q82ua3 nitrosomona
438	Q5AQ12_EMENI	2	1086	49.3	36	Q5aq12 aspergillus	511	35	47.9	281	2	Q9KDU4_BACHD	Q9kdj4 bacillus ha
439	Q9M180_ARATH	2	1113	49.3	36	Q9m180 arabidopsis	512	35	47.9	282	2	Q7NRA5_CHRVO	Q7nra5 chromobacte
440	MFD_ECOLI	1	1148	49.3	36	P30958 escherichia	513	35	47.9	285	2	Q9SGQ2_ARATH	Q9sgq2 arabidopsis
441	Q7UCW0_SHIFL	2	1148	49.3	36	Q7ucw0 shigella fl	514	35	47.9	286	2	Q65PE5_BACLD	Q65pe5 bacillus li
442	Q7AP75_ECO57	2	1148	49.3	36	Q7ap75 escherichia	515	35	47.9	287	1	FLAA_LISIN	Q62dw3 listeria in
443	Q57QD9_SALCH	2	1148	49.3	36	Q57qd9 salmonella	516	35	47.9	287	1	FLAA_LISMO	Q62dw3 listeria in
444	Q8ZQ01_SALTY	2	1148	49.3	36	Q8zq01 salmonella	517	35	47.9	287	1	Q5Y832_LISMO	Q5y832 listeria mo
445	Q8X8E7_ECO57	2	1148	49.3	36	Q8x8e7 escherichia	518	35	47.9	287	2	Q5Y833_LISMO	Q5y833 listeria mo
446	Q83R81_SHIFL	2	1148	49.3	36	Q83rs1 shigella fl	519	35	47.9	287	2	Q5Y831_LISMO	Q5y831 listeria mo
447	Q7N3A4_PHOLL	2	1148	49.3	36	Q7n3a4 photorhabdu	520	35	47.9	287	2	Q722K7_LISMF	Q722k7 listeria mo
448	Q8Z711_SALTI	2	1148	49.3	36	Q8z711 salmonella	521	35	47.9	287	2	Q81SP2_BACAN	Q81sf2 bacillus an
449	Q5PGK4_SALPA	2	1148	49.3	36	Q5pgk4 salmonella	522	35	47.9	300	2	Q916U1_PSEAE	Q916u1 pseudomonas
450	Q6D666_ERWCT	2	1149	49.3	36	Q6d666 erwinia car	523	35	47.9	304	2	Q5DY03_ECOLI	Q5dy03 escherichia
451	KCNT1_CHICK	1	1201	49.3	36	Q8qfv0 gallus gall	524	35	47.9	311	2	Q57KA3_SALCH	Q57ka3 salmonella
452	Q7YSX3_9TRYP	2	1219	49.3	36	Q7ysx3 trypanosoma	525	35	47.9	311	2	Q7CPV5_SALTY	Q7cpv5 salmonella
453	KCNT1_HUMAN	2	1230	49.3	36	Q8jvk3 homo sapien	526	35	47.9	311	2	Q5PEP7_SALPA	Q5pep7 salmonella
454	Q7PRW4_ANOGA	2	1383	49.3	36	Q7prw4 anopheles g	527	35	47.9	311	2	Q8XGD5_SALTI	Q8xgd5 salmonella
455	Q7PC83_ARATH	2	1397	49.3	36	Q7pc83 arabidopsis	528	35	47.9	318	2	Q8BUT1_MOUSE	Q8bvt1 m mus muscu
456	Q7PC89_ARATH	2	1400	49.3	36	Q7pc89 arabidopsis	529	35	47.9	323	2	Q7SAH9_NEUCR	Q7sah9 neurospora
457	Q9ZUT8_ARATH	2	1413	49.3	36	Q9zut8 arabidopsis	530	35	47.9	324	2	Q97397_PHACE	Q97397 phaedon coc
458	Q7S0S1_NEUCR	2	1559	49.3	36	Q7s0s1 neurospora	531	35	47.9	326	2	Q98VE6_9HEPC	Q98ve6 hepatitis c
459	GUIN_CALSA	2	1742	49.3	36	P22534 caldocellum	532	35	47.9	327	2	Q6CWR4_KLULA	Q6cwr4 kluyveromyc
460	Q4ST61_TETNG	2	2195	49.3	36	Q4st61 tetraodon n	533	35	47.9	328	2	Q9AQV6_ORYSA	Q9aqv6 oryza sativ
461	Q4FY29_LEIMA	2	3155	49.3	36	Q4fy29 leishmania	534	35	47.9	329	2	Q9AQV6_ORYSA	Q9aqv6 nycteris th
462	Q4QEB7_LEIMA	2	3551	49.3	36	Q4qeb7 leishmania	535	35	47.9	333	2	Q4KAL3_PSEFS	Q4kal3 pseudomonas
463	Q15142_HUMAN	2	3638	49.3	36	Q15142 homo sapien	536	35	47.9	334	2	Q9VA93_DROME	Q9va93 drosophila
464	PKD1_HUMAN	1	4303	49.3	36	P98161 homo sapien	537	35	47.9	335	2	Q614N9_CAEBR	Q614n9 caenorhabdi
465	COLL3_HUMAN	1	98	48.6	35.5	Q99616 h small ind	538	35	47.9	338	1	G3P_TRIHA	P87197 trichoderma
466	Q6IC06_HUMAN	2	98	48.6	35.5	Q6icq6 homo sapien	539	35	47.9	341	2	Q71P88_9MAGN	Q71p88 cocculus la
467	Q9KKW5_VIBCH	2	319	48.6	35.5	Q9kkw5 vibrio chol	540	35	47.9	343	1	ENGC_PSEPK	Q8adca pseudomonas
468	Q4IDL6_GIBZE	2	486	48.6	35.5	Q4idl6 gibberella	541	35	47.9	343	2	Q59SU6_CANAL	Q59suc candida alb
469	Q4P0H2_USTMA	2	649	48.6	35.5	Q4p0h2 ustilago ma	542	35	47.9	343	2	Q4KJ82_PSEFS	Q4kj82 pseudomonas

543	35	47.9	345	2	Q87UD4_PSESM	Q87ud4 pseudomonas
544	35	47.9	347	1	ADH_SULSO	P39462 trypanosoma
545	35	47.9	348	2	Q57WF4_9TRYP	Q57wf4 trypanosoma
546	35	47.9	353	1	EGSA_METRA	Q8tw08 methanopyru
547	35	47.9	353	2	Q5M6T9_CAMJE	Q5met9 campylobact
548	35	47.9	354	2	Q4V4B1_DROME	Q4v4b1 dirosophila
549	35	47.9	357	2	Q6ANG3_DRSPS	Q6ang3 desulfotale
550	35	47.9	367	1	FLIC2_PROMI	P42273 proteus mir
551	35	47.9	368	2	Q6CLX8_KLUULA	Q6cli8 kluyveromyc
552	35	47.9	368	2	Q9TMG5_9ASPA	Q9tmg5 polyxena co
553	35	47.9	373	2	Q9TMF7_9ASPA	Q9tmf7 nolina recu
554	35	47.9	373	2	Q9TMG6_9ASPA	Q9tmg6 maesonnia de
555	35	47.9	377	2	Q9TMG7_9ASPA	Q9tmg7 hyacinthus
556	35	47.9	378	2	Q9TMH1_POLOD	Q9tmh1 polygonatum
557	35	47.9	381	2	Q7S8S6_NEUCR	Q7s8s6 neurospora
558	35	47.9	402	2	Q8TIJ8_METAC	Q8tij8 methanosarc
559	35	47.9	403	2	Q6C3I5_YARLI	Q6c3i5 yarrowia li
560	35	47.9	407	2	Q8HW65_9WAGN	Q8hw65 cocculus or
561	35	47.9	408	1	CH60_RICFI	Q3a198 rickettsia
562	35	47.9	423	2	Q4TGT1_TETNG	Q4tgt1 tetradon n
563	35	47.9	425	2	Q7IMV8_9LILI	Q7imv8 heliconia s
564	35	47.9	425	2	Q7IMV9_HELRS	Q7imv9 heliconia r
565	35	47.9	427	2	Q5V142_HALMA	Q5v142 haloarcula
566	35	47.9	430	2	QANE91_9MICC	Qane91 arthrobacte
567	35	47.9	438	1	TOLC_VIBCH	Q9k2y1 vibrio chol
568	35	47.9	450	2	Q5X8Z7_LEGPA	Q5x8z7 legionella
569	35	47.9	454	2	Q6ITT7_SPISO	Q6itt7 episula sol
570	35	47.9	454	2	Q7N5K3_PHOLL	Q7n5k3 photorhabd
571	35	47.9	455	2	Q6ITT6_SPISO	Q6itt6 episula sol
572	35	47.9	458	2	Q6AZI8_XENLA	Q6azi8 xenopus lae
573	35	47.9	463	1	DESM_CHICK	P02542 gallus gall
574	35	47.9	464	2	Q6IWI7_CABBR	Q6iwi7 caenorhabd
575	35	47.9	466	2	Q7S7P9_ASHGO	Q7s7p9 ashbya goss
576	35	47.9	466	2	Q5RJQ2_RAT	Q5rjq2 rattus norv
577	35	47.9	468	1	CNRLA_FUGRU	Q9894 fugu rubrip
578	35	47.9	468	1	DESM_CANFA	Q5xfn2 canis famil
579	35	47.9	468	1	DESM_MESAU	P02541 mesocricetu
580	35	47.9	468	1	DESM_MOUSE	P1001 mus musculus
581	35	47.9	468	1	DESM_RAT	P48675 rattus norv
582	35	47.9	468	1	Q4RQX1_TETNG	Q4rqx1 tetradon n
583	35	47.9	469	1	DESM_BOVIN	Q62654 bos taurus
584	35	47.9	469	1	DESM_HUMAN	P17661 homo sapien
585	35	47.9	469	2	Q54A54_MESAU	Q54a94 mesocricetu
586	35	47.9	469	2	Q6P725_RAT	Q6p725 rattus norv
587	35	47.9	470	1	DESM_PIG	P02540 sus scrofa
588	35	47.9	470	2	Q9H3I9_HUMAN	Q9h3i9 homo sapien
589	35	47.9	470	2	Q53S85_HUMAN	Q53sb5 homo sapien
590	35	47.9	470	2	Q549R7_HUMAN	Q549r7 homo sapien
591	35	47.9	470	2	Q549R8_HUMAN	Q549r8 homo sapien
592	35	47.9	470	2	Q549R9_HUMAN	Q549r9 homo sapien
593	35	47.9	470	2	Q80IM1_XENLA	Q80im1 xenopus lae
594	35	47.9	473	1	CISY_SCHPO	Q10306 schizosacch
595	35	47.9	473	2	Q9DDC8_LAMFL	Q9ddc8 lampetra fl
596	35	47.9	487	2	Q75HW3_ORYSA	Q75hw3 oryza sativ
597	35	47.9	488	2	Q8XSR9_RALSO	Q8xsr9 ralsconla s
598	35	47.9	489	2	Q977W6_METTE	Q977w6 methanosarc
599	35	47.9	491	2	Q6IFV0_RAT	Q6ifv0 rattus norv
600	35	47.9	499	2	Q8RP06_BACAM	Q8rpq6 bacillus am
601	35	47.9	500	2	Q6AU71_ORYSA	Q6au71 oryza sativ
602	35	47.9	502	2	Q5ZJG6_CHICK	Q5zjg6 gallus gall
603	35	47.9	504	2	Q7VRW4_CANBF	Q7vrw4 candidatus
604	35	47.9	505	2	Q82Y67_NITEU	Q82y67 nitrosomona
605	35	47.9	506	2	Q5WUQ1_LEGPL	Q5wuq1 legionella
606	35	47.9	506	2	Q5X394_LEGPA	Q5x394 legionella
607	35	47.9	511	2	Q5YAS1_9POAL	Q5yas1 tillandsia
608	35	47.9	511	2	Q5YAS2_9POAL	Q5yas2 tillandsia
609	35	47.9	511	2	Q5YAS3_9POAL	Q5yas3 tillandsia
610	35	47.9	511	2	Q8HV05_9LILI	Q8hv05 heliconia i
611	35	47.9	517	2	Q5ZTC9_LEGPH	Q5ztc9 legionella
612	35	47.9	518	2	Q6LA16_9ASPA	Q6la16 pleomele th
613	35	47.9	518	2	Q9TN83_9ASPA	Q9tn83 asparagus f
614	35	47.9	518	2	Q9TN84_9ASPA	Q9tn84 asparagus c
615	35	47.9	518	2	Q9TN85_9ASPA	Q9tn85 dracaena dr

Q9tn86	dracaena an	Q9TN86_9ASPA	518	2	Q9TN86_9ASPA	Q9tn86 dracaena an
Q9cn98	ophiopogon	Q9TN98_9ASPA	518	2	Q9TN98_9ASPA	Q9cn98 ophiopogon
Q9tn87	ruscus acul	Q9TN88_9ASPA	519	2	Q9TN88_9ASPA	Q9tn87 ruscus acul
Q5tky9	beaucarnea	Q5TKY9_9ASPA	520	1	MATK_RUSAC	Q5tky9 beaucarnea
Q7jdn5	diaporopsis	Q7JDN5_9ASPA	520	2	Q9JHB6_9ASPA	Q7jdn5 diaporopsis
Q9ghb6	polygonatum	Q9GHB6_9ASPA	520	2	Q9JHB6_9ASPA	Q9ghb6 polygonatum
Q9t3z6	diaporopsis	Q9T3Z6_9ASPA	520	2	Q9T3Z6_9ASPA	Q9t3z6 diaporopsis
Q9chn7	peliosanthe	Q9THK7_9ASPA	520	2	Q9THK7_9ASPA	Q9chn7 peliosanthe
Q9chl2	ophiopogon	Q9THL2_9ASPA	520	2	Q9THL2_9ASPA	Q9chl2 ophiopogon
Q9chl3	ophiopogon	Q9THL3_9ASPA	520	2	Q9THL3_9ASPA	Q9chl3 ophiopogon
Q9tn89	nolina recu	Q9TN89_9ASPA	520	2	Q9TN89_9ASPA	Q9tn89 nolina recu
Q9tn91	peliosanthe	Q9TN91_9ASPA	520	2	Q9TN91_9ASPA	Q9tn91 peliosanthe
Q9tn92	peliosanthe	Q9TN92_9ASPA	520	2	Q9TN92_9ASPA	Q9tn92 peliosanthe
Q9cn93	ophiopogon	Q9TN93_9ASPA	520	2	Q9TN93_9ASPA	Q9cn93 ophiopogon
Q9tn95	ophiopogon	Q9TN95_9ASPA	520	2	Q9TN95_9ASPA	Q9tn95 ophiopogon
Q9tn96	ophiopogon	Q9TN96_9ASPA	520	2	Q9TN96_9ASPA	Q9tn96 ophiopogon
Q9tn97	ophiopogon	Q9TN97_9ASPA	520	2	Q9TN97_9ASPA	Q9tn97 ophiopogon
Q9tn99	ophiopogon	Q9TN99_9ASPA	520	2	Q9TN99_9ASPA	Q9tn99 ophiopogon
Q9tna0	liriope spi	Q9TNA0_9ASPA	520	2	Q9TNA0_9ASPA	Q9tna0 liriope spi
Q9tna1	liriope pla	Q9TNA1_LIRPL	520	2	Q9TNA1_LIRPL	Q9tna1 liriope pla
Q9tna2	liriope min	Q9TNA2_9ASPA	520	2	Q9TNA2_9ASPA	Q9tna2 liriope min
Q9tnb5	diaporopsis	Q9TNB5_9ASPA	520	2	Q9TNB5_9ASPA	Q9tnb5 diaporopsis
Q9tnb6	heteropolys	Q9TNB6_9ASPA	520	2	Q9TNB6_9ASPA	Q9tnb6 heteropolys
Q9cnb7	polygonatum	Q9TNB7_9ASPA	520	2	Q9TNB7_9ASPA	Q9cnb7 polygonatum
Q9cnb8	polygonatum	Q9TNB8_9ASPA	520	2	Q9TNB8_9ASPA	Q9cnb8 polygonatum
Q9cnb9	polygonatum	Q9TNB9_9ASPA	520	2	Q9TNB9_9ASPA	Q9cnb9 polygonatum
Q9cnc0	polygonatum	Q9TNCO_9ASPA	520	2	Q9TNCO_9ASPA	Q9cnc0 polygonatum
Q9tn90	peliosanthe	Q9TN90_9ASPA	522	2	Q9TN90_9ASPA	Q9tn90 peliosanthe
Q9wvg9	mus musculus	M53L11_MOUSE	525	1	M53L11_MOUSE	Q9wvg9 mus musculus
Q6fnj1	candida gla	Q6FNU1_CANGA	528	2	Q6FNU1_CANGA	Q6fnj1 candida gla
Q4fwp3	leishmania	Q4FWP3_LEIMA	533	2	Q4FWP3_LEIMA	Q4fwp3 leishmania
Q7p996	rickettsia	Q7P996_RICSI	547	2	Q7P996_RICSI	Q7p996 rickettsia
Q4umf2	rickettsia	Q4UMF2_RICFTE	547	2	Q4UMF2_RICFTE	Q4umf2 rickettsia
Q8a2j6	bacteroides	Q8A2J6_BACTN	547	2	Q8A2J6_BACTN	Q8a2j6 bacteroides
Q92h04	rickettsia	CH60_RICCN	548	1	CH60_RICCN	Q92h04 rickettsia
Q89x76	bradyrhizob	Q89X76_BRAJA	548	2	Q89X76_BRAJA	Q89x76 bradyrhizob
Q83ye7	streptomyces	Q83YE7_STRHY	548	2	Q83YE7_STRHY	Q83ye7 streptomyces
Q7mv80	porphyromon	Q7MV80_PORGI	595	2	Q7MV80_PORGI	Q7mv80 porphyromon
Q83032	streptomyces	Q83032_STRCO	598	2	Q83032_STRCO	Q83032 streptomyces
Q10i010	streptomyces	Q9L010_STRCO	599	2	Q9L010_STRCO	Q10i010 streptomyces
Q8h6i9	zea mays	Q8H6I9_MAI2E	639	2	Q8H6I9_MAI2E	Q8h6i9 zea mays
Q7sdj1	neurospora	Q7SDJ1_NEUCR	639	2	Q7SDJ1_NEUCR	Q7sdj1 neurospora
Q4qn06	leishmania	Q4QH06_LEIMA	653	2	Q4QH06_LEIMA	Q4qn06 leishmania
Q5grx2	woibachia s	Q5GRX2_WOLTR	654	2	Q5GRX2_WOLTR	Q5grx2 woibachia s
Q75cl7	ashbya goss	Q75CL7_ASHGO	657	2	Q75CL7_ASHGO	Q75cl7 ashbya goss
Q4kry9	tomato chlo	Q4KRY9_9CLOS	669	2	Q4KRY9_9CLOS	Q4kry9 tomato chlo
Q9ke00	bacillus ha	Q9KE00_BACHD	682	2	Q9KE00_BACHD	Q9ke00 bacillus ha
Q7xv75	oryza sativ	Q7XV75_ORYSA	693	2	Q7XV75_ORYSA	Q7xv75 oryza sativ
Q9fvc7	oryza sativ	Q9FVC7_ORYSA	736	2	Q9FVC7_ORYSA	Q9fvc7 oryza sativ
Q51pb6	magnaporthe	Q51PB6_MAGGR	760	2	Q51PB6_MAGGR	Q51pb6 magnaporthe
Q9sfw8	arabidopsis	Q9SPW8_ARATH	808	2	Q9SPW8_ARATH	Q9sfw8 arabidopsis
Q03823	saccharomyc	YM35_YEAST	816	1	YM35_YEAST	Q03823 saccharomyc
Q4lhn8	burkholderi	Q4LHN8_BURXK	820	2	Q4LHN8_BURXK	Q4lhn8 burkholderi
Q4ep11	tetradon n	Q4SP11_TETNG	828	2	Q4SP11_TETNG	Q4ep11 tetradon n
Q4in90	gibberella	Q4IN90_GIBZE	840	2	Q4IN90_GIBZE	Q4in90 gibberella
Q14186	schizosacch	YDSB_SCHPO	846	1	YDSB_SCHPO	Q14186 schizosacch
Q61l75	caenorhabdi	Q61L75_CAEBR	857	2	Q61L75_CAEBR	Q61l75 caenorhabdi
Q4wnl3	aspergillus	Q4WNL3_ASPFU	921	2	Q4WNL3_ASPFU	Q4wnl3 aspergillus
Q5lht6	bacteroides	Q5LHT6_BACFN	982	2	Q5LHT6_BACFN	Q5lht6 bacteroides
Q64yt8	bacteroides	Q64YT8_BACFR	982	2	Q64YT8_BACFR	Q64yt8 bacteroides
Q4n733	theileria p	Q4N733_THEPA	995	2	Q4N733_THEPA	Q4n733 theileria p
Q51n11	magnaporthe	Q51N11_MAGGR	1008	2	Q51N11_MAGGR	Q51n11 magnaporthe
Q6bk70	debaryomyce	Q6BK70_DEBHA	1050	2	Q6BK70_DEBHA	Q6bk70 debaryomyce
Q5bge6	aspergillus	Q5BGE6_EMENI	1067	2	Q5BGE6_EMENI	Q5bge6 aspergillus
Q8lbr5	plasmodium	Q8LBR5_PLAF7	1106	2	Q8LBR5_PLAF7	Q8lbr5 plasmodium
Q4q9r1	leishmania	Q4Q9R1_LEIMA	1118	2	Q4Q9R1_LEIMA	Q4q9r1 leishmania
Q4n216	theileria p	Q4N216_THEPA	1123	2	Q4N216_THEPA	Q4n216 theileria p
Q6amn5	desulfotale	Q6AMN5_DESPS	1128	2	Q6AMN5_DESPS	Q6amn5 desulfotale
Q4ubk4	theileria a	Q4UBK4_THEAN	1130	2	Q4UBK4_THEAN	Q4ubk4 theileria a
Q4peb1	ustilago ma	Q4PEB1_USTMA	1173	2	Q4PEB1_USTMA	Q4peb1 ustilago ma
Q7s8g1	neurospora	Q7S8G1_NEUCR	1286	2	Q7S8G1_NEUCR	Q7s8g1 neurospora

689	35	47.9	1346	2	Q7PU00	ANOQA	Q7puq0	anopheles g	762	34	46.6	93	2	Q7BY0	9HEPC	Q7by0	hepatitis c
690	35	47.9	1378	2	Q8G450	BIFLO	Q8g4s0	bifidobacte	763	34	46.6	93	2	Q7BY2	9HEPC	Q7by2	hepatitis c
691	35	47.9	1386	2	Q7FMW1	ORYSA	Q7fmw1	oryza sativ	764	34	46.6	93	2	Q7BY3	9HEPC	Q7by3	hepatitis c
692	35	47.9	1431	2	Q8A039	BACTIN	Q8a039	bacteroides	765	34	46.6	93	2	Q7BY4	9HEPC	Q7by4	hepatitis c
693	35	47.9	1474	2	Q5VMX7	ORYSA	Q5vmx7	oryza sativ	766	34	46.6	93	2	Q7BY5	9HEPC	Q7by5	hepatitis c
694	35	47.9	1487	2	Q5N6Y2	ORYSA	Q5n6y2	oryza sativ	767	34	46.6	93	2	Q7BY6	9HEPC	Q7by6	hepatitis c
695	35	47.9	1490	2	Q9M1C7	ARATH	Q9m1c7	arabidopsis	768	34	46.6	93	2	Q7BY7	9HEPC	Q7by7	hepatitis c
696	35	47.9	2196	2	Q4RT37	TEUNG	Q4rt37	tetradodon n	769	34	46.6	93	2	Q7BY8	9HEPC	Q7by8	hepatitis c
697	35	47.9	3124	2	Q6CQ11	KULUA	Q6cq11	kluyveromyc	770	34	46.6	93	2	Q7BY9	9HEPC	Q7by9	hepatitis c
698	34.5	47.3	431	2	Q26924	METH	Q26924	methanobact	771	34	46.6	93	2	Q7B20	9HEPC	Q7b20	hepatitis c
699	34.5	47.3	470	2	Q16776	CABEL	Q16776	caenorhabdi	772	34	46.6	93	2	Q7B21	9HEPC	Q7b21	hepatitis c
700	34	46.6	52	2	Q6YZ29	ORYSA	Q6yz29	oryza sativ	773	34	46.6	93	2	Q7B22	9HEPC	Q7b22	hepatitis c
701	34	46.6	52	2	Q8F062	LEPIN	Q8f062	leptospira	774	34	46.6	93	2	Q7B23	9HEPC	Q7b23	hepatitis c
702	34	46.6	57	2	Q6FA86	ACIAD	Q6fa86	acinobact	775	34	46.6	93	2	Q7B24	9HEPC	Q7b24	hepatitis c
703	34	46.6	59	2	Q88M29	PSEPK	Q88m29	pseudomonas	776	34	46.6	93	2	Q7B25	9HEPC	Q7b25	hepatitis c
704	34	46.6	59	2	Q8V5T5	NUCL	Q8v5t5	helicoverpa	777	34	46.6	93	2	Q7B26	9HEPC	Q7b26	hepatitis c
705	34	46.6	68	2	Q8Z2E1	SALTI	Q8z2e1	salmonella	778	34	46.6	93	2	Q7B27	9HEPC	Q7b27	hepatitis c
706	34	46.6	69	2	Q571E4	SALCH	Q571e4	salmonella	779	34	46.6	93	2	Q7B28	9HEPC	Q7b28	hepatitis c
707	34	46.6	69	2	Q5PLR2	SALPA	Q5plr2	salmonella	780	34	46.6	93	2	Q7B29	9HEPC	Q7b29	hepatitis c
708	34	46.6	69	2	Q8ZL66	SALTY	Q8zl66	salmonella	781	34	46.6	93	2	Q7C10	9HEPC	Q7c10	hepatitis c
709	34	46.6	70	2	Q88D99	RHILO	Q88d99	rhizobium l	782	34	46.6	93	2	Q7C11	9HEPC	Q7c11	hepatitis c
710	34	46.6	83	2	Q7VTP5	BORPE	Q7vtp5	bordetella	783	34	46.6	93	2	Q7C12	9HEPC	Q7c12	hepatitis c
711	34	46.6	83	2	Q7W155	BORPA	Q7w155	bordetella	784	34	46.6	93	2	Q7C13	9HEPC	Q7c13	hepatitis c
712	34	46.6	83	2	Q7WNUS	BORBR	Q7wnus	bordetella	785	34	46.6	93	2	Q7C14	9HEPC	Q7c14	hepatitis c
713	34	46.6	90	2	Q6FVY8	CANGA	Q6fvy8	candida gla	786	34	46.6	93	2	Q7C15	9HEPC	Q7c15	hepatitis c
714	34	46.6	93	2	Q95334	HUMAN	Q95334	homo sapien	787	34	46.6	93	2	Q7C16	9HEPC	Q7c16	hepatitis c
715	34	46.6	93	2	Q7TBP3	9HEPC	Q7tbp3	hepatitis c	788	34	46.6	93	2	Q7C17	9HEPC	Q7c17	hepatitis c
716	34	46.6	93	2	Q7TBP4	9HEPC	Q7tbp4	hepatitis c	789	34	46.6	93	2	Q7C18	9HEPC	Q7c18	hepatitis c
717	34	46.6	93	2	Q7TBP5	9HEPC	Q7tbp5	hepatitis c	790	34	46.6	93	2	Q7C19	9HEPC	Q7c19	hepatitis c
718	34	46.6	93	2	Q7TBP6	9HEPC	Q7tbp6	hepatitis c	791	34	46.6	93	2	Q7C20	9HEPC	Q7c20	hepatitis c
719	34	46.6	93	2	Q7TBP7	9HEPC	Q7tbp7	hepatitis c	792	34	46.6	93	2	Q7C21	9HEPC	Q7c21	hepatitis c
720	34	46.6	93	2	Q7TBP8	9HEPC	Q7tbp8	hepatitis c	793	34	46.6	93	2	Q7C22	9HEPC	Q7c22	hepatitis c
721	34	46.6	93	2	Q7TBP9	9HEPC	Q7tbp9	hepatitis c	794	34	46.6	93	2	Q7C23	9HEPC	Q7c23	hepatitis c
722	34	46.6	93	2	Q7TBQ0	9HEPC	Q7tbq0	hepatitis c	795	34	46.6	93	2	Q7C24	9HEPC	Q7c24	hepatitis c
723	34	46.6	93	2	Q7TBQ6	9HEPC	Q7tbq6	hepatitis c	796	34	46.6	93	2	Q7C27	9HEPC	Q7c27	hepatitis c
724	34	46.6	93	2	Q7TBQ8	9HEPC	Q7tbq8	hepatitis c	797	34	46.6	93	2	Q7C35	9HEPC	Q7c35	hepatitis c
725	34	46.6	93	2	Q7TBX1	9HEPC	Q7tbx1	hepatitis c	798	34	46.6	93	2	Q7C36	9HEPC	Q7c36	hepatitis c
726	34	46.6	93	2	Q7TBX2	9HEPC	Q7tbx2	hepatitis c	799	34	46.6	93	2	Q7C37	9HEPC	Q7c37	hepatitis c
727	34	46.6	93	2	Q7TBX3	9HEPC	Q7tbx3	hepatitis c	800	34	46.6	93	2	Q7C38	9HEPC	Q7c38	hepatitis c
728	34	46.6	93	2	Q7TBX4	9HEPC	Q7tbx4	hepatitis c	801	34	46.6	93	2	Q7C39	9HEPC	Q7c39	hepatitis c
729	34	46.6	93	2	Q7TBX5	9HEPC	Q7tbx5	hepatitis c	802	34	46.6	93	2	Q7C40	9HEPC	Q7c40	hepatitis c
730	34	46.6	93	2	Q7TBX6	9HEPC	Q7tbx6	hepatitis c	803	34	46.6	93	2	Q7C42	9HEPC	Q7c42	hepatitis c
731	34	46.6	93	2	Q7TBX7	9HEPC	Q7tbx7	hepatitis c	804	34	46.6	93	2	Q7C43	9HEPC	Q7c43	hepatitis c
732	34	46.6	93	2	Q7TBX8	9HEPC	Q7tbx8	hepatitis c	805	34	46.6	93	2	Q7C45	9HEPC	Q7c45	hepatitis c
733	34	46.6	93	2	Q7TBX9	9HEPC	Q7tbx9	hepatitis c	806	34	46.6	93	2	Q7C46	9HEPC	Q7c46	hepatitis c
734	34	46.6	93	2	Q7TBS0	9HEPC	Q7tbs0	hepatitis c	807	34	46.6	93	2	Q7C47	9HEPC	Q7c47	hepatitis c
735	34	46.6	93	2	Q7TBS1	9HEPC	Q7tbs1	hepatitis c	808	34	46.6	93	2	Q7C48	9HEPC	Q7c48	hepatitis c
736	34	46.6	93	2	Q7TBS2	9HEPC	Q7tbs2	hepatitis c	809	34	46.6	93	2	Q7C49	9HEPC	Q7c49	hepatitis c
737	34	46.6	93	2	Q7TBW9	9HEPC	Q7tbw9	hepatitis c	810	34	46.6	93	2	Q7C50	9HEPC	Q7c50	hepatitis c
738	34	46.6	93	2	Q7TBW0	9HEPC	Q7tbw0	hepatitis c	811	34	46.6	93	2	Q7C51	9HEPC	Q7c51	hepatitis c
739	34	46.6	93	2	Q7TBW1	9HEPC	Q7tbw1	hepatitis c	812	34	46.6	93	2	Q7C52	9HEPC	Q7c52	hepatitis c
740	34	46.6	93	2	Q7TBW2	9HEPC	Q7tbw2	hepatitis c	813	34	46.6	93	2	Q7C53	9HEPC	Q7c53	hepatitis c
741	34	46.6	93	2	Q7TBW8	9HEPC	Q7tbw8	hepatitis c	814	34	46.6	93	2	Q7C54	9HEPC	Q7c54	hepatitis c
742	34	46.6	93	2	Q7TBW0	9HEPC	Q7tbw0	hepatitis c	815	34	46.6	93	2	Q7C55	9HEPC	Q7c55	hepatitis c
743	34	46.6	93	2	Q7TBW1	9HEPC	Q7tbw1	hepatitis c	816	34	46.6	93	2	Q7C56	9HEPC	Q7c56	hepatitis c
744	34	46.6	93	2	Q7TBW2	9HEPC	Q7tbw2	hepatitis c	817	34	46.6	93	2	Q7C57	9HEPC	Q7c57	hepatitis c
745	34	46.6	93	2	Q7TBW3	9HEPC	Q7tbw3	hepatitis c	818	34	46.6	93	2	Q7C58	9HEPC	Q7c58	hepatitis c
746	34	46.6	93	2	Q7TBW4	9HEPC	Q7tbw4	hepatitis c	819	34	46.6	93	2	Q7C59	9HEPC	Q7c59	hepatitis c
747	34	46.6	93	2	Q7TBW5	9HEPC	Q7tbw5	hepatitis c	820	34	46.6	93	2	Q7C60	9HEPC	Q7c60	hepatitis c
748	34	46.6	93	2	Q7TBW6	9HEPC	Q7tbw6	hepatitis c	821	34	46.6	93	2	Q7C61	9HEPC	Q7c61	hepatitis c
749	34	46.6	93	2	Q7TBW7	9HEPC	Q7tbw7	hepatitis c	822	34	46.6	93	2	Q7C62	9HEPC	Q7c62	hepatitis c
750	34	46.6	93	2	Q7TBW8	9HEPC	Q7tbw8	hepatitis c	823	34	46.6	93	2	Q7C63	9HEPC	Q7c63	hepatitis c
751	34	46.6	93	2	Q7TBW9	9HEPC	Q7tbw9	hepatitis c	824	34	46.6	93	2	Q7C64	9HEPC	Q7c64	hepatitis c
752	34	46.6	93	2	Q7TBX0	9HEPC	Q7tbx0	hepatitis c	825	34	46.6	93	2	Q7C65	9HEPC	Q7c65	hepatitis c
753	34	46.6	93	2	Q7TBX1	9HEPC	Q7tbx1	hepatitis c	826	34	46.6	93	2	Q7C66	9HEPC	Q7c66	hepatitis c
754	34	46.6	93	2	Q7TBX2	9HEPC	Q7tbx2	hepatitis c	827	34	46.6	93	2	Q7C67	9HEPC	Q7c67	hepatitis c
755	34	46.6	93	2	Q7TBX3	9HEPC	Q7tbx3	hepatitis c	828	34	46.6	93	2	Q7C68	9HEPC	Q7c68	hepatitis c
756	34	46.6	93	2	Q7TBX4	9HEPC	Q7tbx4	hepatitis c	829	34	46.6	93	2	Q7C69	9HEPC	Q7c69	hepatitis c
757	34	46.6	93	2	Q7TBX5	9HEPC	Q7tbx5	hepatitis c	830	34	46.6	93	2	Q7C70	9HEPC	Q7c70	hepatitis c
758	34	46.6	93	2	Q7TBX6	9HEPC	Q7tbx6	hepatitis c	831	34	46.6	93	2	Q7C71	9HEPC	Q7c71	hepatitis c
759	34	46.6	93	2	Q7TBX7	9HEPC	Q7tbx7	hepatitis c	832	34	46.6	93	2	Q7C72	9HEPC	Q7c72	hepatitis c
760	34	46.6	93	2	Q7TBX8	9HEPC	Q7tbx8	hepatitis c	833	34	46.6	93	2	Q7C73	9HEPC	Q7c73	hepatitis c
761	34	46.6	93	2	Q7TBX9	9HEPC	Q7tbx9	hepatitis c	834	34	46.6	93	2	Q7C78	9HEPC	Q7c78	hepatitis c

981 34 46.6 130 2 Q91ZN9_9HEPC Q91zn9 hepatitis c
 982 34 46.6 130 2 Q91ZP0_9HEPC Q91zp0 hepatitis c
 983 34 46.6 130 2 Q91ZP1_9HEPC Q91zp1 hepatitis c
 984 34 46.6 130 2 Q91ZP2_9HEPC Q91zp2 hepatitis c
 985 34 46.6 130 2 Q91ZP3_9HEPC Q91zp3 hepatitis c
 986 34 46.6 130 2 Q91ZP4_9HEPC Q91zp4 hepatitis c
 987 34 46.6 130 2 Q91ZP5_9HEPC Q91zp5 hepatitis c
 988 34 46.6 130 2 Q91ZQ1_9HEPC Q91zq1 hepatitis c
 989 34 46.6 130 2 Q91ZQ2_9HEPC Q91zq2 hepatitis c
 990 34 46.6 130 2 Q91ZQ3_9HEPC Q91zq3 hepatitis c
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 992 34 46.6 130 2 Q91ZQ5_9HEPC Q91zq5 hepatitis c
 993 34 46.6 130 2 Q91ZQ6_9HEPC Q91zq6 hepatitis c
 994 34 46.6 130 2 Q66M93_9HEPC Q66m93 hepatitis c
 995 34 46.6 132 1 Z1AR_SVNV3 Q55940 synechoyast
 996 34 46.6 135 2 Q68190_9HEPC Q68190 hepatitis c
 997 34 46.6 135 2 Q68196_9HEPC Q68196 hepatitis c
 998 34 46.6 136 2 Q66MA9_9HEPC Q66ma9 hepatitis c
 999 34 46.6 137 2 Q66MA8_9HEPC Q66ma8 hepatitis c
 1000 34 46.6 137 2 Q911E9_9HEPC Q911e9 hepatitis c

ALIGNMENTS

RESULT 1

CCL2_HUMAN
 ID _CCL2_HUMAN STANDARD; PRT; 99 AA.
 AC P13500; Q9UDF3;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1) (MCP-1) (Monocyte chemoattractant protein 1) (Monocyte chemoattractant and activating factor) (MCAF) (Monocyte secretory protein JE) (HC11).
 DE Chemotactic and activating factor (MCAF) (Monocyte secretory protein JE) (HC11).
 DE Name=CCL2; Synonyms=MCP1, SCYA2;
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 [1]
 RP MEDLINE=99165862; PubMed=2923622;
 RA Furutani Y., Nomura H., Notake M., Oyama Y., Fukui T., Yamada M., Larsen C.G., Oppenheim J.J., Matsushima K.;
 RT "Cloning and sequencing of the cDNA for human monocyte chemoattractant and activating factor (MCAF).";
 RL Biochem. Biophys. Res. Commun. 159:249-255(1989).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=90097880; PubMed=2513477;
 RA Rollins B.J., Stier P., Ernst T., Wong G.G.;
 RT "The human homolog of the JE gene encodes a monocyte secretory protein.";
 RL Mol. Cell. Biol. 9:4687-4695(1989).
 [3]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89153605; PubMed=2465924; DOI=10.1016/0014-5793(89)80590-3;
 RA Yoshimura T., Yuhki N., Moore S.K., Appella E., Lerman M.I., Leonard E.J.;
 RT "Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expression in mitogen-stimulated blood mononuclear leukocytes, and sequence similarity to mouse competence gene JE.";
 RL FEBS Lett. 244:487-493(1989).
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 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=90290466; PubMed=2357211;
 RA Shyy Y.J., Li Y.S., Kolattukudy P.E.;
 RT "Structure of human monocyte chemoattractant protein gene and its regulation by TPA.";
 RL Biochem. Biophys. Res. Commun. 169:346-351(1990).

[5]
 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91207938; PubMed=2518726;
 RA Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.;
 RT "Cloning and expression of a gamma-interferon-inducible gene in monocytes: a new member of a cytokine gene family.";
 RL Int. Immunol. 1:388-399(1989).
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 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94150478; PubMed=8107690;
 RA Li Y.S., Shyy Y.J., Wright J.G., Valente A.J., Cornhill J.F., Kolattukudy P.E.;
 RT "The expression of monocyte chemoattractant protein (MCP-1) in human vascular endothelium in vitro and in vivo.";
 RL Mol. Cell. Biochem. 126:61-68(1993).
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 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92095166; PubMed=1661560;
 RA Yoshimura T., Leonard E.J.;
 RT "Human monocyte chemoattractant protein-1 (MCP-1).";
 RL Adv. Exp. Med. Biol. 305:47-56(1991).
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 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=91301709; PubMed=2071154;
 RA Rollins B.J., Morton C.C., Ledbetter D.H., Eddy R.L. Jr., Shows T.B.;
 RT "Assignment of the human small inducible cytokine A2 gene, SCYA2 (encoding JE or MCP-1), to 17q11.2-12: evolutionary relatedness of cytokines clustered at the same locus.";
 RL Genomics 10:489-492(1991).
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 RN NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20374005; PubMed=10918580; DOI=10.1038/sj.onc.1203643;
 RA Finzer P., Soto U., Delius H., Patzelt A., Poustka A., Coy J.F., zur Hausen H., Roel F.;
 RT "Differential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic HPV 18 positive cells: the role of the chromatin structure and AP-1 composition.";
 RL Oncogene 19:3235-3244(2000).
 [10]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RA Kainane N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y., Phelan M., Farmer A.;
 RT "Cloning of human full-length CDSs in BD Creator(TM) system donor vector.";
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 [11]
 RN NUCLEOTIDE SEQUENCE [GENOMIC DNA].
 RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
 RT "SeattleSNPs, NHLBI HL66682 program for genomic applications, UW-FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 [12]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Pancreas;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[13]
RP PROTEIN SEQUENCE OF 24-99.
RX MEDLINE=83184525; PubMed=2648385;
RA Robinson E.A., Yoshimura T., Leonard E.J., Tanaka S., Griffin P.R.,
RA Shabanowitz J., Hunt D.F., Appella E.;
RT "Complete amino acid sequence of a human monocyte chemoattractant, a
RT putative mediator of cellular immune reactions.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1850-1854 (1989).
[14]
RP PROTEIN SEQUENCE OF 29-53 AND 82-92.
RX MEDLINE=90211336; PubMed=232286;
RA Decock B., Conings R., Lenaerts J.-P., Billiau A., van Damme J.;
RT "Identification of the monocyte chemotactic protein from human
RT osteosarcoma cells and monocytes: detection of a novel N-terminally
RT processed form.";
RL Biochem. Biophys. Res. Commun. 167:904-909 (1990).
[15]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=91312872; PubMed=1857712;
RA Gronenborn A.M., Clore G.M.;
RT "Modeling the three-dimensional structure of the monocyte chemo-
RT attractant and activating protein MCP-1 on the basis of the
RT solution structure of interleukin-8.";
RL Protein Eng. 4:263-269 (1991).
[16]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=97143315; PubMed=8989326;
RA Lubkowski J., Bujacz G., Domaille P.J., Handel T.M., Wlodawer A.;
RT "The structure of MCP-1 in two crystal forms provides a rare example
RT of variable quaternary interactions.";
RL Nat. Struct. Biol. 4:64-69 (1997).
[17]
RP STRUCTURE BY NMR.
RX MEDLINE=96234959; PubMed=8639605; DOI=10.1021/bi960270;
RA Handel T.M., Domaille P.J.;
RT "Heteronuclear (1H, 13C, 15N) NMR assignments and solution structure
RT of the monocyte chemoattractant protein-1 (MCP-1) dimer.";
RL Biochemistry 35:6569-6584 (1996).
[18]
RP EFFECT OF DELETION OF N-TERMINAL RESIDUES.
RX MEDLINE=96195223; PubMed=8627182; DOI=10.1084/jem.183.2.681;
RA Weber M., Uguccioni M., Baggiolini M., Clark-Lewis I., Dahinden C.A.;
RT "Deletion of the NH2-terminal residue converts monocyte chemotactic
RT protein 1 from an activator of basophil mediator release to an
RT eosinophil chemoattractant.";
RL J. Exp. Med. 183:681-685 (1996).
[19]
RP MUTAGENESIS.
RX MEDLINE=94253189; PubMed=8195247;
RA Zhang Y.J., Rutledge B.J., Rollins B.J.;
RT "Structure/activity analysis of human monocyte chemoattractant
RT protein-1 (MCP-1) by mutagenesis. Identification of a mutated protein
RT that inhibits MCP-1 mediated monocyte chemotaxis.";
RL J. Biol. Chem. 269:15918-15924 (1994).
[20]
RP SUBUNIT.
RX MEDLINE=97053697; PubMed=8898111; DOI=10.1016/0014-5793(96)01024-1;
RA Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;
RT "Structural characterization of a monomeric chemokine: monocyte
RT chemoattractant protein-3.";
RL FEBS Lett. 395:277-282 (1996).
CC -1- FUNCTION: Chemotactic factor that attracts monocytes and basophils
CC but not neutrophils or eosinophils. Augments monocyte anti-tumor
CC activity. Has been implicated in the pathogenesis of diseases
CC characterized by monocyte infiltrates, like psoriasis, rheumatoid
CC arthritis or atherosclerosis. May be involved in the recruitment
CC of monocytes into the arterial wall during the disease process of
CC atherosclerosis. Binds to CCR2 and CCR4.

CC -1- SUBUNIT: Monomer or homodimer; in equilibrium.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: Processing at the N-terminus can regulate receptor and target
CC cell selectivity. Deletion of the N-terminal residue converts it
CC from an activator of basophil to an eosinophil chemoattractant.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ISVORLASRYRITSSK 16
DB 43 ISVORLASRYRITSSK 58
RESULT 2
CCL2_MACFA STANDARD; PRT; 99 AA.
ID CCL2_MACFA
AC P61274; Q9MYN4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
DE protein 1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=MCPI, SCYA2;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Studer C., Urfer R.;
RT "Cloning and expression of cynomolgus monkey chemoattractant protein-
RT 1.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Chemotactic factor that attracts monocytes and basophils
CC but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By
CC similarity).
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC EMBL; AF276081; AAF81899.1; -; mRNA.
CC HSSP; P13500; 1DOK.
DR SMC; P61274; 24-93.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Pyrilidone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 99 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By
FT similarity).
FT CARBOHYD 37 37 N-linked (GlcNAc...) (potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
FT SEQUENCE 99 AA; 11007 MW; 433CB98C64EE7A4F CRC64;

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 43 ISVQRLASYRRITSSK 58

RESULT 3

CCL2 MACMU CCL2 MACMU STANDARD; PRT; 99 AA.
AC P61275; Q9MNA4;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=MCPI, SCYA2;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Studer C., Urfer R.;
RT "Cloning and expression of rhesus monkey monocyte chemoattractant protein-1";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemotactic factor that attracts monocytes and basophils but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By similarity).
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.

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EMBL; AF255343; AAF67756.1; -; mRNA.
HSP; P13500; IDOX.
SMR; P61275; 24-93.
InterPro; IPR000827; CC_chemokine_sml.
InterPro; IPR001811; Chemokine IL8.
Pfam; PF00048; IL8; 1.
PRINTS; PR01721; FRACTALKINE.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
Pyrridone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 99 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By similarity).
FT CARBOHYD 37 37 N-linked (GlcNAc...) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 11007 MW; 433CB88C64EE7A4F CRC64;

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 43 ISVQRLASYRRITSSK 58

RESULT 4

CCL2 PONPY CCL2 PONPY STANDARD; PRT; 99 AA.
AC OSRA36;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2).
GN Name=CCL2;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC The German cDNA consortium;
RG TISSUE=Kidney;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemotactic factor that attracts monocytes and basophils but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By similarity).
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.

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EMBL; CR859186; CAH91374.1; -; mRNA.
SMR; OSRA36; 24-94.
InterPro; IPR000827; CC_chemokine_sml.
InterPro; IPR001811; Chemokine IL8.
InterPro; IPR008097; Fractalkine.
Pfam; PF00048; IL8; 1.
PRINTS; PR01721; FRACTALKINE.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
Pyrridone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 99 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By similarity).
FT CARBOHYD 37 37 N-linked (GlcNAc...) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 11015 MW; 45FCA8CC64FF8A4F CRC64;

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 43 ISVQRLASYRRITSSK 58

RESULT 5

O6XVNS MACNE O6XVNS MACNE PRELIMINARY; PRT; 99 AA.
AC O6XVNS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Monocyte chemoattractant protein-1.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecoidea; Macaca.

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OX NCBI_TaxID=9545;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Coleman G.D., Clements J.E., Zink M.C.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY206692; AAOS2733.1; -; mRNA.
DR HSSP; P78423; 1B2T.
DR SMR; Q6XVNS; 24-93.
DR GO; GO:000576; C:extracellular region; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC:chemokine IEA.
DR InterPro; IPR001811; Chemokine IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
SQ SEQUENCE 99 AA; 11007 MW; 433CB88C64EE7A4F CRC64;

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
Db |||||
43 ISVQRLASYRRITSSK 58

RESULT 6
Q71ME7 MACMU
ID Q71ME7 MACMU PRELIMINARY; PRT; 99 AA.
AC Q71ME7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Chemokine CCL2/MCP-1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RX Baev S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXCL,
RT and CX3C families of chemokines.";
RL Cytokine 18:140-148(2002).
DR EMBL; AF449265; AAN76069.1; -; mRNA.
SQ SEQUENCE 99 AA; 11007 MW; 433CB88C64EE7A4F CRC64;

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 5.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
Db |||||
43 ISVQRLASYRRITSSK 58

RESULT 7
CCL2 CANPA
ID CCL2 CANPA STANDARD; PRT; 101 AA.
AC P52203;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant
protein 1) (MCP-1) (Monocyte chemoattractant protein 1).

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GN Name=CCL2; Synonyms=MCP1, SCYA2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
RN [1]_TaxID=9615;
RX NCBI_TaxID=9615;
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Jugular vein endothelial;
RX MEDLINE=97176620; PubMed=9024159;
RA Kumar A.G., Ballantyne C.M., Michael L.H., Kukielka G.L., Youker K.A.,
RA Lindsley M.L., Hawkins H.K., Birdsall H.H., Mackay C.R., Larosa G.J.,
RA Rossen R.D., Smith C.W., Bateman M.L.;
RT "Induction of monocyte chemoattractant protein-1 in the small veins of
RT the ischemic and reperused canine myocardium.";
RL Circulation 95:693-700(1997).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils. Important factor in the course of the inflammatory
CC reaction to reperfusion of the previously ischemic myocardium. May
CC play a significant role in monocyte trafficking into the
CC reperused myocardium.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Endothelium of small veins and intrafascicular
CC veins, and infiltrating leukocytes.
CC -!- INDUCTION: By TNF-alpha.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U29653; AAA84911.1; -; mRNA.
DR HSSP; P13500; 1DOM.
DR SMR; P52203; 24-94.
DR Ensembl; ENSCAFG00000018349; Canis familiaris.
DR InterPro; IPR000827; CC:chemokine sm1.
DR InterPro; IPR001811; Chemokine IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR PROSITE; PS00472; SMALL_CYTOKINES CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response;
KW Pyroglutamate carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 101 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyroglutamate carboxylic acid (By
FT similarity).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 101 AA; 11121 MW; CDD7E2B1901A7267 CRC64;

Query Match 93.2%; Score 68; DB 1; Length 101;
Best Local Similarity 81.2%; Pred. No. 5.4e-05;
Matches 13; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
Db |||||
43 ISVQRLASYRRITSSK 58

RESULT 8
MCPB BOVIN
ID MCPB BOVIN STANDARD; PRT; 74 AA.
AC P80343;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Monocyte chemoattractant protein 1B (MCP-1B) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=95034774; PubMed=7947749;
RA Proost P., Wuyts A., Lenaerts J.-P., van Damme J.;
RT "Purification, sequence analysis, and biological characterization of a
second bovine monocyte chemoattractant protein-1 (Bo MCP-1B).";
RL Biochemistry 33:13406-13412(1994).
CC -1- FUNCTION: Chemoattractant factor that attracts monocytes, but not
neutrophils. Augments monocyte anti-tumor activity. Also induces
the release of gelatinase B. This protein can bind heparin.
CC -1- PM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR HSSP; P13500; 1DOK.
DR SMR; P80343; 1-68.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
DR Chemotaxis; Cytokine; direct protein sequencing; Heparin-binding;
KW Sensory transduction.
FT DISULFID 9 34 By similarity.
FT DISULFID 10 50 By similarity.
FT NON_TER 1 1
SQ SEQUENCE 74 AA; 8363 MW; FAAF72B970EB16E3 CRC64;

Query Match 87.7%; Score 64; DB 1; Length 74;
Best Local Similarity 81.2%; Pred. No. 0.00023;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ISVORLASVRRITSSK 16
DB 18 ISMQRLMSVRRITSSK 33
|||:|||||:|||||

RESULT 9
Q9TTS6 BOVIN PRELIMINARY; PRT; 97 AA.
AC Q9TTS6;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Eotaxin.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Vogel B., Klinder A., Sittig D., Aust G.;
RT "Bovine eotaxin (CCL11) - an unusual member of the eotaxin group -
attracts eosinophils in vitro but is not responsible for eosinophilia
in the ovary.";
RL Vet. Immunol. Immunopathol. 107:67-77(2005).
DR EMBL; AJ132003; CAB61617.1; -; mRNA.
DR HSSP; P51671; 1EOT.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.

DR SMART; SM00199; SCY; 1.
SQ SEQUENCE 97 AA; 10965 MW; 9E65F23E1DDEB743 CRC64;
Query Match 87.7%; Score 64; DB 2; Length 97;
Best Local Similarity 81.2%; Pred. No. 0.00031;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 ISVORLASVRRITSSK 16
DB 41 ISIQLQSYRKITSSK 56
|||:|||||:|||||

RESULT 10
CCL2_PIG STANDARD; PRT; 99 AA.
AC P42831;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1) (MCP-1) (MCP-1) (Monocyte chemoattractant protein 1).
DE Name=CCL2; Synonyms=SCYA2;
GN Sus scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OX Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94183284; PubMed=7510962;
RA Hosang K., Knoke I., Klaidiny J., Wempe P., Wuttke W., Scheit K.H.;
RT "Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): analysis by polymerase chain reaction and cDNA cloning.";
RL Biochem. Biophys. Res. Commun. 199:962-968(1994).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Zach O.R.P.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Chemoattractant factor that attracts monocytes, but not neutrophils.
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
DR EMBL; Z48479; CAA8370.1; -; mRNA.
DR EMBL; X79416; CAA55945.1; -; mRNA.
DR PIR; JC2136; JC2136.
DR HSSP; P13500; 1DOM.
DR SMR; P42831; 24-98.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response;
FT Pyridolone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 99 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyridolone carboxylic acid (By similarity).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 10976 MW; 4C0AC6278D4F0A09 CRC64;
Query Match 87.7%; Score 64; DB 1; Length 99;
Best Local Similarity 81.2%; Pred. No. 0.00032;

Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISVQRLASRYRRTSSK 16
||:|||||:|||||
Db 43 ISMQRLMSYRRVTSSK 58

RESULT 11

MCQA_BOVIN STANDARD; PRT; 99 AA.
AC P28291;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Monocyte chemotactic protein 1A precursor (MCP-1A) (MCP-1) (Acidic
seminal fluid protein).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Seminal plasma;
RX MEDLINE=92096117; PubMed=1721821;
RA Wempe F., Henschen A., Scheit K.H.;
RT "Gene expression and cDNA cloning identified a major basic protein
constituent of bovine seminal plasma as bovine monocyte-
chemoattractant protein-1 (MCP-1).";
RL DNA Cell Biol. 10:671-679 (1991).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Seminal plasma;
RX MEDLINE=92181448; PubMed=1543494;
RA Wempe F., Einspanier R., Scheit K.H.;
RT "Characterization by cDNA cloning of the mRNA of a new growth factor
from bovine seminal plasma: acidic seminal fluid protein.";
RL Biochem. Biophys. Res. Commun. 183:232-237 (1992).
RN [3]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94338337; PubMed=8060303;
RA Wempe F., Kuhlmann J.K., Scheit K.H.;
RT "Characterization of the bovine monocyte chemoattractant protein-1
gene.";
RL Biochem. Biophys. Res. Commun. 202:1272-1279 (1994).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
neutrophils.
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC
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removed.
CC
CC EMBL; L32659; AAA60956.1; -; Genomic_DNA.
DR EMBL; M84602; AAA30651.1; -; mRNA.
DR PIR; A39296; A39296.
DR HSSP; P13500; 1ML0.
DR SMR; P28291; 24-98.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Pyrralidone carboxylic acid;
KW Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 99 Monocyte chemotactic protein 1A.
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By
similarity).
FT DISULFID 34 59 By similarity.
FT FT 35 75 By similarity.

SQ SEQUENCE 99 AA; 11114 MW; 0FD79FC1AB0CB88 CRC64;

Query Match 83.6%; Score 61; DB 1; Length 99;
Best Local Similarity 75.0%; Pred. No. 0.0012;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ISVQRLASRYRRTSSK 16
||:|||||:|||||
Db 43 ISMQRLMSYRRVTSSK 58

RESULT 12

CCL11_HORSE STANDARD; PRT; 100 AA.
AC Q9TTQ4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Botaxin precursor (Small inducible cytokine A11) (CCL11).
GN Name=CCL11; Synonyms=SCYA11;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21061912; PubMed=11044560; DOI=10.1016/S0165-2427(00)00222-1;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
Collins M.E.;
RT "Cloning of equine chemokines eotaxin, monocyte chemoattractant
protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and
induction by IL-4 in dermal fibroblasts.";
RL Vet. Immunol. Immunopathol. 76:283-298 (2000).
CC -!- FUNCTION: In response to the presence of allergens, this protein
directly promotes the accumulation of eosinophils, a prominent
feature of allergic inflammatory reactions. Binds to CCR3 (By
similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC
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the European Bioinformatics Institute. There are no restrictions on its
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removed.
CC
CC EMBL; AJ251188; CAB61624.1; -; mRNA.
DR HSSP; P51671; 1EOT.
DR SMR; Q9TTQ4; 25-96.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 100 Eotaxin.
FT CARBOHYD 94 94 O-linked (GalNAc..) (By similarity).
FT DISULFID 32 57 By similarity.
FT DISULFID 33 73 By similarity.
SQ SEQUENCE 100 AA; 11247 MW; 11F08EC00E75D50B CRC64;

Query Match 82.2%; Score 60; DB 1; Length 100;
Best Local Similarity 81.2%; Pred. No. 0.0019;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ISVQRLASRYRRTSSK 16
||:|||||:|||||
Db 41 ISFQRLQSYRKITSK 56

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RESULT 13
CCL2_HORSE
ID_CCL2_HORSE STANDARD; PRT; 99 AA.
AC Q9TTQ3;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1).
DE protein 1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=MCP1, SCYA2;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=21061912; PubMed=11044560; DOI=10.1016/S0165-2427(00)00222-1;
RA Benarafa C., Cunningham F.M., Hamblin A.S., Horchov D.W.,
RA Collins M.E.;
RA "Cloning of equine chemokines eotaxin, monocyte chemoattractant protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and induction by IL-4 in dermal fibroblasts.";
RT Vet. Immunol. Immunopathol. 76:283-298(2000).
RL
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not neutrophils (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
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-----
DR EMBL; AJ251189; CAB61625.1; -; mRNA.
DR HSSP; P13500; 1DOM.
DR SMR; Q9TTQ3; 24-38.
DR InterPro; IPR000827; CC_chemokine_sml.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Inflammatory response;
KW Pyrolydione carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 99 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyrolydione carboxylic acid (By similarity).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 10790 MW; BA1448F79F3423D2 CRC64;

Query Match 80.8%; Score 59; DB 1; Length 99;
Best Local Similarity 75.0%; Pred No. 0.003;
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
||| ||| ||| ||| |||
Db 43 ISSQRLGSYKRVITSSK 58

RESULT 14
Q92318_CAVPO
ID Q92318_CAVPO PRELIMINARY; PRT; 97 AA.
AC Q92318;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Monocyte Chemoattractant Protein-3 (MCP-3).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC Hystriocognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RA Asano K., Nakamura M., Oguma T., Fukunaga K., Matsubara H.,
RA Ishizaka A., Yanaguchi K., Kanazawa M.;
RA Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB014340; BAA36456.1; -; mRNA.
DR HSSP; P51671; 1EOT.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 97 AA; 11159 MW; E1B9A17C165C2421 CRC64;

Query Match 78.1%; Score 57; DB 2; Length 97;
Best Local Similarity 81.2%; Pred. No. 0.0071;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
||| ||| ||| ||| |||
Db 41 IRVQRLSYRRITSSK 56

RESULT 15
CCL11_HUMAN
ID CCL11_HUMAN STANDARD; PRT; 97 AA.
AC P51671; P50877; Q92490; Q92491;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Eotaxin precursor (Small inducible cytokine A11) (CCL11) (Eosinophil chemotactic protein)-SCYA11;
DE Name=CCL11; Synonyms=SCYA11;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96181758; PubMed=8597956; DOI=10.1038/nm0496-449;
RA Garcia-Zepeda E.A., Rothenberg M.E., Ownbey T.R., Leder P.,
RA Luster A.D.;
RA "Human eotaxin is a specific chemoattractant for eosinophil cells and provides a new mechanism to explain tissue eosinophilia.";
RL Nat. Med. 2:449-456(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96189937; PubMed=8609214;
RA Ponath P.D., Qin S., Ringler D.J., Clark-Lewis I., Wang J., Kassam N.,
RA Smith H., Shi X., Gonzalo J.A., Newman W., Gutierrez-Ramos J.C.,
RA Mackay C.R.;
RA "Cloning of the human eosinophil chemoattractant, eotaxin. Expression, receptor binding, and functional properties suggest a mechanism for the selective recruitment of eosinophils.";
RL J. Clin. Invest. 97:604-612(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Small intestine;
RX MEDLINE=96205964; PubMed=8631813; DOI=10.1074/jbc.271.13.7725;
RA Kitaura M., Nakajima T., Imai T., Harada S., Combadiere C.,
RA Tiffany H.L., Murphy P.M., Yoshie O.;
RT Molecular cloning of human eotaxin, an eosinophil-selective CC chemokine, and identification of a specific eosinophil eotaxin receptor, CC chemokine receptor 3.;
RT

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RL J. Biol. Chem. 271:7725-7730(1996).
RN [4]
RP NUCLEOTIDE SEQUENCE, PROTEIN SEQUENCE OF 60-65 AND 75-88, AND
RP VARIANTS.
RC TISSUE=ForeSkin;
RX MEDLINE=96374440; PubMed=8780731; DOI=10.1006/bbrc.1996.1292;
RA Bartels J., Schluter C., Richter E., Noso N., Kulke R.,
RA Christophers E., Schroeder J.-M.;
RT "Human dermal fibroblasts express eotaxin: molecular cloning, mRNA
RT expression, and identification of eotaxin sequence variants";
RL Biochem. Biophys. Res. Commun. 225:1045-1051(1996).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=97312708; PubMed=9169149; DOI=10.1006/geno.1997.4656;
RA Garcia-Zepeda E.A., Rothenberg M.E., Weremowicz S., Sarafi M.N.,
RA Morton C.C., Luster A.D.;
RT "Genomic organization, complete sequence, and chromosomal location of
RT the gene for human eotaxin (SCYA11), an eosinophil-specific CC
RT chemokine";
RL Genomics 41:471-476(1997).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=97445071; PubMed=9299399; DOI=10.1006/bbrc.1997.7169;
RA Hein H., Schluter C., Kulke R., Christophers E., Schroeder J.-M.,
RA Bartels J.;
RT "Genomic organization, sequence, and transcriptional regulation of the
RT human eotaxin gene";
RL Biochem. Biophys. Res. Commun. 237:537-542(1997).
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.E., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP CARBOHYDRATE-LINKAGE SITE.
RC TISSUE=Blood;
RX MEDLINE=98237580; PubMed=9578468;
RA Noso N., Bartels J., Maillet A.I., Mochizuki M., Christophers E.,
RA Schroeder J.-M.;
RT "Delayed production of biologically active O-glycosylated forms of
RT human eotaxin by tumor-necrosis-factor-alpha-stimulated dermal
RT fibroblasts";
RL Eur. J. Biochem. 253:114-122(1998).
RN [9]
RP STRUCTURE BY NMR.
RX MEDLINE=98380469; PubMed=9712872; DOI=10.1074/jbc.273.35.22471;
RA Crump M.P., Rajarathnam K., Kim K.S., Clark-Lewis I., Sykes B.D.;
RT "Solution structure of eotaxin, a chemokine that selectively recruits
RT eosinophils in allergic inflammation";
RL J. Biol. Chem. 273:22471-22479(1998).
CC -I- FUNCTION: In response to the presence of allergens, this protein
CC directly promotes the accumulation of eosinophils, a prominent

CC feature of allergic inflammatory reactions. Binds to CCR3.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- INDUCTION: By TNF-alpha, interleukin-1 alpha and interferon gamma.
CC -I- PTM: O-linked glycan consists of a Gal-GalNAc disaccharide which
CC is modified with up to 2 sialic acid residues.
CC -I- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -I- DATABASE: NAME=RD Systems' cytokine source book: SCYA11;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=196".
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; U46573; AAA98957.1; -; mRNA.
CC EMBL; U34780; AAC50369.1; -; Genomic_DNA.
CC EMBL; D49372; BAA08370.1; -; mRNA.
CC EMBL; D69291; CAA93258.1; -; mRNA.
CC EMBL; Z75668; CAA99997.1; -; mRNA.
CC EMBL; Z75669; CAA99998.1; -; mRNA.
CC EMBL; U46572; AAC51297.1; -; Genomic_DNA.
CC EMBL; Z92709; CAB07027.1; -; Genomic_DNA.
CC EMBL; BC017850; AAH17850.1; -; mRNA.
CC PIR; JC4912; JC4912.
CC PDB; 1BOT; NMR; @=24-97.
CC PDB; 2BOT; NMR; @=24-97.
CC Ensembl; ENSG00000172156; Homo sapiens.
CC HGNC; HGNC:10610; CCL11.
CC H-InvDB; HIX0013715; -.
CC MIM; 601156; -.
CC GO; GO:0008009; F:chemokine activity; TAS.
CC GO; GO:0006874; P:calcium ion homeostasis; TAS.
CC GO; GO:0007155; P:cell adhesion; TAS.
CC GO; GO:0006935; P:chemotaxis; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0006488; P:protein amino acid phosphorylation; TAS.
CC GO; GO:0009334; P:response to radiation; TAS.
CC GO; GO:0009615; P:response to virus; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR000827; CC chemokine sm.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC PROSITE; PS00472; SMALL CYTOKINES CC; 1.
CC 3D-structure; Chemotaxis; Cytokine; Direct protein sequencing;
CC Glycoprotein; Inflammatory response; Polymorphism;
CC Sensory transduction; Signal.
CC
CC SIGNAL 1 23
CC CHAIN 24 97 Botaxin.
CC CARBOHYD 94 94 O-linked (GalNAc. .).
CC DISULFID 32 57
CC DISULFID 33 73
CC VARIANT 7 7
CC
CC L -> P (in clone 34).
CC /FTID=VAR_001634.
CC A -> T (in clone 53; dbSNP:3744508).
CC /FTID=VAR_001635.
CC R -> S (in clone 34).
CC /FTID=VAR_001636.
CC K -> R (in clone 53).
CC /FTID=VAR_001637.
CC
CC TURN 44 45
CC STRAND 46 52
CC STRAND 61 66
CC TURN 67 68
CC STRAND 71 74
CC TURN 76 77
CC TURN 79 91
CC HELIX 79 91
CC
CC SQ SEQUENCE 97 AA; 10732 MW; B433C30FDA4C71A7 CRC64;
CC
CC Query Match 76.7%; Score 56; DB 1; Length 97;
CC Best Local Similarity 75.0%; Pred. No. 0.011;
CC Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 ISVQRLASYRRITSSK 16
| : ||| ||||| |
Db 41 IPLQLRLESYRRITSSK 56

RESULT 16
Q619T4 HUMAN
ID Q619T4 HUMAN PRELIMINARY; PRT; 97 AA.
AC Q619T4
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE CCL11 protein.
GN Name=CCL11;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; CR457421; CAG33702.1; -; mRNA.
SQ SEQUENCE 97 AA; 10732 MW; B433C30FDA4C71A7 CRC64;

Query Match 76.7%; Score 56; DB 2; Length 97;
Best Local Similarity 75.0%; Pred. No. 0.011;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
| : ||| ||||| |
Db 41 IPLQLRLESYRRITSSK 56

RESULT 17
CCL2 RABIT
ID CCL2 RABIT STANDARD; PRT; 125 AA.
AC P28292;
DT 01-DEC-1992 (Rel. 24, Created)
DT 13-SEP-2005 (Rel. 24, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1) (MCP-1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=SCY22;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=New Zealand white; TISSUE=Spleen;
RX MEDLINE=91225489; PubMed=2026877;
RA Yoshimura T., Yuhki N.;
RT "Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein-1 in rabbit. CDNA cloning and their expression in spleen cells.";
RL J. Immunol. 146:3483-3488(1991).
CC -!- FUNCTION: Chemoattractant factor that attracts monocytes, but not neutrophils.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
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CC
CC EMBL; M57440; AAA31386.1; -; mRNA.
CC PIR; I46857; I46857.
```

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DR HSSP; P13500; IDOM.
DR SMR; P28292; 24-99.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Pyrrolidone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23
FT CHAIN 24 125
FT MOD_RES 24 24
FT CARBOHYD 40 40
FT CARBOHYD 55 55
FT CARBOHYD 112 112
FT DISULFID 34 59
FT DISULFID 35 75
SQ SEQUENCE 125 AA; 13776 MW; 24C3A542CB6A47EE CRC64;

Query Match 76.7%; Score 56; DB 1; Length 125;
Best Local Similarity 75.0%; Pred. No. 0.015;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSSK 16
| : ||| ||||| |
Db 43 ISVKRLMSYRRINSTK 58

RESULT 18
Q516F8 CANFA
ID Q516F8 CANFA PRELIMINARY; PRT; 99 AA.
AC Q516F8;
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
DE Monocyte chemoattractant protein 3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Peters I.R., Peeters D., Clercx C., Day M.J.;
RT "Identification of Coding Sequence of Canine MCP-3 (CCL-7).";
RL Submitted (DEC-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY849795; AAW34061.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC_chemokine_sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SQ SEQUENCE 99 AA; 11256 MW; 48A5B4A7932DEEC9 CRC64;

Query Match 74.0%; Score 54; DB 2; Length 99;
Best Local Similarity 73.3%; Pred. No. 0.028;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ISVQRLASYRRITSS 15
| : ||| ||||| |
Db 43 IPIQKLKSYRRITSS 57

RESULT 19
CCL11 CAVPO
ID CCL11 CAVPO STANDARD; PRT; 96 AA.
AC P80325;
DT 01-JUN-1994 (Rel. 29, Created)
```

01-OCT-1996 (Rel. 34, Last sequence update)
 10-MAY-2005 (Rel. 47, Last annotation update)
 Eotaxin precursor (Small inducible cytokine A11) (CCL11) (Eosinophil chemotactic protein)
 Name=CCL11; Synonyms=SCV11;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Hystriognathi; Caviidae; Cavia.
 NCBI_TaxID=10141;
 (1)
 NUCLEOTIDE SEQUENCE.
 TISSUE=Lung;
 MEDLINE=95173589; PubMed=7869037; DOI=10.1084/jem.181.3.1211;
 RA Rothenberg M.E., Luster A.D., Lilly C.M., Drazen J.M., Leder P.;
 RT "Constitutive and allergen-induced expression of eotaxin mRNA in the guinea pig lung.";
 RL J. Exp. Med. 181:1211-1216 (1995).
 (2)
 NUCLEOTIDE SEQUENCE.
 MEDLINE=95091818; PubMed=7999113;
 RA Jose P.J., Adcock I.M., Griffiths-Johnson D.A., Berkman N., Wells T.C., Williams T.J., Power C.A.;
 RT "Eotaxin: cloning of an eosinophil chemoattractant cytokine and increased mRNA expression in allergen-challenged guinea-pig lungs.";
 RL Biochem. Biophys. Res. Commun. 205:788-794 (1994).
 (3)
 PROTEIN SEQUENCE OF 24-96.
 STRAIN=Hartley; TISSUE=Lung;
 MEDLINE=94157409; PubMed=7509365; DOI=10.1084/jem.179.3.881;
 RA Jose P.J., Griffiths-Johnson D.A., Collins P.D., Walsh D.T., Moser R., Totty N.P., Truong O., Huan J.J., Williams T.J.;
 RT "Eotaxin: a potent eosinophil chemoattractant cytokine detected in a guinea pig model of allergic airways inflammation.";
 RL J. Exp. Med. 179:881-887 (1994).
 CC -I- FUNCTION: In response to the presence of allergens, this protein directly promotes the accumulation of eosinophils, a prominent feature of allergic inflammatory reactions.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- TISSUE SPECIFICITY: Lung.
 CC -I- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
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 CC -----
 DR EMBL; U18941; AAC52180.1; -; mRNA.
 DR EMBL; X77603; CAA54698.1; -; mRNA.
 DR PIR; I48099; I48099.
 DR HSP; P51671; 180T.
 DR InterPro; IPR000827; CC chemokine sm1.
 DR InterPro; IPR001811; Chemokine_IL8.
 DR Pfam; PF00048; IL8; 1.
 DR SMART; SM00199; SCY; 1.
 DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
 DR Chemotaxis; Cytokine; Direct protein sequencing; Glycoprotein;
 KW Inflammatory response; Sensory transduction; Signal.
 FT SIGNAL 1 23
 FT CHAIN 24 96 Eotaxin.
 FT CARBOHYD 93 93 O-linked (Potential).
 FT DISULFID 31 56 By similarity.
 FT DISULFID 32 72 By similarity.
 FT CONFLICT 88 88 D -> G (in Ref. 2).
 SQ SEQUENCE 96 AA; 10753 MW; 62C856645BC6AC99 CRC64;
 Query Match 71.2%; Score 52; DB 1; Length 96;
 Best Local Similarity 75.0%; Pred. No. 0.066;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 || ||| ||: |||||

Qy

Db 40 ISFORLKSXYKIITSSK 55
 RESULT 20
 CCL12 MOUSE
 ID CCL12 MOUSE STANDARD; PRT; 104 AA.
 AC Q62401; O9QVD6;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Small inducible cytokine A12 precursor (CCL12 protein 5) (MCP-5) (MCP-1-related chemokine).
 DE Name=CCL12; Synonyms=Mcp5, Scyal2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 (1)
 NUCLEOTIDE SEQUENCE.
 MEDLINE=97079149; PubMed=8920881; DOI=10.1084/jem.184.5.1939;
 RA Jia G.-Q., Gonzalo J.A., Lloyd C., Kremer L., Lu L., Martinez A.C., Wershil B.K., Gutierrez-Ramos J.C.;
 RT "Distinct expression and function of the novel mouse chemokine monocyte chemotactic protein-5 in lung allergic inflammation.";
 RL J. Exp. Med. 184:1939-1951 (1996).
 (2)
 NUCLEOTIDE SEQUENCE.
 MEDLINE=97149438; PubMed=8996246; DOI=10.1084/jem.185.1.99;
 RA Sarafi M.N., Garcia-Zepeda E.A., McLean J.A., Charo I.F., Luster A.D.;
 RT "Murine monocyte chemoattractant protein (MCP)-5: a novel CC chemokine that is a structural and functional homologue of human MCP-1.";
 RL J. Exp. Med. 185:99-109 (1997).
 (3)
 NUCLEOTIDE SEQUENCE.
 STRAIN=B10.S/J, BALB/c, DBA/2J, NOD/LtJ, and SJL/J; TISSUE=Spleen;
 MEDLINE=99370037; PubMed=10438970;
 RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.P., Doerge R.W., Blankenhorn E.P.;
 RT "Sequence polymorphisms in the chemokines Scyal (TCA-3), Scyal2 (monocyte chemoattractant protein (MCP)-1), and Scyal2 (MCP-5) are candidates for eae7, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis.";
 RL J. Immunol. 163:2262-2266 (1999).
 (4)
 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 TISSUE=Mammary gland;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Iqbalano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -I- FUNCTION: Chemotactic factor that attracts eosinophils, monocytes, and lymphocytes but not neutrophils. Potent monocyte active chemokine that signals through CCR2. Involved in allergic inflammation and the host response to pathogens and may play a pivotal role during early stages of allergic lung inflammation.
 CC

RA Zhang L., Soares M.P., Guan Y., Sirotina-Meisher A.,
RA Matheravidathu S., Iliff S.A., Mudgett J.S., Springer M.S.,
RA Daugherty B.L.,
RT "Molecular cloning of eotaxin/CC111 and CCR3 from rhesus monkey.
RT Functional expression and characterization of rhesus monkey CCR3 in
RT murine Li-2 cells; generation of antibodies against rhesus CCR3.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: In response to the presence of allergens, this protein
CC directly promotes the accumulation of eosinophils, a prominent
CC feature of allergic inflammatory reactions. Binds to CCR3 (By
CC similarity).
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
CC
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL: AY049019; AAL13086.1; -; mRNA.
CC SMR: Q8MT77; 24-97.
CC InterPro: IPR000827; CC_chemkine_sml.
CC InterPro: IPR001811; Chemokine_IL8.
CC Pfam: PF00048; IL8; 1.
CC SMART: SM00199; SCY; 1.
CC PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
CC Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 97 Eotaxin.
FT CARBOHYD 94 94 O-linked (GalNAc...) (By similarity).
FT DISULFID 32 57 By similarity.
FT DISULFID 33 73 By similarity.
SQ SEQUENCE 97 AA; 10855 MW; 9BCA0FD6D95B02DD CRC64;

Query Match 68.5%; Score 50; DB 1; Length 97;
Best Local Similarity 68.8%; Pred. No. 0.16;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| : ||| ||||| |
Db 41 IPLQRLSYRRITSSK 56
| : ||| ||||| |

RESULT 25
Q8HXZ5 MACMU PRELIMINARY; PRT; 97 AA.
AC Q8HXZ5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine CC111/EOTAXIN.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OK NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
RA Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
RT chemokine cDNAs reveals evolutionary conservation among C, CC, CXCL,
RT and CX3C families of chemokines.";
RL Cytochrome 18:140-148(2002).
DR EMBL: AF449270; AAN76074.1; -; mRNA.
DR HSSP: P51671; 1EOT.
DR SMR: Q8HXZ5; 24-97.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0008009; F:chemokine activity; IEA.
DR GO: GO:0006935; P:chemotaxis; IEA.
DR GO: GO:0006955; P:immune response; IEA.

DR InterPro: IPR000827; CC_chemkine_sml.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 97 AA; 10795 MW; EDUCD4B2860A47C9 CRC64;

Query Match 68.5%; Score 50; DB 2; Length 97;
Best Local Similarity 68.8%; Pred. No. 0.16;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| : ||| ||||| |
Db 41 IPLQRLSYRRITSSK 56
| : ||| ||||| |

RESULT 26
Q9Z292_9RODE PRELIMINARY; PRT; 106 AA.
AC Q9Z292;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Monocyte chemoattractant protein 1 (fragment).
OS Cricetulus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Cricetinae; Cricetulus.
OK NCBI_TaxID=10031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bachtrati C.Z., Downes S., Raske I.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081141; AAD03677.1; -; mRNA.
DR HSSP: P13500; 1ML0.
DR GO: GO:0005576; C:extracellular region; IEA.
DR GO: GO:0008009; F:chemokine activity; IEA.
DR GO: GO:0006955; P:immune response; IEA.
DR InterPro: IPR001811; Chemokine_IL8.
DR Pfam: PF00048; IL8; 1.
DR SMART: SM00199; SCY; 1.
FT NON_TER 1
SQ SEQUENCE 106 AA; 11876 MW; 3F670AE9F360355A CRC64;

Query Match 68.5%; Score 50; DB 2; Length 106;
Best Local Similarity 68.8%; Pred. No. 0.18;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| : ||| ||||| |
Db 7 IPEKRLSYRRITSSK 22
| : ||| ||||| |

RESULT 27
Q8CGM5 SIGHI PRELIMINARY; PRT; 150 AA.
ID Q8CGM5 SIGHI PRELIMINARY; PRT; 150 AA.
AC Q8CGM5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monocyte chemoattractant protein-1.
GN Name=MCP-1/JE;
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Sigmodontinae; Sigmodon.
OK NCBI_TaxID=42415;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14980081; DOI=10.1089/10799900477219873;
RA Blanco J.C., Pletneva L., Boukhvalova M., Richardson J.Y.,
RA Harris K.A., Prince G.A.;
RT "The cotton rat: an underutilized animal model for human infectious

RX MEDLINE=89093129; PubMed=2910858;
RA Kawahara R.S., Devel T.P.;
RT "Platelet-derived growth factor-inducible gene JE is a member of a
RT family of small inducible genes related to platelet factor 4.";
RL J. Biol. Chem. 264:679-682(1989).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89234501; PubMed=3287374;
RA Rollins B.J., Morrison E.D., Stiles C.D.;
RT "Cloning and expression of JE, a gene inducible by platelet-derived
RT growth factor and whose product has cytokine-like properties.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:3738-3742(1988).
RN [3]
RP NUCLEOTIDE SEQUENCE, AND VARIANTS GLY-50 AND GLN-92.
RC STRAIN=B10.S/J, BALB/C, DBA/2J, NOD/LtJ, and SJL/J, TISSUE=Spleen;
RX MEDLINE=99370037; PubMed=10438970;
RA Teuscher C., Butterfield R.J., Ma R.Z., Zachary J.F., Doerge R.W.,
RA Blankenhorn E.P.;
RT "Sequence polymorphisms in the chemokines Scya1 (TCA-3), Scya2
RT (monocyte chemoattractant protein (MCP)-1), and Scya12 (MCP-5) are
RT candidates for eae7, a locus controlling susceptibility to monophasic
RT remitting/nonrelapsing experimental allergic encephalomyelitis.";
RL J. Immunol. 163:2262-2266(1999).
RN [4]
RP PROTEIN SEQUENCE OF 26-42.
RX MEDLINE=91293127; PubMed=2065676;
RA van Damme J.J., Decock B., Bertini R., Conings R., Lenaerts J.-P.,
RA Put W., Opendakker G., Mantovani A.;
RT "Production and identification of natural monocyte chemotactic protein
RT from virally infected murine fibroblasts. Relationship with the
RT product of the mouse competence (JE) gene.";
RL Eur. J. Biochem. 199:223-229(1991).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes, but not
CC neutrophils.
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- INDUCTION: By platelet-derived growth factor.
CC -!- POLYMORPHISM: The polymorphisms in strain SJL/J may be associated
CC with severity of clinical symptoms of experimental allergic
CC encephalomyelitis, an animal model of multiple sclerosis, and
CC susceptibility to the monophasic remitting/nonrelapsing form of
CC the disease.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC EMBL; J04467; AAA37685.1; -; Genomic DNA.
CC EMBL; M19681; AAA37684.1; -; Genomic DNA.
CC EMBL; AF065929; AAF15379.1; -; mRNA.
CC EMBL; AF065930; AAF15380.1; -; mRNA.
CC EMBL; AF065931; AAF15381.1; -; mRNA.
CC EMBL; AF065932; AAF15382.1; -; mRNA.
CC EMBL; AF065933; AAF15383.1; -; mRNA.
CC F01; A30209; A30209.
CC F01; S16226; S16226.
CC HSSP; P13500; IDOK.
CC Ensembl; ENSMUSG00000035385; Mus musculus.
CC MGI; MGI:98259; Ccl2.
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0001664; F:G-protein-coupled receptor binding; IDA.
CC GO; GO:0005515; F:protein binding; IDA.
CC InterPro; IPR000827; CC chemokine sm1.
CC InterPro; IPR001811; Chemokine_IL8.
CC Pfam; PF00048; IL8; 1.
CC SMART; SM00199; SCY; 1.
CC PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
CC Chemotaxis; Cytokine; Direct protein sequencing; Glycoprotein;
KW Inflammatory response; Polymorphism; Pyrrolidone carboxylic acid;
KW Sensory transduction; Signal.

FT SIGNAL 1 23 By similarity.
FT CHAIN 24 148 Small inducible cytokine A2.
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By
FT similarity).
FT CARBOHYD 126 126 N-linked (GlcNAc...) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
FT VARIANT 50 50 S -> G (in strain SJL/J).
FT VARIANT 92 92 R -> Q (in strain SJL/J).
SQ SEQUENCE 148 AA; 16326 MW; 29A5505FC6D94837 CRC64;
Query Match 67.1%; Score 49; DB 1; Length 148;
Best Local Similarity 62.5%; Pred. No. 0.42;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ISVORLASYYRITSSK 16
| : ||| : ||| : ||| :
Db 43 IPMSRLSEYKRITSSR 58
RESULT 31
Q5SVU3_MOUSE PRELIMINARY; PRT; 148 AA.
ID Q5SVU3_MOUSE
AC Q5SVU3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Chemokine (C-C motif) ligand 2 (Ccl2 protein).
GN Name=Ccl2; ORFName=RP23-350GL.3-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Whitehead S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE
RA Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
RA Mollenhauer J., Wiemann S., Schick M., Korn B.;
RT "Cloning of mouse full open reading frames in Gateway(R) system entry
RT vector (pDONR201)." ;
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL626807; CA125305.1; -; Genomic DNA.
DR EMBL; CT010187; CA18395.1; -; mRNA.
DR Ensembl; ENSMUSG00000035385; Mus musculus.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 148 AA; 16326 MW; 29A5505FC6D94837 CRC64;
Query Match 67.1%; Score 49; DB 2; Length 148;
Best Local Similarity 62.5%; Pred. No. 0.42;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 ISVORLASYYRITSSK 16
| : ||| : ||| : ||| :
Db 43 IPMSRLSEYKRITSSR 58
RESULT 32
Q5MKC8_HORSE PRELIMINARY; PRT; 99 AA.
ID Q5MKC8_HORSE
AC Q5MKC8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE MCP-2. Equus caballus (Horse).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.

OX NCBI_TaxID=9796;

RN [1]_TaxID=9796;

RP NUCLEOTIDE SEQUENCE.

RA Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF506972; AAM34214.1; -; mRNA.

DR HSSP; P80075; 1ESR.

DR GO; GO:0005576; C:extracellular region; IEA.

DR GO; GO:0008009; F:chemokine activity; IEA.

DR GO; GO:0008955; P:immune response; IEA.

DR InterPro; IPR001811; Chemokine_IL8.

DR Pfam; PF00048; IL8; 1.

DR SMART; SM00199; SCY; 1.

SQ SEQUENCE 99 AA; 11028 MW; 94F5D8E540889228 CRC64;

Query Match 65.8%; Score 48; DB 2; Length 99;

Best Local Similarity 56.2%; Pred. NO. 0.41;

Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ISVQLASVRRITSSK 16

DB 43 VPIQRVESYTRITSSQ 58

RESULT 33

CCL7_HUMAN

ID CCL7_HUMAN STANDARD; PRT; 99 AA.

AC P80098;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Small inducible cytokine A7 precursor (CCL7) (Monocyte chemoattractant protein 3) (MCP-3) (MCP-3) (Monocyte chemoattractant protein 3) (NC28).

GN Name=CCL7; Synonyms=MCP3, SCYA7;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RP [1]

RN NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 31-67 AND 71-99.

RA MEDLINE=93213290; PubMed=8461011;

RA Opdenakker G., Froyen G., Fiten P., Proost P., van Damme J.;

RT "Human monocyte chemoattractant protein-3 (MCP-3): molecular cloning of the cDNA and comparison with other chemokines.";

RL Biochem. Biophys. Res. Commun. 191:535-542(1993).

RN [2]

RP NUCLEOTIDE SEQUENCE.

EX MEDLINE=94375065; PubMed=7916328;

RA Opdenakker G., Fiten P., Nys G., Froyen G., van Roy N., Speleman F., Laureys G., van Damme J.;

RA "The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the C-C chemokine gene cluster on chromosome 17q11.2-q12.";

RT Eur. Cytokine Netw. 4:99-110(1993).

RL Genomics 21:403-408(1994).

RN [3]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=93305913; PubMed=8318676;

RA Minty A., Chalou P., Guillemot J.C., Kaghad M., Liauzun P., Magazin M., Miloux B., Miny C., Ramond P., Vita N., Lupker J., Shire D., Ferrara P., Caput D.;

RA "Molecular cloning of the MCP-3 chemokine gene and regulation of its expression.";

RT Eur. Cytokine Netw. 4:99-110(1993).

RL Eur. Cytokine Netw. 4:99-110(1993).

RN [4]

RP NUCLEOTIDE SEQUENCE OF 24-99.

RA Jang J.S., Kim B.E.;

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [5]

RP PROTEIN SEQUENCE OF 30-99.

RC TISSUE=Osteosarcoma;

RX MEDLINE=92308855; PubMed=16133466; DOI=10.1084/jem.176.1.59;

RA van Damme J., Proost P., Lenaerts J.-P., Opdenakker G.;

RT "Structural and functional identification of two human, tumor-derived monocyte chemoattractant proteins (MCP-2 and MCP-3) belonging to the chemokine family.";

RT J. Exp. Med. 176:59-65(1992).

RL [6]

RN PROTEIN SEQUENCE OF 24-38.

RX PubMed=15340161; DOI=10.1110/ps.04682504;

RA Zhang Z., Hensel W.J.;

RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites.";

RL Protein Sci. 13:2819-2824(2004).

RN [7]

RP STRUCTURE BY NMR, AND SUBUNIT.

RX MEDLINE=97053697; PubMed=8898111; DOI=10.1016/0014-5793(96)01024-1;

RA Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;

RT "Structural characterization of a monomeric chemokine: monocyte chemoattractant protein-3.";

RL FEBS Lett. 395:277-282(1996).

RN [8]

RP STRUCTURE BY NMR.

RX MEDLINE=97263733; PubMed=9109648; DOI=10.1021/bi9627929;

RA Meunier S., Bernassau J.-M., Guillemot J.-C., Ferrara P., Darbon H.;

RT "Determination of the three-dimensional structure of CC chemokine monocyte chemoattractant protein 3 by 1H two-dimensional NMR spectroscopy.";

RL Biochemistry 36:4412-4422(1997).

RN [9]

RP STRUCTURE BY NMR.

RA Kwon D., Lee D., Sykes B.D., Kim K.-S.;

RL Submitted (AUG-1998) to the PDB data bank.

CC -!- FUNCTION: Chemotactic factor that attracts monocytes and eosinophils, but not neutrophils. Augments monocyte anti-tumor activity. Also induces the release of gelatinase B. This protein can bind heparin. Binds to CCR1, CCR2 and CCR3.

CC -!- SUBUNIT: Monomer.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- PTM: O-glycosylated.

CC -!- SIMILARITY: Belongs to the interzine beta (chemokine CC) family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC EMBL; X72308; CAA51055.1; ALT INIT; mRNA.

DR EMBL; X72309; -; NOT ANNOTATED CDS; Genomic_DNA.

DR EMBL; X71087; CAA50407.1; -; mRNA.

DR EMBL; X71087; CAA50406.1; ALT INIT; mRNA.

DR EMBL; X71087; CAA50405.1; ALT INIT; mRNA.

DR EMBL; AF043338; AAC03538.1; -; mRNA.

DR PDB; 1BOO; NMR; @=24-99.

DR PDB; 1NCV; NMR; A/B=24-99.

DR Ensembl; ENSG00000108688; Homo sapiens.

DR HGNC; HGNC:10634; CCL7.

DR MIM; 158106; -.

DR GO; GO:0005615; C:extracellular space; TAS.

DR GO; GO:0008009; F:chemokine activity; TAS.

DR GO; GO:0006874; P:calcium ion homeostasis; TAS.

DR GO; GO:0007267; P:cell-cell signaling; TAS.

DR GO; GO:0006935; P:chemotaxis; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

DR InterPro; IPR000827; CC chemokine sm1.

DR InterPro; IPR001811; Chemokine_IL8.

DR Pfam; PF00048; IL8; 1.

DR SMART; SM00199; SCY; 1.

DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.

KW 3D-structure; Chemotaxis; Cytokine; Direct protein sequencing;

KW Glycoprotein; Heparin-binding; Inflammatory response;
KW Pyroglutamate carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23
FT CHAIN 24 99
FT MOD RES 24 24 Small inducible cytokine A7.
FT CARBOHYD 29 29 Pyroglutamate carboxylic acid.
FT DISULFID 34 59 N-linked (GlcNAc...) (Potential).
FT DISULFID 35 75
FT CONFLICT 30 30
FT CONFLICT 68 70
FT TURN 45 47
FT TURN 45 47
FT STRAND 48 53
FT TURN 56 58
FT STRAND 64 68
FT TURN 69 70
FT STRAND 73 76
FT TURN 78 79
FT HELIX 81 91
SQ SEQUENCE 99 AA; 11200 MW; 96048B371C25D00E CRC64;

Query Match 64.4%; Score 47; DB 1; Length 99;
Best Local Similarity 73.3%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVQRLASRYRRTSS 15
| | | | | | | | | |
Db 43 IPKQRLSYRRTSS 57

RESULT 34
Q569J6 HUMAN PRELIMINARY; PRT; 99 AA.
AC Q569J6; 23
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Chemokine (C-C motif) ligand 7.
GN Name=CCL7;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092436; AAH92436.1; -; mRNA.

SQ SEQUENCE 99 AA; 11200 MW; 96048B371C25D00E CRC64;
Query Match 64.4%; Score 47; DB 2; Length 99;
Best Local Similarity 73.3%; Pred. No. 0.65;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ISVQRLASRYRRTSS 15
| | | | | | | | | |
Db 43 IPKQRLSYRRTSS 57
RESULT 35
Q7Z7Q8 HUMAN PRELIMINARY; PRT; 109 AA.
AC Q7Z7Q8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Monocyte chemotactic protein-3.
GN Name=MCP-3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94375065; PubMed=7916328;
RA Opdenakker G., Fiten P., Nys G., Froyen G., van Roy N., Speleman F.,
RA Laureys G., van Damme J.;
RT "The human MCP-3 gene (SCYA7): cloning, sequence analysis, and
RT assignment to the C-C chemokine gene cluster on chromosome 17q11.2-
RT Q12."
RL Genomics 21:403-408(1994).
DR EMBL; X72309; CAB59723.1; -; Genomic_DNA.
DR HSSP; P80098; 1B00.
DR SMR; Q7Z7Q8; 34-109.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; F:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006935; P:immune response; IEA.
DR InterPro; IPR000827; CC chemokine smi.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 109 AA; 12356 MW; 63980669F0A2157D CRC64;

Query Match 64.4%; Score 47; DB 2; Length 109;
Best Local Similarity 73.3%; Pred. No. 0.72;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ISVQRLASRYRRTSS 15
| | | | | | | | | |
Db 53 IPKQRLSYRRTSS 67
RESULT 36
Q9BG83 PONPY PRELIMINARY; PRT; 44 AA.
AC Q9BG83;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Monocyte chemotactic protein 1 (Fragment).
GN Name=MCP1;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

RA Avi T.C., Chew X.L.A., Yap P.H.E.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF324463; AAKJ3442.1; -; mRNA.
DR HSSP; P13500; 1DOK.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
FT NON TER 1 1
FT NON TER 44 44
SQ SEQUENCE 44 AA; 4830 MW; 1DE3C10EB83CD190 CRC64;

Query Match 63.0%; Score 46; DB 2; Length 44;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ISVQLASVYR 10
|:|||||
DB 35 ISVQLASVYR 44

RESULT 37
Q865F4_MACNE PRELIMINARY; PRT; 99 AA.
ID Q865F4;
AC Q865F4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Monocyte chemoattractant protein-2.
OS Macaca nemestrina (pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinæ; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Coleman G.D., Clements J.E., Zink M.C.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY206693; AAO52734.1; -; mRNA.
DR HSSP; P80075; 1ESR.
DR SMR; O865F4; 24-99.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR00827; CC chemokine sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRCTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 99 AA; 11261 MW; 9D6797974A88B9BF CRC64;

Query Match 63.0%; Score 46; DB 2; Length 99;
Best Local Similarity 56.2%; Pred. No. 1;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ISVQLASVYRITSSK 16
|:|||||
DB 43 IPIQLQSYTRITNTQ 58

RESULT 38
Q8HYQ0_MACMU PRELIMINARY; PRT; 99 AA.
ID Q8HYQ0;
AC Q8HYQ0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Chemokine CCL8/MCP-2.

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OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheidae; Cercopithecinæ; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22123042; PubMed=12126650; DOI=10.1006/cyto.2002.0875;
Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
RT "Molecular cloning and sequencing of 25 different rhesus macaque
chemokine cDNAs reveals evolutionary conservation among C, CC, CXC,
RT and CX3C families of chemokines.";
RL Cytokine 18:140-148(2002).
DR EMBL; AF449269; AAN76073.1; -; mRNA.
DR HSSP; P80075; 1ESR.
DR SMR; Q8HYQ0; 24-99.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008009; P:chemokine activity; IEA.
DR GO; GO:0006935; P:chemotaxis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR00827; CC chemokine sml.
DR InterPro; IPR001811; Chemokine_IL8.
DR InterPro; IPR008097; Fractalkine.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRCTALKINE.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
SQ SEQUENCE 99 AA; 11263 MW; 9D6797974A88B97F CRC64;

Query Match 63.0%; Score 46; DB 2; Length 99;
Best Local Similarity 56.2%; Pred. No. 1;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 ISVQLASVYRITSSK 16
|:|||||
DB 43 IPIQLQSYTRITNTQ 58

RESULT 39
CCL2_RAT STANDARD; PRT; 148 AA.
ID CCL2_RAT
AC P14844;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant
protein 1) (MCP-1) (Monocyte chemoattractant protein 1) (Immediate-
early serum-responsive JE protein).
DE Name=CCL2; Synonyms=Je, Mcp1, Scy2;
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WAG/RIJ; TISSUE=Kidney;
RX MEDLINE=90174947; PubMed=2106664;
Timmers H.T.M., Pronk G.J., Bos J.L., van der Eb A.J.;
RT "Analysis of the rat JE gene promoter identifies an AP-1 binding site
essential for basal expression but not for TPA induction.";
RL Nucleic Acids Res. 18:23-34(1990).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91128376; PubMed=1704226;
Yoshimura T., Takeya M., Takahashi K.;
RT "Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1)
and its expression in rat spleen cells and tumor cell lines.";
RL Biochem. Biophys. Res. Commun. 174:504-509(1991).
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, but not
neutrophils.
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).

```


Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lennard B., Lyons P.A.,
RA Maglott D.R., Maitala L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertele G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempole C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Vardaro R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imocani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
[8]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISSUE=Testis;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kravinsky M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Chemotactic factor that attracts monocytes and
CC eosinophils, but not neutrophils. Augments monocyte anti-tumor
CC activity (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL: Z12297; CAA78169.1; -; mRNA.
CC EMBL: L04694; AAA37516.1; -; mRNA.
CC EMBL: S71251; AAB30997.1; -; mRNA.
CC EMBL: X70058; CAA49662.1; -; Genomic_DNA.
CC EMBL: AF128193; AAF22534.1; -; mRNA.
CC EMBL: AF128194; AAF22535.1; -; mRNA.
CC EMBL: AK078827; BAC37413.1; -; mRNA.
CC EMBL: BC061126; AAB61126.1; -; mRNA.
CC PIR: A48093; A48093.
CC HSSP: P80098; 1B00.
CC Ensembl: ENSMUG00000035373; Mus musculus.
CC MG1: MG1-99512; Ccl17.
CC GO: GO:0005615; C:extracellular space; TAS.
CC InterPro: IPR000827; CC_chemokine_sml.
CC InterPro: IPR001811; Chemokine_IL8.

DR PFAM: PF00048; IL8; 1.
DR PROSITE: PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Heparin-binding;
KW Inflammatory response; Pyrilidone carboxylic acid;
KW Sensory transduction; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 97 Small inducible cytokine A7.
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By
FT similarity).
FT CARBOHYD 29 29 N-linked (GlcNAc..) (Potential).
FT DISULFID 33 57 By similarity.
FT DISULFID 34 73 By similarity.
FT CONFLICT 57 63 Missing (in Ref. 5).
FT CONFLICT 74 74 A -> R (in Ref. 4).
SQ SEQUENCE 97 AA; 10999 MW; B94FDA6DF1EF6140 CRC64;
Query Match 61.6%; Score 45; DB 1; Length 97;
Best Local Similarity 62.5%; Pred. No. 1.6;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ISVORLASYYRRITSSK 16
| : ||||| :
Db 41 IPKRNLSYYRRITSSR 56
RESULT 42
QSSVUO MOUSE
ID QSSVUO MOUSE PRELIMINARY; PRT; 97 AA.
AC QSSVUO;
DT 10-MAY-2005 (TRENBLrel. 30, Created)
DT 10-MAY-2005 (TRENBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TRENBLrel. 30, Last annotation update)
DE Chemokine (C-C motif) ligand 7.
GN Name=Ccl17; ORFNames=RP23-350G1.4-001;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Whitehead S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL626807; CA125304.1; -; Genomic DNA.
SQ SEQUENCE 97 AA; 10999 MW; B94FDA6DF1EF6140 CRC64;
Query Match 61.6%; Score 45; DB 2; Length 97;
Best Local Similarity 62.5%; Pred. No. 1.6;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ISVORLASYYRRITSSK 16
| : ||||| :
Db 41 IPKRNLSYYRRITSSR 56
RESULT 43
Q4PIY1 9ZZZZ
ID Q4PIY1 9ZZZZ PRELIMINARY; PRT; 97 AA.
AC Q4PIY1;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)
DE MARC.
GN Name=MARC;
OS unidentified.
OC unclassified.
OX NCBI_TaxID=32644;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93094785; PubMed=1281219; DOI=10.1084/jem.176.6.1773;
RA Kulmburg P.A.; Huber N.E.; Scheer B.J.; Wrann M.; Baumruker T.;
RT "Immunoglobulin E plus antigen challenge induces a novel
RT intercrine/chemokine in mouse mast cells.";

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RL J. Exp. Med. 176:1773-1778 (1992).
DR EMBL; S50588; AAA12542.1; -; mRNA
SQ SEQUENCE 97 AA; 10999 MW; B94FDA6DF1EF6140 CRC64;

Query Match 61.6%; Score 45; DB 2; Length 97;
Best Local Similarity 62.5%; Pred. No. 1.6;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
Db 41 IPKENLKSYYRITSSR 56
| : | | | | | | | | | |
| : | | | | | | | | | |

RESULT 44
CCL8 CANFA STANDARD; PRT; 99 AA.
AC Q69AY;
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
GN Name=CCL8; Synonyms=MCP2; SCYA10, SCYA8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OC NCBI_TaxID=9615;
OX [1]
RN NUCLEOTIDE SEQUENCE [MRNA].
RA Tsukui T., Sakaguchi M., Maeda S., Koyanagi M., Masuda K., Ohno K.,
RA Tsujimoto H., Iwabuchi S.;
RT "Expression analysis of chemokine gene in canine atopic dermatitis.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
[2]
RN NUCLEOTIDE SEQUENCE [MRNA].
RA Peters I.R., Peeters D., Clercx C., Day M.J.;
RT "Identification of coding sequences for canine monocyte chemotactic
RT protein-2 (CCL8), eotaxin 2 (CCL24), eotaxin 3 (CCL26) and C-C
RT chemokine receptor 3 (CCR3).";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Chemotactic factor that attracts monocytes. This protein
CC can bind heparin (By similarity).
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.
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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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DR EMBL; AB163436; BAD37149.1; -; mRNA.
DR EMBL; AY675234; AAU14059.1; -; mRNA.
DR Ensembl; ENSCAFG00000018348; Canis familiaris.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine I18.
DR Pfam; PF00048; IL8; 1.
DR PRINTS; PR01721; FRACTALKINE.
DR SMART; SM00189; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Heparin-binding; Inflammatory response;
KW Pyrilidone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 99 Small inducible cytokine A8.
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By
FT similarity).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 11263 MW; FD56D8405DC010E8 CRC64;

Query Match 60.3%; Score 44; DB 1; Length 99;
Best Local Similarity 56.2%; Pred. No. 2.5;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
Db 43 IPMQKLESYRITNSQ 58
| : | | | | | | | | | |
| : | | | | | | | | | |

RESULT 45
CCL8 HUMAN STANDARD; PRT; 99 AA.
AC P80075; P78388;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
DE protein 2) (MCP-2) (Monocyte chemoattractant protein 2) (HC14)
DE [Contains: MCP-2 (6-76)].
GN Name=CCL8; Synonyms=MCP2, SCYA10, SCYA8;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE, AND VARIANT GLN-69.
RX MEDLINE=97237052; PubMed=9119400; DOI=10.1006/geno.1996.4594;
RA van Coillie E., Fiten P., Nomiya H., Sakaki Y., Miura R., Fiten P.,
RA van Damme J., Odenakker G.;
RT "The human MCP-2 gene (SCYA8): cloning, sequence analysis, tissue
RT expression, and assignment to the CC chemokine gene contig on
RT chromosome 17q11.2.";
RL Genomics 40:323-331 (1997).
[2]
RN NUCLEOTIDE SEQUENCE, AND VARIANT GLN-69.
RX TISSUE=Bone marrow;
RX MEDLINE=97224420; PubMed=9070881; DOI=10.1006/bbrc.1997.6177;
RA van Coillie E., Froyen F., Nomiya H., Miura R., Fiten P.,
RA van Aelst I., van Damme J., Odenakker G.;
RT "Human monocyte chemotactic protein-2: cDNA cloning and regulated
RT expression of mRNA in mesenchymal cells.";
RL Biochem. Biophys. Res. Commun. 231:726-730 (1997).
[3]
RN NUCLEOTIDE SEQUENCE OF 23-99.
RX MEDLINE=91207938; PubMed=2518726;
RA Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.;
RT "Cloning and expression of a gamma-interferon-inducible gene in
RT monocytes: a new member of a cytokine gene family.";
RL Int. Immunol. 1:388-399 (1989).
[4]
RN PROTEIN SEQUENCE OF 26-99.
RX TISSUE=Osteosarcoma;
RX MEDLINE=92308855; PubMed=1613466; DOI=10.1084/jem.176.1.59;
RA van Damme J., Proost P., Lenaerts J.-P., Odenakker G.;
RT "Structural and functional identification of two human, tumor-derived
RT monocyte chemotactic proteins (MCP-2 and MCP-3) belonging to the
RT chemokine family.";
RL J. Exp. Med. 176:59-65 (1992).
[5]
RN SUBUNIT.
RX MEDLINE=97053697; PubMed=8898111; DOI=10.1016/0014-5793(96)01024-1;
RA Kim K.-S., Rajaratnam K., Clark-Lewis I., Sykes B.D.;
RT "Structural characterization of a monomeric chemokine: monocyte
RT chemoattractant protein-3.";
RL FEBS Lett. 395:277-282 (1996).
[6]
RN IDENTIFICATION OF MCP-2 (6-76), MASS SPECTROMETRY, N-TERMINAL
RN PROCESSING, AND FUNCTION.
RX PubMed=9558113;
RA Proost P., Struyf S., Couvreur M., Lenaerts J.-P., Conings R.,
RA Menten P., Verhaert P., Wuyts A., Van Damme J.;
RT "Posttranslational modifications affect the activity of the human

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monocyte chemotactic proteins MCP-1 and MCP-2: identification of MCP-2 (6-76) as a natural chemokine inhibitor.";

J. Immunol. 160:4034-4041(1998).

-1- FUNCTION: Chemotactic factor that attracts monocytes, lymphocytes, basophils and eosinophils. May play a role in neoplasia and inflammatory host responses. This protein can bind heparin. The processed form MCP-2(6-76) does not show monocyte chemotactic activity, but inhibits the chemotactic effect most predominantly of CCL7, and also of CCL2 and CCL5 and CCL8.

-1- SUBUNIT: Monomer or homodimer; in equilibrium.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: Highest expression found in the small intestine and peripheral blood cells. Intermediate levels seen in the heart, placenta, lung, skeletal muscle, thymus, colon, ovary, spinal cord and pancreas. Low levels seen in the brain, liver, spleen and prostate.

-1- INDUCTION: By interferon gamma, mitogens and interleukin-1.

-1- PTM: N-terminal processed form MCP-2(6-76) is produced by proteolytic cleavage after secretion from peripheral blood monocytes.

-1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.

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EMBL; X99886; CAA68168.1; ALT INIT; Genomic_DNA.
EMBL; Y10802; CAA71760.1; -; mRNA.
EMBL; Y16645; CAA76341.1; -; mRNA.
PIR; JC5295; JCS295.
PDB; 1ESR; X-ray; A=24-99.
Ensembl; ENSG00000108700; Homo sapiens.
HGNC; HGNC:10635; CCL8.
MIM; 602283; -.
GO; GO:0008009; F:chemokine activity; TAS.
GO; GO:0004871; F:signal transducer activity; TAS.
GO; GO:0006816; P:calcium ion transport; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0006935; P:chemotaxis; TAS.
GO; GO:0006887; P:exocytosis; TAS.
GO; GO:0009615; P:response to virus; TAS.
GO; GO:0007165; P:signal transduction; TAS.
InterPro; IPR000827; CC chemokine sm1.
InterPro; IPR001811; Chemokine IL8.
Pfam; PF000048; IL8; 1.
PRINTS; PR01721; FRACTALKINE.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
3D-structure; Chemotaxis; Cytokine; Direct protein sequencing; Heparin-binding; Inflammatory response; Polymorphism; Pyrrolidone carboxylic acid; Sensory transduction; Signal.
SIGNAL 1 23 Probable.
CHAIN 24 99 Small inducible cytokine A8.
CHAIN 29 99 MCP-2(6-76).
MOD RES 24 24 Pyrrolidone carboxylic acid.
DISULFID 34 59 By similarity.
DISULFID 35 75 By similarity.
VARIANT 69 69 K-> Q (in dbSNP:3138038).
FT TURN 26 29
FT HELIX 45 47
FT STRAND 48 53
FT TURN 57 58
FT STRAND 64 68
FT TURN 69 70
FT STRAND 73 76
FT TURN 78 79
FT HELIX 81 96
SQ SEQUENCE 99 AA; 11246 MW; 9D67976BB9422F2A CRC64;

Query Match 60.3%; Score 44; DB 1; Length 99;

Best Local Similarity 64.3%; Pred. No. 2.5;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 ISVQLASVRRITSS 14
|:|:|:|:|:|:|:
DB 43 IPIQLBSYTRITN 56

RESULT 46
Q621J4_CABBR
ID Q621J4_CABBR PRELIMINARY; PRT; 253 AA.
AC Q621J4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein CBG02465.
GN Name=CBG02465;
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6238;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG The C.briggsae Sequencing Consortium;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; CAC01000012; CAB59159.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 253 AA; 28604 MW; 461744764A01B3EF CRC64;

Query Match 60.3%; Score 44; DB 2; Length 253;
Best Local Similarity 71.4%; Pred. No. 7.4;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SVQELASVRRITSS 15
|:|:|:|:|:|:|:
DB 56 SLQNLASARKITSS 69

RESULT 47
Q5XPM8_ERWAM
ID Q5XPM8_ERWAM PRELIMINARY; PRT; 271 AA.
AC Q5XPM8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Flc (Fragment).
GN Name=flc;
OS Erwinia amylovora.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Erwinia.
OX NCBI_TaxID=552;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CFBP 1430;
RA Cesbron S., Bissot M.-N., Tharaud M., Paulin J.-P.;
"Erwinia amylovora genes involved in motility,";
Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY743588; AAU90046.1; -; Genomic_DNA.
DR GO; GO:0009420; C:flagellar filament (sensu Bacteria); IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0001539; P:ciliary or flagellar motility; IEA.
DR InterPro; IPR001029; Flagellin_C.
DR InterPro; IPR001492; Flagellin_N.
DR Pfam; PF00700; Flagellin_C; 1.
DR Pfam; PF00669; Flagellin_N; 1.
DR PRINTS; PD00207; FLAGELLIN.
DR ProDom; PD000316; Flagellin_C; 1.
FT NON TER 271 271
SQ SEQUENCE 271 AA; 28638 MW; 7F1EDE7853451F27 CRC64;

Query Match 60.3%; Score 44; DB 2; Length 271;
Best Local Similarity 66.7%; Pred. NO. 8;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
|:|:|:|:|:|:|
Db 28 SMERLSSGSRITSSK 42

RESULT 48

	Q8D3D7	WIGBR	PRT;	421 AA.
ID	Q8D3D7_WIGBR	PRELIMINARY;		
AC	Q8D3D7;			
DT	01-MAR-2003	(TrEMBLrel_23, Created)		
DT	01-MAR-2003	(TrEMBLrel_23, Last sequence update)		
DT	01-JUN-2003	(TrEMBLrel_24, Last annotation update)		
DE	Flic protein.			
GN	Name=flic; OrderedLocusNames=WGBR0640;			
OS	Bacterioworthia glossinidia Brevipalpis.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales;			
OX	Enterobacteriaceae; Wigglesworthia.			
CX	NCBI_TaxId=36870;			
RN	[1]	NUCLEOTIDE SEQUENCE.		
RP	MEDLINE=2297718; PubMed=1219091; DOI=10.1038/ng986;			
RX	Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M,			
RA	Aksay S. ;			
RT	"Genome sequence of the endocellular obligate symbiont of tsetse			
RL	fliers, Wigglesworthia glossinidia."			
RM	Nat. Genet. 32:402-407(2002).			
RL	EWBL; BA000021; BAC24210.1; -; Genomic_DNA.			
DR	HSSP; Q67803; IORV;			
DR	GO; GO:0009420; C:flagellar filament (sensu Bacteria); IEA.			
DR	GO; GO:0005198; F:structural molecule activity; IEA.			
DR	GO; GO:0001539; P:ciliary or flagellar motility; IEA.			
DR	InterPro; IPRO01029; Flagellin_C.			
DR	InterPro; IPRO01492; Flagellin_N.			
DR	pfam; PF00700; Flagellin_C; 1.			
DR	pfam; PF00669; Flagellin_N; 1.			
DR	PRINTS; PR00207; FLAGELLIN.			
DR	ProDom; PD000316; FLAGELLIN-C; 1.			
KW	SOURCE 421 AA; 45963 MW; AA6952B2CEC2CA8C CRG64;			
LK	SEQUENCE COMPLETE.			
SK	COMPLETE proteome.			

Query Match	58.9%	Score 43;	DB 2;	Length 421;
Best Local Similarity	66.7%	Pred. No. 21;		
Matches	10;	Conservative	2;	Mismatches 3;
		Indels	0;	Gaps 0;

Qy 2 SVQR LASYRRITSSK 16
| : | | : | | |
Dh 28 STORLSSGLRINSSK 42

RESULT 49

AD0015	Q40115	LEIMA PRELIMINARY;	PRT;	447 AA.
ID	Q40115	LEIMA PRELIMINARY;		
AC	Q40115			
DT	13-SEP-2005	(TREMBLrel. 31, Created)		
DT	13-SEP-2005	(TREMBLrel. 31, Last sequence update)		
DT	13-SEP-2005	(TREMBLrel. 31, Last annotation update)		
DE	Tyrosine aminotransferase, putative (EC 2.6.1.5).			
DE	ORFNames=LmjF36.2360;			
GN	Leishmania major.			
OS	Leishmania major.			
OC	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.			
OX	NCBI_TaxID=5664;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	STRAIN=Frieldin;			
RA	Peacock C.S.; Murphy L.; Ivens A.C.; Berriman M.; Blackwell J.,			
RA	Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neill S.,			
RA	Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;			
RL	Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; CT005272; CAJ09194.1; -; Genomic DNA.			

KW AminoTRANSFERase; TRANSFERase.
SQ SEQUENCE 447 AA; 49590 MW; 8AB5E91CFAC64A14 CRC64;
Query Match 58.9%; Score 43; DB 2; Length 447;
Best Local Similarity 90.0%; Pred. No. 22;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ASYRRITSSK 16
|||:|||||
Db 38 ASFRRITSSK 47

RESIST 50

YRHL_AZOVI	STANDARD;	PRT;	60 AA.
ID	YRHL_AZOVI		
AC	Q44557;		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Hypothetical protein in rhda 5' region (ORF1) (Fragment).		
DE	Hypothetical protein in rhda 5' region (ORF1) (Fragment).		
OS	Azotobacter vinelandii.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		
OC	Pseudomonadaceae; Azotobacter.		
OX	NCBI_TaxID=354;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [GENOMIC DNA].		
RC	STRAIN=OP / UWI136;		
RC	STRAIN=OP / UWI136;		
FX	MEDLINE=96184904; PubMed=8617271;		
RA	Clonghi R., Paganì S., Kennedy C., Drummond M.;		
RA	"Cloning, sequence analysis and overexpression of the rhodanese gene		
RT	of Azotobacter vinelandii.";		
RL	Eur. J. Biochem. 236:240-248(1996).		

CC -i- SIMILARITY: To E.coli yjeQ and H.influenzae HI1714.
CC -----
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CC -----
DR EMBL: L42346: AAB03237.1: -; Genomic DNA.

DR
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DR pfam; PF03193; DUF258; 1.
KW Hypothetical protein.

FT	NON TER	1	1
SO	SEQUENCE	60 AA.	699

SV SEQUENCE	00 AM, 0000 PM, 21023437500004200	Score 43: DB 1: Length
Query: Match	57 58:	

Query Match	57.5%;	Score 42;	DB 1;	Length 60;
Best local similarity	50.0%;	Score 34;	DB 2;	Length 40;

Best Local Similarity	60.0%	Freq. No.	3.4
Matches	9	Conservative	2
		Mismatches	4
		Indels	0
		Gaps	0

Qy 1 ISVQLASYRRITSS 15

Db 40 IQPQRMASRYHILAS 54

Search completed: February 6, 2006, 14:29:19
Job time : 276 secs

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OM protein - protein search, using sw model

Run on: February 6, 2006, 14:29:34 ; Search time 47 Seconds
(without alignments)

Title: US-10-644-277-149 COPY 20 35

Perfect score: 73

Sequence: 1 ISVQLASYRRITSSK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
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107	47	64.4	99	2	US-09-067-447B-18	Sequence 18, Appl	180	36	49.3	1614	2	US-08-422-582-2	Sequence 2, Appl
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122	46	63.0	70	2	US-08-613-822-17	Sequence 17, Appl	195	35.5	48.6	98	2	US-08-852-212-2	Sequence 2, Appl
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276	34	46.6	409	1	US-08-440-542-21	Sequence 21, Appl	349	33	45.2	186	2	US-09-270-767-60031	Sequence 60031, A
277	34	46.6	409	1	US-08-440-542-24	Sequence 24, Appl	350	33	45.2	187	2	US-09-252-991A-20027	Sequence 20027, A
278	34	46.6	409	1	US-08-231-368-21	Sequence 21, Appl	351	33	45.2	245	2	US-09-583-110-3499	Sequence 3499, Ap
279	34	46.6	409	1	US-08-231-368-24	Sequence 24, Appl	352	33	45.2	254	2	US-09-107-433-3222	Sequence 3222, Ap
280	34	46.6	409	1	US-08-440-210-21	Sequence 21, Appl	353	33	45.2	277	2	US-09-543-681A-8237	Sequence 8237, Ap
281	34	46.6	409	2	US-09-046-604-21	Sequence 21, Appl	354	33	45.2	286	2	US-09-540-236-3046	Sequence 3046, Ap
282	34	46.6	409	2	US-09-046-604-21	Sequence 21, Appl	355	33	45.2	294	2	US-09-489-039A-12425	Sequence 12425, A
283	34	46.6	409	2	US-09-046-604-24	Sequence 24, Appl	356	33	45.2	296	2	US-09-252-991A-30042	Sequence 30042, A
284	34	46.6	410	1	US-08-188-281B-18	Sequence 18, Appl	357	33	45.2	304	2	US-09-248-796A-19355	Sequence 19355, A
285	34	46.6	410	4	PCT-US94-07280-18	Sequence 18, Appl	358	33	45.2	309	2	US-10-101-464A-602	Sequence 602, App
286	34	46.6	410	4	PCT-US95-01087-18	Sequence 18, Appl	359	33	45.2	348	2	US-09-949-016-11586	Sequence 11586, A
287	34	46.6	417	1	US-08-188-281B-19	Sequence 19, Appl	360	33	45.2	350	2	US-09-252-991A-26068	Sequence 26068, A
288	34	46.6	417	4	PCT-US94-07280-19	Sequence 19, Appl	361	33	45.2	366	2	US-09-252-991A-28917	Sequence 28917, A
289	34	46.6	417	4	PCT-US95-01087-19	Sequence 19, Appl	362	33	45.2	387	2	US-09-270-767-3219	Sequence 3219, A
290	34	46.6	434	1	US-08-188-281B-10	Sequence 10, Appl	363	33	45.2	387	2	US-09-270-767-48436	Sequence 48436, A
291	34	46.6	434	4	PCT-US94-07280-10	Sequence 10, Appl	364	33	45.2	437	2	US-09-198-452A-204	Sequence 204, App
292	34	46.6	434	4	PCT-US95-01087-10	Sequence 10, Appl	365	33	45.2	437	2	US-09-438-185A-190	Sequence 190, App
293	34	46.6	441	1	US-08-188-281B-21	Sequence 21, Appl	366	33	45.2	471	2	US-09-126-420A-20	Sequence 20, Appl
294	34	46.6	441	4	PCT-US94-07280-21	Sequence 21, Appl	367	33	45.2	472	1	US-08-278-091-5	Sequence 5, Appli
295	34	46.6	441	4	PCT-US95-01087-21	Sequence 21, Appl	368	33	45.2	472	1	US-08-483-859-5	Sequence 5, Appli
296	34	46.6	447	1	US-08-188-281B-20	Sequence 20, Appl	369	33	45.2	472	1	US-08-472-173-5	Sequence 5, Appli
297	34	46.6	447	4	PCT-US94-07280-20	Sequence 20, Appl	370	33	45.2	472	1	US-08-487-167-5	Sequence 5, Appli
298	34	46.6	447	4	PCT-US95-01087-20	Sequence 20, Appl	371	33	45.2	472	1	US-08-482-816-5	Sequence 5, Appli
299	34	46.6	453	1	US-08-188-281B-16	Sequence 16, Appl	372	33	45.2	472	1	US-08-296-149-5	Sequence 5, Appli
300	34	46.6	453	4	PCT-US94-07280-16	Sequence 16, Appl	373	33	45.2	472	1	US-08-801-499-5	Sequence 5, Appli
301	34	46.6	453	4	PCT-US95-01087-16	Sequence 16, Appl	374	33	45.2	472	1	US-08-615-271-5	Sequence 5, Appli
302	34	46.6	490	1	US-08-188-281B-15	Sequence 15, Appl	375	33	45.2	472	2	US-09-074-660-5	Sequence 5, Appli
303	34	46.6	490	4	PCT-US94-07280-15	Sequence 15, Appl	376	33	45.2	472	2	US-09-074-659-5	Sequence 5, Appli
304	34	46.6	490	4	PCT-US95-01087-15	Sequence 15, Appl	377	33	45.2	472	2	US-09-106-468-5	Sequence 5, Appli
305	34	46.6	500	2	US-09-248-796A-25507	Sequence 25507, A	378	33	45.2	472	2	US-09-106-466A-5	Sequence 5, Appli
306	34	46.6	537	1	US-08-453-552-4	Sequence 4, Appli	379	33	45.2	472	2	US-09-106-467-5	Sequence 5, Appli
307	34	46.6	537	1	US-08-710-637-4	Sequence 4, Appli	380	33	45.2	502	2	US-09-499-302A-7	Sequence 7, Appli
308	34	46.6	537	4	PCT-US93-00907-4	Sequence 4, Appli	381	33	45.2	509	2	US-09-499-302A-8	Sequence 8, Appli
309	34	46.6	571	2	US-09-248-796A-20375	Sequence 20375, A	382	33	45.2	552	2	US-09-792-024-84	Sequence 84, Appl
310	34	46.6	608	2	US-09-107-532A-5702	Sequence 5702, Ap	383	33	45.2	572	2	US-09-248-796A-27399	Sequence 27399, A
311	34	46.6	615	2	US-09-540-236-2639	Sequence 2639, Ap	384	33	45.2	606	2	US-09-270-767-45656	Sequence 45656, A
312	34	46.6	620	2	US-09-538-092-1285	Sequence 1285, Ap	385	33	45.2	616	2	US-09-248-796A-20955	Sequence 20955, A
313	34	46.6	687	2	US-09-252-991A-26621	Sequence 26621, A	386	33	45.2	714	2	US-09-792-024-117	Sequence 117, App
314	34	46.6	967	1	US-08-188-281B-13	Sequence 13, Appl	387	33	45.2	1046	2	US-09-540-236-2376	Sequence 2376, Ap
315	34	46.6	967	4	PCT-US94-07280-13	Sequence 13, Appl	388	33	45.2	1439	2	US-09-902-540-14072	Sequence 14072, A
316	34	46.6	967	4	PCT-US95-01087-13	Sequence 13, Appl	389	33	43.8	36	2	US-10-464-939-5	Sequence 5, Appli
317	34	46.6	1157	1	US-07-876-280-30	Sequence 30, Appl	390	32	43.8	43	2	US-10-318-675-38	Sequence 38, Appl
318	34	46.6	1157	1	US-07-812-180A-2	Sequence 2, Appli	391	32	43.8	43	2	US-10-318-675-40	Sequence 40, Appl
319	34	46.6	1157	1	US-08-315-468-2	Sequence 2, Appli	392	32	43.8	61	1	US-08-194-211A-3	Sequence 3, Appli

393	32	43.8	61	2	US-08-456-748B-3	Sequence 3, Appl1	466	32	43.8	567	2	US-09-711-164-374	Sequence 374, App
394	32	43.8	61	2	US-09-492-709A-357	Sequence 357, App	467	32	43.8	623	2	US-10-464-939-12	Sequence 12, Appl
395	32	43.8	67	2	US-09-489-039A-10090	Sequence 10090, A	468	32	43.8	664	2	US-08-957-063-18	Sequence 18, Appl
396	32	43.8	68	2	US-09-543-681A-5321	Sequence 5321, Ap	469	32	43.8	664	2	US-09-487-685-18	Sequence 18, Appl
397	32	43.8	72	2	US-09-134-000C-4792	Sequence 4792, Ap	470	32	43.8	664	2	US-08-802-805D-18	Sequence 18, Appl
398	32	43.8	87	2	US-09-248-796A-22966	Sequence 22966, A	471	32	43.8	664	2	US-09-388-316C-18	Sequence 18, Appl
399	32	43.8	100	2	US-09-513-999C-6473	Sequence 6473, Ap	472	32	43.8	675	2	US-09-171-878-1	Sequence 1, Appl
400	32	43.8	105	2	US-09-471-276-908	Sequence 908, Ap	473	32	43.8	757	2	US-09-419-679-6	Sequence 6, Appl
401	32	43.8	106	2	US-09-270-767-31649	Sequence 31649, A	474	32	43.8	759	2	US-09-252-991A-17841	Sequence 17841, A
402	32	43.8	106	2	US-09-270-767-46866	Sequence 46866, A	475	32	43.8	831	1	US-08-073-384C-5	Sequence 5, Appl
403	32	43.8	117	2	US-09-248-796A-19723	Sequence 19723, A	476	32	43.8	831	1	US-08-254-359A-5	Sequence 5, Appl
404	32	43.8	151	2	US-09-583-110-2927	Sequence 2927, Ap	477	32	43.8	831	1	US-08-483-043-5	Sequence 5, Appl
405	32	43.8	165	2	US-09-107-433-4649	Sequence 4649, Ap	478	32	43.8	831	1	US-08-481-238-5	Sequence 5, Appl
406	32	43.8	170	2	US-09-248-796A-19501	Sequence 19501, A	479	32	43.8	831	1	US-08-471-066B-5	Sequence 5, Appl
407	32	43.8	190	2	US-09-252-991A-22245	Sequence 22245, A	480	32	43.8	831	1	US-08-484-956-5	Sequence 5, Appl
408	32	43.8	209	2	US-09-270-767-35218	Sequence 35218, A	481	32	43.8	831	1	US-08-757-653-5	Sequence 5, Appl
409	32	43.8	209	2	US-09-270-767-50435	Sequence 50435, A	482	32	43.8	831	1	US-08-559-491-5	Sequence 5, Appl
410	32	43.8	218	2	US-09-107-532A-3957	Sequence 3957, Ap	483	32	43.8	831	1	US-08-756-386-5	Sequence 5, Appl
411	32	43.8	232	1	US-08-456-670B-39	Sequence 39, Appl	484	32	43.8	831	1	US-08-823-516-5	Sequence 5, Appl
412	32	43.8	232	2	US-09-372-036-39	Sequence 39, Appl	485	32	43.8	831	1	US-08-682-853A-5	Sequence 5, Appl
413	32	43.8	235	2	US-09-252-991A-29622	Sequence 29622, A	486	32	43.8	831	2	US-08-759-038-5	Sequence 5, Appl
414	32	43.8	258	2	US-09-328-352-6852	Sequence 6852, Ap	487	32	43.8	831	2	US-08-758-314-5	Sequence 5, Appl
415	32	43.8	263	2	US-09-270-767-57472	Sequence 57472, A	488	32	43.8	831	2	US-09-350-309-5	Sequence 5, Appl
416	32	43.8	269	2	US-09-252-991A-16773	Sequence 16773, A	489	32	43.8	831	2	US-08-520-346-5	Sequence 5, Appl
417	32	43.8	294	2	US-09-270-767-57095	Sequence 57095, A	490	32	43.8	831	2	US-09-684-938-5	Sequence 5, Appl
418	32	43.8	306	2	US-09-270-767-33158	Sequence 33158, A	491	32	43.8	831	2	US-09-308-825A-5	Sequence 5, Appl
419	32	43.8	306	2	US-09-270-767-48375	Sequence 48375, A	492	32	43.8	831	2	US-09-758-282B-5	Sequence 5, Appl
420	32	43.8	308	2	US-09-640-211A-644	Sequence 644, App	493	32	43.8	831	2	US-09-655-378A-5	Sequence 5, Appl
421	32	43.8	311	2	US-09-614-912-198	Sequence 198, App	494	32	43.8	831	2	US-09-940-244-5	Sequence 5, Appl
422	32	43.8	314	2	US-09-583-545-15	Sequence 15, Appl	495	32	43.8	831	2	US-09-333-145-5	Sequence 5, Appl
423	32	43.8	314	2	US-09-134-000C-4530	Sequence 4530, Ap	496	32	43.8	831	2	US-09-577-304A-5	Sequence 5, Appl
424	32	43.8	314	2	US-09-514-245-24	Sequence 24, Appl	497	32	43.8	831	2	US-09-381-212-5	Sequence 5, Appl
425	32	43.8	314	2	US-10-112-540-2	Sequence 2, Appl	498	32	43.8	831	2	US-10-081-806-5	Sequence 5, Appl
426	32	43.8	320	2	US-09-212-247C-13	Sequence 13, Appl	499	32	43.8	831	2	US-10-190-967-16	Sequence 16, Appl
427	32	43.8	320	2	US-10-076-157-13	Sequence 13, Appl	500	32	43.8	831	2	US-09-713-601A-5	Sequence 5, Appl
428	32	43.8	321	2	US-09-270-767-42852	Sequence 42852, A	501	32	43.8	974	2	US-09-949-016A-11563	Sequence 11563, A
429	32	43.8	333	2	US-09-252-991A-29336	Sequence 29336, A	502	32	43.8	1106	2	US-09-248-796A-15028	Sequence 15028, A
430	32	43.8	344	2	US-09-199-637A-108	Sequence 108, App	503	32	43.8	1159	2	US-09-328-352-7624	Sequence 7624, Ap
431	32	43.8	409	2	US-09-232-931A-31003	Sequence 31003, A	504	32	43.8	1195	2	US-09-540-236-3165	Sequence 3165, Ap
432	32	43.8	432	2	US-09-602-777A-140	Sequence 140, App	505	32	43.8	1227	2	US-09-252-991A-16636	Sequence 16636, A
433	32	43.8	445	2	US-08-861-990-11	Sequence 11, Appl	506	32	43.8	1380	2	US-09-252-991A-25722	Sequence 25722, A
434	32	43.8	447	2	US-09-614-912-192	Sequence 192, App	507	32	43.8	2472	2	US-09-252-991A-17052	Sequence 17052, A
435	32	43.8	456	2	US-09-270-767-42198	Sequence 42198, A	508	31	42.5	30	2	US-09-333-768-1	Sequence 1, Appl
436	32	43.8	464	2	US-08-957-063-6	Sequence 6, Appl	509	31	42.5	43	2	US-10-318-675-42	Sequence 42, Appl
437	32	43.8	464	2	US-09-487-685-6	Sequence 6, Appl	510	31	42.5	43	2	US-10-318-675-45	Sequence 45, Appl
438	32	43.8	464	2	US-08-802-805D-6	Sequence 6, Appl	511	31	42.5	43	2	US-10-318-675-48	Sequence 48, Appl
439	32	43.8	464	2	US-08-861-990-2	Sequence 2, Appl	512	31	42.5	48	1	US-08-637-759B-480	Sequence 480, App
440	32	43.8	464	2	US-09-388-316C-6	Sequence 6, Appl	513	31	42.5	48	2	US-08-871-355A-480	Sequence 480, App
441	32	43.8	472	2	US-09-826-509-469	Sequence 469, App	514	31	42.5	48	2	US-09-201-945-480	Sequence 480, App
442	32	43.8	474	2	US-09-248-796A-15826	Sequence 15826, A	515	31	42.5	59	1	US-08-637-759B-99	Sequence 99, Appl
443	32	43.8	475	1	US-08-278-031-6	Sequence 6, Appl	516	31	42.5	59	2	US-08-871-355A-99	Sequence 99, Appl
444	32	43.8	475	1	US-08-483-859-6	Sequence 6, Appl	517	31	42.5	59	2	US-09-201-945-99	Sequence 99, Appl
445	32	43.8	475	1	US-08-472-173-6	Sequence 6, Appl	518	31	42.5	65	2	US-09-186-276B-65	Sequence 65, Appl
446	32	43.8	475	1	US-08-487-167-6	Sequence 6, Appl	519	31	42.5	65	2	US-08-842-445-65	Sequence 65, Appl
447	32	43.8	475	1	US-08-482-816-6	Sequence 6, Appl	520	31	42.5	65	2	US-09-186-188B-65	Sequence 65, Appl
448	32	43.8	475	1	US-08-296-149-6	Sequence 6, Appl	521	31	42.5	65	2	US-09-270-767-62105	Sequence 62105, A
449	32	43.8	475	1	US-08-801-439-6	Sequence 6, Appl	522	31	42.5	65	2	US-09-265-585C-65	Sequence 65, Appl
450	32	43.8	475	1	US-08-615-271-6	Sequence 6, Appl	523	31	42.5	67	2	US-09-107-532A-6800	Sequence 6800, Ap
451	32	43.8	475	2	US-09-074-660-6	Sequence 6, Appl	524	31	42.5	72	2	US-09-270-767-61719	Sequence 61719, A
452	32	43.8	475	2	US-09-106-468-6	Sequence 6, Appl	525	31	42.5	79	2	US-09-107-532A-4870	Sequence 4870, Ap
453	32	43.8	475	2	US-09-106-468-6	Sequence 6, Appl	526	31	42.5	81	2	US-09-270-767-46160	Sequence 46160, A
454	32	43.8	475	2	US-09-106-468A-6	Sequence 6, Appl	527	31	42.5	96	2	US-09-366-887A-9	Sequence 9, Appl
455	32	43.8	475	2	US-09-106-467-6	Sequence 6, Appl	528	31	42.5	96	2	US-09-517-204-9	Sequence 9, Appl
456	32	43.8	478	1	US-08-456-670B-40	Sequence 40, Appl	529	31	42.5	101	2	US-09-252-991A-29775	Sequence 29775, A
457	32	43.8	478	2	US-09-372-036-40	Sequence 40, Appl	530	31	42.5	103	2	US-09-902-540-11485	Sequence 11485, A
458	32	43.8	484	1	US-08-127-499A-26	Sequence 26, Appl	531	31	42.5	106	2	US-09-489-039A-9092	Sequence 9092, Ap
459	32	43.8	484	1	US-08-482-847-26	Sequence 26, Appl	532	31	42.5	108	2	US-09-513-999C-6103	Sequence 6103, Ap
460	32	43.8	487	2	US-09-489-039A-12914	Sequence 12914, A	533	31	42.5	110	2	US-09-710-279-894	Sequence 894, App
461	32	43.8	498	2	US-09-648-004-12	Sequence 12, Appl	534	31	42.5	113	1	US-08-248-839C-2	Sequence 2, Appl
462	32	43.8	498	2	US-10-272-419-12	Sequence 12, Appl	535	31	42.5	113	1	US-08-248-839C-4	Sequence 4, Appl
463	32	43.8	545	2	US-09-543-681A-5914	Sequence 5914, Ap	536	31	42.5	113	1	US-08-248-839C-6	Sequence 6, Appl
464	32	43.8	565	2	US-09-270-767-41851	Sequence 41851, A	537	31	42.5	113	1	US-08-248-839C-8	Sequence 8, Appl
465	32	43.8	566	2	US-09-514-245-18	Sequence 18, Appl	538	31	42.5	120	2	US-09-902-540-12861	Sequence 12861, A

539	31	42.5	140	2	US-09-024-020B-11	Sequence 11, Appl	612	31	42.5	502	1	US-08-484-840-3	Sequence 3, Appl
540	31	42.5	140	2	US-09-425-043-11	Sequence 11, Appl	613	31	42.5	502	1	US-08-483-094-3	Sequence 3, Appl
541	31	42.5	147	2	US-09-230-637-43	Sequence 43, Appl	614	31	42.5	503	1	US-08-484-840-4	Sequence 4, Appl
542	31	42.5	150	2	US-09-024-020B-10	Sequence 10, Appl	615	31	42.5	503	1	US-08-483-094-4	Sequence 4, Appl
543	31	42.5	150	2	US-09-425-043-10	Sequence 10, Appl	616	31	42.5	504	2	US-09-902-540-14106	Sequence 14106, A
544	31	42.5	154	2	US-09-270-767-35773	Sequence 35773, A	617	31	42.5	510	2	US-09-248-796A-18513	Sequence 18513, A
545	31	42.5	154	2	US-09-270-767-50990	Sequence 50990, A	618	31	42.5	518	2	US-09-881-578A-4	Sequence 4, Appl
546	31	42.5	168	2	US-09-252-991A-27872	Sequence 27872, A	619	31	42.5	544	2	US-09-614-912-176	Sequence 176, App
547	31	42.5	195	2	US-09-198-452A-126	Sequence 126, App	620	31	42.5	549	2	US-09-115-150-4	Sequence 4, Appl
548	31	42.5	195	2	US-09-438-185A-110	Sequence 110, App	621	31	42.5	549	2	US-09-489-039A-8814	Sequence 8814, Ap
549	31	42.5	204	2	US-09-949-016-9696	Sequence 9696, Ap	622	31	42.5	553	2	US-09-096-399-2	Sequence 2, Appl
550	31	42.5	205	2	US-10-169-048-36	Sequence 36, Appl	623	31	42.5	554	1	US-08-021-623C-6	Sequence 6, Appl
551	31	42.5	208	2	US-09-107-532A-6378	Sequence 6378, Ap	624	31	42.5	559	2	US-09-096-399-4	Sequence 4, Appl
552	31	42.5	214	2	US-09-758-282B-19	Sequence 19, Appl	625	31	42.5	563	2	US-09-614-912-170	Sequence 170, App
553	31	42.5	214	2	US-09-577-304A-19	Sequence 19, Appl	626	31	42.5	574	2	US-09-614-912-172	Sequence 172, App
554	31	42.5	216	2	US-09-294-298A-7	Sequence 7, Appl	627	31	42.5	632	2	US-09-640-958-4	Sequence 4, Appl
555	31	42.5	219	2	US-09-248-796A-20115	Sequence 20115, A	628	31	42.5	633	2	US-09-902-540-15927	Sequence 15927, A
556	31	42.5	234	2	US-09-543-681A-4712	Sequence 4712, Ap	629	31	42.5	634	2	US-09-640-958-10	Sequence 10, Appl
557	31	42.5	236	2	US-09-248-335-68	Sequence 68, Appl	630	31	42.5	654	2	US-09-640-958-12	Sequence 12, Appl
558	31	42.5	245	2	US-09-248-796A-21863	Sequence 21863, A	631	31	42.5	695	1	US-08-484-956-87	Sequence 87, Appl
559	31	42.5	246	2	US-08-858-207A-483	Sequence 483, App	632	31	42.5	695	1	US-08-757-653-87	Sequence 87, Appl
560	31	42.5	247	1	US-08-465-980-3	Sequence 3, Appl	633	31	42.5	695	2	US-08-520-946-87	Sequence 87, Appl
561	31	42.5	247	1	US-09-053-303-3	Sequence 3, Appl	634	31	42.5	695	2	US-09-655-378A-87	Sequence 87, Appl
562	31	42.5	247	4	PCT-US95-07093-3	Sequence 3, Appl	635	31	42.5	711	2	US-09-402-214-4	Sequence 4, Appl
563	31	42.5	247	4	PCT-US95-07093-3	Sequence 3, Appl	636	31	42.5	711	2	US-09-402-214-17	Sequence 17, Appl
564	31	42.5	255	2	US-09-583-110-4397	Sequence 4397, Ap	637	31	42.5	712	2	US-09-949-016-8349	Sequence 8349, Ap
565	31	42.5	263	2	US-09-107-433-2937	Sequence 2937, Ap	638	31	42.5	712	2	US-09-543-681A-5392	Sequence 5392, Ap
566	31	42.5	267	2	US-09-902-540-14601	Sequence 14601, A	639	31	42.5	714	1	US-08-859-201-2	Sequence 2, Appl
567	31	42.5	270	1	US-08-859-201-4	Sequence 4, Appl	640	31	42.5	714	2	US-09-402-214-2	Sequence 2, Appl
568	31	42.5	275	2	US-09-489-039A-7372	Sequence 7372, Ap	641	31	42.5	810	2	US-09-587-856-2	Sequence 2, Appl
569	31	42.5	278	2	US-09-270-767-35188	Sequence 35188, A	642	31	42.5	810	2	US-09-777-537-2	Sequence 2, Appl
570	31	42.5	282	2	US-09-270-767-50405	Sequence 50405, A	643	31	42.5	810	2	US-09-777-538-2	Sequence 2, Appl
571	31	42.5	295	2	US-09-002-298-5	Sequence 5, Appl	644	31	42.5	822	2	US-09-252-991A-30521	Sequence 30521, A
572	31	42.5	295	2	US-09-481-277-5	Sequence 5, Appl	645	31	42.5	822	2	US-09-824-734-3	Sequence 3, Appl
573	31	42.5	297	2	US-09-068-195-12	Sequence 12, Appl	646	31	42.5	832	1	US-07-977-434-2	Sequence 2, Appl
574	31	42.5	299	2	US-09-205-258-265	Sequence 265, App	647	31	42.5	832	1	US-08-156-020-2	Sequence 2, Appl
575	31	42.5	299	2	US-10-004-860-265	Sequence 265, App	648	31	42.5	832	1	US-08-156-020-4	Sequence 4, Appl
576	31	42.5	300	2	US-09-252-991A-27295	Sequence 27295, A	649	31	42.5	832	1	US-08-156-020-6	Sequence 6, Appl
577	31	42.5	302	2	US-09-248-796A-15243	Sequence 15243, A	650	31	42.5	832	1	US-08-156-020-8	Sequence 8, Appl
578	31	42.5	304	2	US-09-902-540-12191	Sequence 12191, A	651	31	42.5	832	1	US-08-156-020-10	Sequence 10, Appl
579	31	42.5	314	1	US-08-859-201-8	Sequence 8, Appl	652	31	42.5	832	1	US-08-073-384C-4	Sequence 4, Appl
580	31	42.5	314	2	US-08-988-876-7	Sequence 7, Appl	653	31	42.5	832	1	US-08-254-359A-4	Sequence 4, Appl
581	31	42.5	314	2	US-09-968-033C-5	Sequence 5, Appl	654	31	42.5	832	1	US-08-483-043-4	Sequence 4, Appl
582	31	42.5	336	2	US-09-120-365-70	Sequence 70, Appl	655	31	42.5	832	1	US-08-458-819-2	Sequence 2, Appl
583	31	42.5	336	2	US-09-515-039-70	Sequence 70, Appl	656	31	42.5	832	1	US-08-481-238-4	Sequence 4, Appl
584	31	42.5	347	2	US-09-252-991A-28131	Sequence 28131, A	657	31	42.5	832	1	US-08-471-066B-4	Sequence 4, Appl
585	31	42.5	353	2	US-09-248-796A-15681	Sequence 15681, A	658	31	42.5	832	1	US-08-484-956-4	Sequence 4, Appl
586	31	42.5	366	2	US-09-605-703B-2130	Sequence 2130, Ap	659	31	42.5	832	1	US-08-757-653-4	Sequence 4, Appl
587	31	42.5	366	2	US-09-605-703B-2132	Sequence 2132, Ap	660	31	42.5	832	1	US-08-599-491-4	Sequence 4, Appl
588	31	42.5	369	2	US-09-902-540-10817	Sequence 10817, A	661	31	42.5	832	1	US-08-756-386-4	Sequence 4, Appl
589	31	42.5	371	2	US-09-199-637A-295	Sequence 295, App	662	31	42.5	832	1	US-08-823-516-4	Sequence 4, Appl
590	31	42.5	371	2	US-09-252-991A-21430	Sequence 21430, A	663	31	42.5	832	2	US-08-682-853A-4	Sequence 4, Appl
591	31	42.5	374	2	US-08-821-994-70	Sequence 70, Appl	664	31	42.5	832	2	US-08-759-038-4	Sequence 4, Appl
592	31	42.5	374	2	US-09-787-084-4	Sequence 4, Appl	665	31	42.5	832	2	US-08-758-314-4	Sequence 4, Appl
593	31	42.5	381	2	US-09-902-540-11854	Sequence 11854, A	666	31	42.5	832	2	US-09-350-309-4	Sequence 4, Appl
594	31	42.5	385	2	US-09-248-796A-17393	Sequence 17393, A	667	31	42.5	832	2	US-08-520-946-4	Sequence 4, Appl
595	31	42.5	393	2	US-09-489-039A-7842	Sequence 7842, Ap	668	31	42.5	832	2	US-08-978-806-2	Sequence 2, Appl
596	31	42.5	395	1	US-08-841-349-9	Sequence 9, Appl	669	31	42.5	832	2	US-09-684-938-4	Sequence 4, Appl
597	31	42.5	395	2	US-09-431-184A-9	Sequence 9, Appl	670	31	42.5	832	2	US-09-308-825A-4	Sequence 4, Appl
598	31	42.5	396	2	US-09-949-016-6783	Sequence 6783, Ap	671	31	42.5	832	2	US-09-758-282B-4	Sequence 4, Appl
599	31	42.5	398	2	US-09-248-796A-18248	Sequence 18248, A	672	31	42.5	832	2	US-09-655-378A-4	Sequence 4, Appl
600	31	42.5	405	2	US-09-270-767-46358	Sequence 46358, A	673	31	42.5	832	2	US-09-940-244-4	Sequence 4, Appl
601	31	42.5	410	2	US-09-252-991A-31937	Sequence 31937, A	674	31	42.5	832	2	US-09-333-145-4	Sequence 4, Appl
602	31	42.5	425	2	US-09-489-039A-8386	Sequence 8386, Ap	675	31	42.5	832	2	US-09-577-304A-4	Sequence 4, Appl
603	31	42.5	432	1	US-08-705-660-18	Sequence 18, Appl	676	31	42.5	832	2	US-09-381-212-4	Sequence 4, Appl
604	31	42.5	432	2	US-08-989-045-18	Sequence 18, Appl	677	31	42.5	832	2	US-10-081-806-4	Sequence 4, Appl
605	31	42.5	432	2	US-09-919-172-9	Sequence 9, Appl	678	31	42.5	832	2	US-10-190-967-3	Sequence 3, Appl
606	31	42.5	432	2	US-09-315-355A-18	Sequence 18, Appl	679	31	42.5	832	2	US-09-713-601A-4	Sequence 4, Appl
607	31	42.5	442	2	US-09-949-016-9762	Sequence 9762, Ap	680	31	42.5	832	4	PCT-US91-07035-2	Sequence 2, Appl
608	31	42.5	467	2	US-08-867-611-24	Sequence 24, Appl	681	31	42.5	833	1	US-08-073-384C-8	Sequence 8, Appl
609	31	42.5	467	2	US-09-690-359-24	Sequence 24, Appl	682	31	42.5	833	1	US-08-254-359A-8	Sequence 8, Appl
610	31	42.5	467	4	PCT-US92-06965A-29	Sequence 29, Appl	683	31	42.5	833	1	US-08-483-043-8	Sequence 8, Appl
611	31	42.5	471	2	US-09-538-092-837	Sequence 837, App	684	31	42.5	833	1	US-08-481-238-8	Sequence 8, Appl

685	31	42.5	833	1	US-08-471-066B-8	Sequence 8, Appli	758	31	42.5	839	2	US-09-758-282B-127	Sequence 137, App
686	31	42.5	833	1	US-08-484-956-8	Sequence 8, Appli	759	31	42.5	839	2	US-09-758-282B-130	Sequence 133, App
687	31	42.5	833	1	US-08-484-956-8	Sequence 85, Appli	760	31	42.5	839	2	US-09-758-282B-133	Sequence 130, App
688	31	42.5	833	1	US-08-757-653-8	Sequence 8, Appli	761	31	42.5	839	2	US-09-758-282B-139	Sequence 139, App
689	31	42.5	833	1	US-08-757-653-85	Sequence 85, Appli	762	31	42.5	839	2	US-09-758-282B-142	Sequence 142, App
690	31	42.5	833	1	US-08-757-653-168	Sequence 168, App	763	31	42.5	839	2	US-09-758-282B-145	Sequence 145, App
691	31	42.5	833	1	US-08-757-653-188	Sequence 188, App	764	31	42.5	839	2	US-09-758-282B-148	Sequence 148, App
692	31	42.5	833	1	US-08-757-653-190	Sequence 190, App	765	31	42.5	839	2	US-09-758-282B-150	Sequence 150, App
693	31	42.5	833	1	US-08-539-491-8	Sequence 8, Appli	766	31	42.5	839	2	US-09-758-282B-153	Sequence 153, App
694	31	42.5	833	1	US-08-756-386-8	Sequence 8, Appli	767	31	42.5	839	2	US-09-758-282B-169	Sequence 169, App
695	31	42.5	833	1	US-08-823-516-8	Sequence 8, Appli	768	31	42.5	839	2	US-09-758-282B-172	Sequence 172, App
696	31	42.5	833	1	US-08-823-516-66	Sequence 66, Appli	769	31	42.5	839	2	US-09-758-282B-175	Sequence 175, App
697	31	42.5	833	1	US-08-823-516-69	Sequence 69, Appli	770	31	42.5	839	2	US-09-758-282B-178	Sequence 178, App
698	31	42.5	833	1	US-08-823-516-71	Sequence 71, Appli	771	31	42.5	839	2	US-09-758-282B-181	Sequence 181, App
699	31	42.5	833	2	US-08-682-853A-8	Sequence 8, Appli	772	31	42.5	839	2	US-09-758-282B-184	Sequence 184, App
700	31	42.5	833	2	US-08-759-038-8	Sequence 8, Appli	773	31	42.5	839	2	US-09-758-282B-187	Sequence 187, App
701	31	42.5	833	2	US-08-759-038-107	Sequence 107, App	774	31	42.5	839	2	US-09-758-282B-190	Sequence 190, App
702	31	42.5	833	2	US-08-759-038-130	Sequence 130, App	775	31	42.5	839	2	US-09-758-282B-200	Sequence 200, App
703	31	42.5	833	2	US-08-759-038-132	Sequence 132, App	776	31	42.5	839	2	US-09-758-282B-202	Sequence 202, App
704	31	42.5	833	2	US-08-758-314-8	Sequence 8, Appli	777	31	42.5	839	2	US-09-758-282B-204	Sequence 204, App
705	31	42.5	833	2	US-08-758-314-107	Sequence 107, App	778	31	42.5	839	2	US-09-758-282B-206	Sequence 206, App
706	31	42.5	833	2	US-08-758-314-130	Sequence 130, App	779	31	42.5	839	2	US-09-758-282B-218	Sequence 218, App
707	31	42.5	833	2	US-09-350-309-8	Sequence 8, Appli	780	31	42.5	839	2	US-09-758-282B-221	Sequence 221, App
708	31	42.5	833	2	US-08-520-946-8	Sequence 85, Appli	781	31	42.5	839	2	US-09-758-282B-226	Sequence 226, App
709	31	42.5	833	2	US-08-520-946-85	Sequence 85, Appli	782	31	42.5	839	2	US-09-758-282B-228	Sequence 228, App
710	31	42.5	833	2	US-08-684-938-8	Sequence 8, Appli	783	31	42.5	839	2	US-09-758-282B-230	Sequence 230, App
711	31	42.5	833	2	US-08-684-938-107	Sequence 107, App	784	31	42.5	839	2	US-09-758-282B-232	Sequence 232, App
712	31	42.5	833	2	US-09-684-938-130	Sequence 130, App	785	31	42.5	839	2	US-09-758-282B-234	Sequence 234, App
713	31	42.5	833	2	US-09-684-938-130	Sequence 130, App	786	31	42.5	839	2	US-09-758-282B-236	Sequence 236, App
714	31	42.5	833	2	US-09-684-938-132	Sequence 132, App	787	31	42.5	839	2	US-09-577-304A-63	Sequence 63, Appli
715	31	42.5	833	2	US-09-308-825A-8	Sequence 8, Appli	788	31	42.5	839	2	US-09-577-304A-73	Sequence 73, Appli
716	31	42.5	833	2	US-09-308-825A-107	Sequence 107, App	789	31	42.5	839	2	US-09-577-304A-81	Sequence 81, Appli
717	31	42.5	833	2	US-09-308-825A-130	Sequence 130, App	790	31	42.5	839	2	US-09-577-304A-83	Sequence 83, Appli
718	31	42.5	833	2	US-09-308-825A-132	Sequence 132, App	791	31	42.5	839	2	US-09-577-304A-89	Sequence 89, Appli
719	31	42.5	833	2	US-09-758-282B-8	Sequence 8, Appli	792	31	42.5	839	2	US-09-577-304A-115	Sequence 115, App
720	31	42.5	833	2	US-09-758-282B-40	Sequence 40, Appli	793	31	42.5	839	2	US-09-577-304A-118	Sequence 118, App
721	31	42.5	833	2	US-09-758-282B-56	Sequence 56, Appli	794	31	42.5	839	2	US-09-577-304A-121	Sequence 121, App
722	31	42.5	833	2	US-09-758-282B-99	Sequence 99, Appli	795	31	42.5	839	2	US-09-577-304A-124	Sequence 124, App
723	31	42.5	833	2	US-09-758-282B-101	Sequence 101, App	796	31	42.5	839	2	US-09-577-304A-127	Sequence 127, App
724	31	42.5	833	2	US-09-655-378A-8	Sequence 8, Appli	797	31	42.5	839	2	US-09-577-304A-130	Sequence 130, App
725	31	42.5	833	2	US-09-655-378A-85	Sequence 85, Appli	798	31	42.5	839	2	US-09-577-304A-133	Sequence 133, App
726	31	42.5	833	2	US-09-940-244-8	Sequence 8, Appli	799	31	42.5	839	2	US-09-577-304A-139	Sequence 139, App
727	31	42.5	833	2	US-09-940-244-66	Sequence 66, Appli	800	31	42.5	839	2	US-09-577-304A-142	Sequence 142, App
728	31	42.5	833	2	US-09-940-244-69	Sequence 69, Appli	801	31	42.5	839	2	US-09-577-304A-145	Sequence 145, App
729	31	42.5	833	2	US-09-940-244-71	Sequence 71, Appli	802	31	42.5	839	2	US-09-577-304A-148	Sequence 148, App
730	31	42.5	833	2	US-09-333-145-8	Sequence 8, Appli	803	31	42.5	839	2	US-09-577-304A-150	Sequence 150, App
731	31	42.5	833	2	US-09-577-304A-8	Sequence 8, Appli	804	31	42.5	839	2	US-09-577-304A-153	Sequence 153, App
732	31	42.5	833	2	US-09-577-304A-40	Sequence 40, Appli	805	31	42.5	839	2	US-09-577-304A-169	Sequence 169, App
733	31	42.5	833	2	US-09-577-304A-56	Sequence 56, Appli	806	31	42.5	839	2	US-09-577-304A-172	Sequence 172, App
734	31	42.5	833	2	US-09-577-304A-99	Sequence 99, Appli	807	31	42.5	839	2	US-09-577-304A-175	Sequence 175, App
735	31	42.5	833	2	US-09-577-304A-101	Sequence 101, App	808	31	42.5	839	2	US-09-577-304A-178	Sequence 178, App
736	31	42.5	833	2	US-09-381-212-8	Sequence 8, Appli	809	31	42.5	839	2	US-09-577-304A-181	Sequence 181, App
737	31	42.5	833	2	US-09-381-212-66	Sequence 66, Appli	810	31	42.5	839	2	US-09-577-304A-184	Sequence 184, App
738	31	42.5	833	2	US-09-381-212-71	Sequence 71, Appli	811	31	42.5	839	2	US-09-577-304A-187	Sequence 187, App
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740	31	42.5	833	2	US-09-713-601A-8	Sequence 8, Appli	813	31	42.5	839	2	US-09-577-304A-200	Sequence 200, App
741	31	42.5	833	2	US-09-713-601A-66	Sequence 66, Appli	814	31	42.5	839	2	US-09-577-304A-202	Sequence 202, App
742	31	42.5	833	2	US-09-713-601A-69	Sequence 69, Appli	815	31	42.5	839	2	US-09-577-304A-204	Sequence 204, App
743	31	42.5	833	2	US-09-713-601A-69	Sequence 71, Appli	816	31	42.5	839	2	US-09-577-304A-206	Sequence 206, App
744	31	42.5	833	2	US-09-713-601A-71	Sequence 71, Appli	817	31	42.5	839	2	US-09-577-304A-218	Sequence 218, App
745	31	42.5	834	2	US-08-539-205A-6	Sequence 6, Appli	818	31	42.5	839	2	US-09-577-304A-221	Sequence 221, App
746	31	42.5	834	2	US-09-392-163A-6	Sequence 6, Appli	819	31	42.5	839	2	US-09-577-304A-226	Sequence 226, App
747	31	42.5	838	2	US-09-758-282B-265	Sequence 265, App	820	31	42.5	839	2	US-09-577-304A-228	Sequence 228, App
748	31	42.5	838	2	US-09-577-304A-265	Sequence 265, App	821	31	42.5	839	2	US-09-577-304A-230	Sequence 230, App
749	31	42.5	839	2	US-09-758-282B-63	Sequence 63, Appli	822	31	42.5	839	2	US-09-577-304A-232	Sequence 232, App
750	31	42.5	839	2	US-09-758-282B-73	Sequence 73, Appli	823	31	42.5	839	2	US-09-577-304A-234	Sequence 234, App
751	31	42.5	839	2	US-09-758-282B-81	Sequence 81, Appli	824	31	42.5	839	2	US-09-577-304A-236	Sequence 236, App
752	31	42.5	839	2	US-09-758-282B-83	Sequence 83, Appli	825	31	42.5	842	2	US-09-758-282B-77	Sequence 77, Appli
753	31	42.5	839	2	US-09-758-282B-89	Sequence 89, Appli	826	31	42.5	842	2	US-09-758-282B-93	Sequence 93, Appli
754	31	42.5	839	2	US-09-758-282B-115	Sequence 115, App	827	31	42.5	842	2	US-09-758-282B-241	Sequence 241, App
755	31	42.5	839	2	US-09-758-282B-118	Sequence 118, App	828	31	42.5	842	2	US-09-758-282B-263	Sequence 263, App
756	31	42.5	839	2	US-09-758-282B-121	Sequence 121, App	829	31	42.5	842	2	US-09-577-304A-77	Sequence 77, Appli
757	31	42.5	839	2	US-09-758-282B-124	Sequence 124, App	830	31	42.5	842	2	US-09-577-304A-93	Sequence 93, Appli

831	31	42.5	842	2	US-09-577-304A-241	Sequence 241, App	904	30.5	41.8	2296	2	US-08-980-357-27	Sequence 27, Appl
832	31	42.5	842	2	US-09-577-304A-263	Sequence 263, App	905	30.5	41.8	2296	1	US-09-357-375-27	Sequence 27, Appl
833	31	42.5	845	2	US-08-804-439A-94	Sequence 94, Appl	906	30	41.1	34	1	US-08-640-847C-16	Sequence 16, Appl
834	31	42.5	845	2	US-08-720-229-94	Sequence 94, Appl	907	30	41.1	49	2	US-09-079-030-26	Sequence 26, Appl
835	31	42.5	846	2	US-09-328-352-6286	Sequence 6286, Ap	908	30	41.1	73	1	US-08-891-837B-2	Sequence 2, Appl
836	31	42.5	908	2	US-09-252-991A-24682	Sequence 24682, A	909	30	41.1	73	2	US-09-107-532A-3851	Sequence 3851, Ap
837	31	42.5	908	2	US-09-623-326-9	Sequence 9, Appl	910	30	41.1	73	2	US-09-270-767-41128	Sequence 41128, A
838	31	42.5	908	2	US-09-623-326-10	Sequence 10, Appl	911	30	41.1	73	2	US-09-270-767-56344	Sequence 56344, A
839	31	42.5	910	2	US-09-623-326-7	Sequence 7, Appl	912	30	41.1	87	2	US-09-513-999C-5681	Sequence 5681, Ap
840	31	42.5	920	2	US-09-623-326-8	Sequence 8, Appl	913	30	41.1	87	2	US-09-513-999C-5683	Sequence 5683, Ap
841	31	42.5	920	2	US-09-640-958-6	Sequence 6, Appl	914	30	41.1	90	1	US-08-326-352-3	Sequence 3, Appl
842	31	42.5	921	2	US-09-902-540-15467	Sequence 15467, A	915	30	41.1	90	1	US-08-326-352-5	Sequence 5, Appl
843	31	42.5	927	2	US-09-270-767-4518	Sequence 4518, A	916	30	41.1	90	1	US-08-591-498-11	Sequence 11, Appl
844	31	42.5	949	2	US-09-623-326-11	Sequence 11, Appl	917	30	41.1	90	2	US-08-404-607-3	Sequence 3, Appl
845	31	42.5	980	2	US-09-379-530B-1	Sequence 1, Appl	918	30	41.1	90	2	US-08-404-607-5	Sequence 5, Appl
846	31	42.5	982	2	US-09-623-326-12	Sequence 12, Appl	919	30	41.1	93	2	US-08-931-858E-134	Sequence 134, App
847	31	42.5	988	2	US-09-949-016-5881	Sequence 5881, Ap	920	30	41.1	93	2	US-08-931-858E-176	Sequence 176, App
848	31	42.5	1036	2	US-09-771-161A-255	Sequence 255, App	921	30	41.1	93	2	US-09-220-407-134	Sequence 134, App
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850	31	42.5	1135	2	US-09-294-238A-21	Sequence 21, Appl	923	30	41.1	93	2	US-09-473-551-5	Sequence 5, Appl
851	31	42.5	1151	1	US-08-286-889-37	Sequence 37, Appl	924	30	41.1	94	2	US-08-931-858E-87	Sequence 87, Appl
852	31	42.5	1151	1	US-08-485-618-37	Sequence 37, Appl	925	30	41.1	94	2	US-08-981-739-87	Sequence 87, Appl
853	31	42.5	1151	1	US-08-362-652-37	Sequence 37, Appl	926	30	41.1	94	2	US-09-128-026-87	Sequence 87, Appl
854	31	42.5	1151	1	US-08-605-672-37	Sequence 37, Appl	927	30	41.1	94	2	US-09-220-616-87	Sequence 87, Appl
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856	31	42.5	1151	1	US-08-943-363-37	Sequence 37, Appl	929	30	41.1	94	2	US-09-220-407-87	Sequence 87, Appl
857	31	42.5	1151	2	US-09-193-043-37	Sequence 37, Appl	930	30	41.1	94	2	US-09-220-407-87	Sequence 87, Appl
858	31	42.5	1151	2	US-09-688-307A-37	Sequence 37, Appl	931	30	41.1	96	4	PCT-US93-08744-4	Sequence 4, Appl
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864	31	42.5	1161	1	US-08-943-363-55	Sequence 55, Appl	937	30	41.1	134	1	US-08-446-383A-2	Sequence 2, Appl
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866	31	42.5	1161	2	US-09-688-307A-55	Sequence 55, Appl	939	30	41.1	134	1	US-08-519-777-78	Sequence 78, Appl
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870	31	42.5	1325	2	US-09-294-298A-6	Sequence 6, Appl	943	30	41.1	134	1	US-08-777-019-78	Sequence 78, Appl
871	31	42.5	1353	2	US-08-894-173-2	Sequence 2, Appl	944	30	41.1	134	1	US-08-777-143-77	Sequence 77, Appl
872	31	42.5	1353	2	US-09-398-193-2	Sequence 2, Appl	945	30	41.1	134	1	US-08-777-143-78	Sequence 78, Appl
873	31	42.5	1353	2	US-10-071-223-3	Sequence 3, Appl	946	30	41.1	134	1	US-08-452-242-4	Sequence 4, Appl
874	31	42.5	1376	2	US-09-294-298A-4	Sequence 4, Appl	948	30	41.1	134	2	US-08-775-414-77	Sequence 77, Appl
875	31	42.5	1423	2	US-09-294-298A-2	Sequence 2, Appl	949	30	41.1	134	2	US-08-775-414-78	Sequence 78, Appl
876	31	42.5	1481	2	US-09-231-899-70	Sequence 70, Appl	950	30	41.1	134	2	US-08-451-374-4	Sequence 4, Appl
877	31	42.5	1581	2	US-09-866-108A-15754	Sequence 15754, A	951	30	41.1	134	2	US-08-935-268A-4	Sequence 4, Appl
878	31	42.5	1695	2	US-09-866-108A-15753	Sequence 15753, A	952	30	41.1	134	2	US-08-931-858E-77	Sequence 77, Appl
879	31	42.5	1876	1	US-08-619-554-2	Sequence 2, Appl	953	30	41.1	134	2	US-08-931-858E-78	Sequence 78, Appl
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881	31	42.5	1895	1	US-08-619-554-4	Sequence 4, Appl	955	30	41.1	134	2	US-08-981-739-78	Sequence 78, Appl
882	31	42.5	1895	1	US-09-487-558B-136	Sequence 136, App	956	30	41.1	134	2	US-08-452-229-4	Sequence 4, Appl
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886	31	42.5	1988	2	US-09-425-043-4	Sequence 4, Appl	960	30	41.1	134	2	US-09-220-616-78	Sequence 78, Appl
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888	31	42.5	2175	2	US-09-693-205A-8	Sequence 8, Appl	962	30	41.1	134	2	US-09-220-527-78	Sequence 78, Appl
889	31	42.5	2209	2	US-10-017-754-1903	Sequence 1903, Ap	963	30	41.1	134	2	US-09-220-407-77	Sequence 77, Appl
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892	31	42.5	2291	2	US-09-357-375-29	Sequence 29, Appl	966	30	41.1	134	2	US-09-219-952-78	Sequence 78, Appl
893	31	42.5	3169	1	US-08-477-451-6	Sequence 6, Appl	967	30	41.1	136	2	US-09-252-991A-23240	Sequence 23240, A
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895	31	42.5	3829	2	US-09-693-205A-2	Sequence 2, Appl	969	30	41.1	147	2	US-09-134-000C-6018	Sequence 6018, Ap
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898	30.5	41.8	326	2	US-09-252-991A-32227	Sequence 32227, A	972	30	41.1	156	2	US-09-270-767-46017	Sequence 46017, Ap
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977 30 41.1 174 2 US-08-311-731A-116 Sequence 116, App
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979 30 41.1 193 2 US-09-107-532A-5253 Sequence 5253, Ap
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981 30 41.1 194 2 US-09-270-767-49020 Sequence 49020, A
982 30 41.1 205 2 US-09-583-110-3163 Sequence 3163, Ap
983 30 41.1 205 2 US-09-107-433-4004 Sequence 4004, Ap
984 30 41.1 211 2 US-09-302-769-10 Sequence 10, Appl
985 30 41.1 211 2 US-09-972-800A-12 Sequence 12, Appl
986 30 41.1 211 2 US-08-962-560C-10 Sequence 10, Appl
987 30 41.1 213 2 US-09-949-016-9423 Sequence 9423, Ap
988 30 41.1 221 2 US-09-248-796A-24110 Sequence 24110, A
989 30 41.1 227 2 US-09-270-767-59033 Sequence 59033, A
990 30 41.1 227 2 US-09-902-540-15523 Sequence 15523, A
991 30 41.1 231 2 US-08-252-991A-17218 Sequence 17218, A
992 30 41.1 232 2 US-08-134-000C-3556 Sequence 3556, Ap
993 30 41.1 235 2 US-09-543-681A-5473 Sequence 5473, Ap
994 30 41.1 235 2 US-09-270-767-37185 Sequence 37185, A
995 30 41.1 235 2 US-09-270-767-52402 Sequence 52402, A
996 30 41.1 241 2 US-10-104-047-2501 Sequence 2501, Ap
997 30 41.1 243 2 US-08-252-991A-29870 Sequence 29870, A
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1000 30 41.1 261 2 US-09-902-540-15280 Sequence 15280, A

ALIGNMENTS

RESULT 1
US-09-463-458A-9
; Sequence 9, Application US/09463458A
; Patent No. 6383782
; GENERAL INFORMATION:
; APPLICANT: Barratt, Derek G
; APPLICANT: Needham, Maurice R.C.
; TITLE OF INVENTION: MCP-1 ANALOGS
; FILE REFERENCE: 1991-186
; CURRENT APPLICATION NUMBER: US/09/463,458A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: PCT/GB98/02179
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: [V9A]MCP-1(9-76)
US-09-463-458A-9

Query Match 100.0%; Score 73; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 12 ISVQRLASYRRITSSK 27
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RESULT 2
US-09-463-458A-26
; Sequence 26, Application US/09463458A
; Patent No. 6383782
; GENERAL INFORMATION:
; APPLICANT: Barratt, Derek G
; APPLICANT: Needham, Maurice R.C.
; TITLE OF INVENTION: MCP-1 ANALOGS
; FILE REFERENCE: 1991-186
; CURRENT APPLICATION NUMBER: US/09/463,458A
; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: PCT/GB98/02179
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: [V9G]MCP-1(9-76)
US-09-463-458A-26

Query Match 100.0%; Score 73; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 12 ISVQRLASYRRITSSK 27
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RESULT 3
US-09-463-458A-29
; Sequence 29, Application US/09463458A
; Patent No. 6383782
; GENERAL INFORMATION:
; APPLICANT: Barratt, Derek G
; APPLICANT: Needham, Maurice R.C.
; TITLE OF INVENTION: MCP-1 ANALOGS
; FILE REFERENCE: 1991-186
; CURRENT APPLICATION NUMBER: US/09/463,458A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: PCT/GB98/02179
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: [V9T]MCP-1(9-76)
US-09-463-458A-29

Query Match 100.0%; Score 73; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 12 ISVQRLASYRRITSSK 27
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RESULT 4
US-09-463-458A-30
; Sequence 30, Application US/09463458A
; Patent No. 6383782
; GENERAL INFORMATION:
; APPLICANT: Barratt, Derek G
; APPLICANT: Needham, Maurice R.C.
; TITLE OF INVENTION: MCP-1 ANALOGS
; FILE REFERENCE: 1991-186
; CURRENT APPLICATION NUMBER: US/09/463,458A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: PCT/GB98/02179
; PRIOR FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 68
; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: MCP1(9-76)
US-09-463-458A-30

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Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
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Db 12 ISVQRLASYRRITSSK 27

RESULT 5

US-09-463-458A-31
; Sequence 31, Application US/09463458A

; Patent No. 6383782

; GENERAL INFORMATION:

; APPLICANT: Barratt, Derek G

; APPLICANT: Needham, Maurice R.C.

; TITLE OF INVENTION: MCP-1 ANALOGS

; FILE REFERENCE: 1991-186

; CURRENT APPLICATION NUMBER: US/09/463,458A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: PCT/GB98/02179

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 31

; LENGTH: 69

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Met-MCP1(9-76)

US-09-463-458A-31

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
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Db 13 ISVQRLASYRRITSSK 28

RESULT 6

US-09-463-458A-32
; Sequence 32, Application US/09463458A

; Patent No. 6383782

; GENERAL INFORMATION:

; APPLICANT: Barratt, Derek G

; APPLICANT: Needham, Maurice R.C.

; TITLE OF INVENTION: MCP-1 ANALOGS

; FILE REFERENCE: 1991-186

; CURRENT APPLICATION NUMBER: US/09/463,458A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: PCT/GB98/02179

; PRIOR FILING DATE: 1998-07-21

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 32

; LENGTH: 69

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: pglu-MCP1(9-76)

; FEATURE:

; NAME/KEY: VARIANT

; LOCATION: ()

; OTHER INFORMATION: Xaa=pglu

US-09-463-458A-32

Query Match 100.0%; Score 73; DB 2; Length 69;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
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Db 13 ISVQRLASYRRITSSK 28

RESULT 7

US-07-956-862A-1

; Sequence 1, Application US/07956862A

; Patent No. 5413778

; GENERAL INFORMATION:

; APPLICANT: KUNKEL, STEVEN L.

; APPLICANT: LYLE, LEON R.

; APPLICANT: STRIETER, ROBERT M.

; TITLE OF INVENTION: LABELLED MONOCYTE CHEMOATTRACTANT

; TITLE OF INVENTION: PROTEIN MATERIAL AND MEDICAL USES

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Rothwell, Figg, Ernst & Kurz

; STREET: Suite 701-E, 555 Thirteenth St., N.W

; CITY: Washington

; STATE: D. C.

; COUNTRY: U.S.A.

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/956,862A

; FILING DATE: 05-OCT-1992

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: REPPER, GEORGE R.

; REGISTRATION NUMBER: 31,414

; REFERENCE/DOCKET NUMBER: 1670-197A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202)783-6040

; TELEFAX: (202)783-6031

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 76 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; FRAGMENT TYPE: N-terminal

US-07-956-862A-1

Query Match 100.0%; Score 73; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
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Db 20 ISVQRLASYRRITSSK 35

RESULT 8

US-08-250-958-1

; Sequence 1, Application US/08250958

; Patent No. 5571713

; GENERAL INFORMATION:

; APPLICANT: LYLE, LEON R.

; APPLICANT: KUNKEL, STEVEN L.

; APPLICANT: STRIETER, ROBERT M.

; TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING

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;
; TITLE OF INVENTION: VASCULAR RESTENOSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,958
; FILING DATE: 27-MAY-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/965,678
; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 2077-206A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
;
US-08-250-958-1
;
Query Match 100.0%; Score 73; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
Db 20 ISVORLASYYRITSSK 35

RESULT 9
US-08-235-659-1
; Sequence 1, Application US/08235659
; Patent No. 5605671
; GENERAL INFORMATION:
; APPLICANT: Lyle, Leon R.
; APPLICANT: Kunkel, Steven L.
; APPLICANT: Strieter, Robert M.
; TITLE OF INVENTION: LABELLED CHEMOKINE MATERIALS AND
; TITLE OF INVENTION: MEDICAL USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: Suite 701-E, 555 Thirteenth St., N.W
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,659
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; FILING DATE: 29-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,862
; FILING DATE: 05-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/956,863
; FILING DATE: 05-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WALKER, Barbara W.
; REGISTRATION NUMBER: 35,400
; REFERENCE/DOCKET NUMBER: 2077-205A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)783-6040
; TELEFAX: (202)783-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
;
US-08-235-659-1
;
Query Match 100.0%; Score 73; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
Db 20 ISVORLASYYRITSSK 35

RESULT 10
US-08-716-188-2
; Sequence 2, Application US/08716188
; Patent No. 5908829
; GENERAL INFORMATION:
; APPLICANT: KELLY, RODNEY W
; TITLE OF INVENTION: USE OF MCP-1 FOR INDUCING RIPENING OF
; TITLE OF INVENTION: THE CERVIX
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,188
; FILING DATE: 30-SEP-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/00733
; FILING DATE: 31-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9406463.1
; FILING DATE: 31-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4091
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 2:
```

SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-716-188-2

Query Match 100.0%; Score 73; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
|||||

Db 20 ISVORLASYYRRTSSK 35

RESULT 11

US-08-615-232A-5
Sequence 5, Application US/08615232A
Patent No. 5993814
GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
APPLICANT: HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,232A
FILING DATE: 13-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9318984
FILING DATE: 14-SEP-1993
APPLICATION NUMBER: GB 9408602
FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 550-32
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-615-232A-5

Query Match 100.0%; Score 73; DB 1; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
|||||

Db 20 ISVORLASYYRRTSSK 35

RESULT 12

US-08-470-323-5
Sequence 5, Application US/08470323A
Patent No. 6031080
GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
APPLICANT: HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
FILE REFERENCE: 550-33
CURRENT APPLICATION NUMBER: US/08/470,323A
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: PCT/GB94/02006
EARLIER FILING DATE: 1994-09-14
EARLIER APPLICATION NUMBER: GB 9318984.3
EARLIER FILING DATE: 1993-09-14
EARLIER APPLICATION NUMBER: GB 94086902.2
EARLIER FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 5
LENGTH: 76
TYPE: PRT
ORGANISM: human
US-08-470-323-5

Query Match 100.0%; Score 73; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
|||||

Db 20 ISVORLASYYRRTSSK 35

RESULT 13

US-09-195-457-5
Sequence 5, Application US/09195457
Patent No. 6605702
GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
APPLICANT: HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
FILE REFERENCE: 550-33
CURRENT APPLICATION NUMBER: US/09/195,457
CURRENT FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 08/470,323
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: PCT/GB94/02006
PRIOR FILING DATE: 1994-09-14
PRIOR APPLICATION NUMBER: GB 9318984.3
PRIOR FILING DATE: 1993-09-14
PRIOR APPLICATION NUMBER: GB 94086902.2
PRIOR FILING DATE: 1994-04-29
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 5
LENGTH: 76
TYPE: PRT
ORGANISM: human
US-09-195-457-5

Query Match 100.0%; Score 73; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
|||||

Db 20 ISVORLASYYRRTSSK 35

RESULT 14

US-09-291-038-5
; Sequence 5, Application US/09291038
; Patent No. 6635251
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; JOSE, PETER J.
; GRIFFITHS-JOHNSON, DAVID A.
; HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/291,038
; FILING DATE: 14-Apr-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/615,232A
; FILING DATE: 13-AUG-1996
; APPLICATION NUMBER: GB 9318984
; FILING DATE: 14-SEP-1993
; APPLICATION NUMBER: GB 9408602
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 550-32
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-291-038-5

Query Match 100.0%; Score 73; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASVRRITSSK 35

RESULT 15

US-09-043-861-31
; Sequence 31, Application US/09043861
; Patent No. 6793917
; GENERAL INFORMATION:
; APPLICANT: IMAI, Toshio
; APPLICANT: YOSHIDA, Tetsuya
; APPLICANT: YOSHIE, Osamu
; TITLE OF INVENTION: TYPE CC CHEMOKINE-LIKE PROTEIN
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.

; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/043,861
; FILING DATE: 27-MAR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP96/02801
; FILING DATE: 27-SEP-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 56044/1996
; FILING DATE: 13-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 249457/1995
; FILING DATE: 27-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wegner, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 74129/432
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5393
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 76 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-043-861-31

Query Match 100.0%; Score 73; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASVRRITSSK 35

RESULT 16

US-08-330-163-12
; Sequence 12, Application US/08330163
; Patent No. 5656724
; GENERAL INFORMATION:
; APPLICANT: Daly, Thomas J.
; APPLICANT: Larosa, Gregory J.
; TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
; TITLE OF INVENTION: Use
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/330,163
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 00231/080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-330-163-12

Query Match 100.0%; Score 73; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRTSSK 16
|||||
Db 22 ISVQRLASYRRTSSK 37

RESULT 17
US-08-482-111-12
Sequence 12, Application US/08482111
Patent No. 5789539

GENERAL INFORMATION:
APPLICANT: Daly, Thomas J.
TITLE OF INVENTION: Chemokine-Like Proteins and Methods of
USE
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,111
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 00231/080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-111-12

Query Match 100.0%; Score 73; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRTSSK 16
|||||

Db 22 ISVQRLASYRRTSSK 37

RESULT 18

US-09-567-225-14
Sequence 14, Application US/09567225
Patent No. 6713052
GENERAL INFORMATION:
APPLICANT: White, John R.
APPLICANT: Pelus, Louis
APPLICANT: Li, Haodong
APPLICANT: Kreider, Brent L.
TITLE OF INVENTION: No. 6713052el Chemokine for Mobilizing Stem Cells
FILE REFERENCE: 1488.1550004
CURRENT APPLICATION NUMBER: US/09/567,225
CURRENT FILING DATE: 2000-10-09
PRIOR APPLICATION NUMBER: US 09/225,501
PRIOR FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: US 60/006,051
PRIOR FILING DATE: 1995-10-24
PRIOR APPLICATION NUMBER: US 08/740,033
PRIOR FILING DATE: 1996-10-23
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 78
TYPE: PRT
ORGANISM: MCP-1
US-09-567-225-14

Query Match 100.0%; Score 73; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRTSSK 16
|||||
Db 22 ISVQRLASYRRTSSK 37

RESULT 19

PCT-US95-00605-1
Sequence 1, Application PC/TUS9500605
GENERAL INFORMATION:
APPLICANT: Lyle, Leon
APPLICANT: Thomas-Miller, Beth
TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING
TITLE OF INVENTION: VASCULAR RESTENOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mallinckrodt Medical, Inc.
STREET: 675 McDonnell Boulevard, P.O. Box 5840
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63134

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00605
FILING DATE: 13-JAN-1995
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/182,917
FILING DATE: 14-JAN-1994
APPLICATION NUMBER: US 07/965,678
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vacca, Rita D.
REGISTRATION NUMBER: 33,624
REFERENCE/DOCKET NUMBER: 0783.2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 314-895-7215
TELEFAX: 314-895-2156
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 5..22
PCT-US95-00605-1

Query Match 100.0%; Score 73; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 22 ISVQRLASYRRITSSK 37

RESULT 20

US-08-127-499A-35
Sequence 35, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown

US-08-127-499A-35

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 43 ISVQRLASYRRITSSK 58

RESULT 21

US-08-482-847-35
Sequence 35, Application US/08482847
Patent No. 5556757
GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown

US-08-482-847-35

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 43 ISVQRLASYRRITSSK 58

RESULT 22

US-08-347-492B-8
Sequence 8, Application US/08347492B
Patent No. 5602008
GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
TITLE OF INVENTION: PRODUCTION AND USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,492B
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0024
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 487124
US-08-347-492B-8

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 23
US-08-449-19
Sequence 19, Application US/08480449
Patent No. 5688927
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,449
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gase, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/32779

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "Hu MCP-1"
US-08-480-449-19

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 24
US-08-479-126B-5
Sequence 5, Application US/08479126B
Patent No. 5866373
GENERAL INFORMATION:
APPLICANT: LI, HAODONG
APPLICANT: RUBEN, STEVEN M
APPLICANT: SUTTON, GRANGER G III
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING HUMAN MONOCYTE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,126B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STREFF, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-479-126B-5

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58
|||||

RESULT 25

US-08-421-144A-5
; Sequence 5, Application US/08421144A
; Patent No. 5874211
; GENERAL INFORMATION:
; APPLICANT: BANDMAN, OLGA
; APPLICANT: COLEMAN, ROGER
; APPLICANT: STUART, SUSAN G.
; TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN EOSINOPHILS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/421,144A
; FILING DATE: 13-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF-0031 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-421-144A-5

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58
|||||

RESULT 26

US-08-726-830A-5
; Sequence 5, Application US/08726830A
; Patent No. 5880263
; GENERAL INFORMATION:
; APPLICANT: LI, HAODONG
; APPLICANT: RUBEN, STEVEN M
; APPLICANT: SUTTON, GRANGER G III
; TITLE OF INVENTION: MONOCYTE CHEMOTACTIC PROTEIN-4
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600

; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,830A
; FILING DATE: 08-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,126
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,425
; FILING DATE: 21-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05384
; FILING DATE: 16-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0340002

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-726-830A-5

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58
|||||

RESULT 27
US-08-660-542-19
; Sequence 19, Application US/08660542
; Patent No. 5932703
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
; TITLE OF INVENTION: ANALOGS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,542
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/558,658
FILING DATE: 16-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,620
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/33318
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "Hu MCP-1"
FEATURE:
NAME/KEY: Protein
LOCATION: 1..76
US-08-660-542-19

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 43 ISVQRLASYRRITSSK 58

RESULT 28
US-08-798-143-8
Sequence 8, Application US/08798143
Patent No. 5936068
GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
TITLE OF INVENTION: PRODUCTION AND USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,143
FILING DATE: 10-FEB-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,492
FILING DATE: 29-NOV-1994
APPLICATION NUMBER: 08/303,241
FILING DATE: 07-SEP-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
ATTORNEY/AGENT INFORMATION:

NAME: Luther, Barbara J
REGISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: PF-0024
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 487124
US-08-798-143-8

Query Match 100.0%; Score 73; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 43 ISVQRLASYRRITSSK 58

RESULT 29
US-07-927-391-24
Sequence 24, Application US/07927391
Patent No. 6001649
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: MILOUX, Brigitte
APPLICANT: MINTY, Adrian
APPLICANT: VITA, Natalio
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500, 1800 Diagonal
STREET: Road, PO Box 299
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/927,391
FILING DATE: 19920929
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/369
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899143
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-927-391-24

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 43 ISVQRLASYRRITSSK 58

RESULT 30

US-08-995-156A-5
; Sequence 5, Application US/08995156A
; Patent No. 6028169
; GENERAL INFORMATION:
; APPLICANT: KREIDER, BRENT L.
; APPLICANT: RUBEN, STEVEN M.
; APPLICANT: OLSEN, HENRIK S.
; TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995.156A
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/042,269
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0340004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-995-156A-5

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 43 ISVQRLASYRRITSSK 58

RESULT 31

US-09-044-856A-5
; Sequence 5, Application US/09044856A
; Patent No. 6075124
; GENERAL INFORMATION:
; APPLICANT: LI, HAODONG
; APPLICANT: RUBEN, STEVEN M
; APPLICANT: SUTTON, GRANGER G III
; TITLE OF INVENTION: HUMAN CHEMOTACTIC PROTEIN
; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,856A
; FILING DATE: HEREWITH
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/726,830
; FILING DATE: 08-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,126
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,425
; FILING DATE: 21-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05384
; FILING DATE: 16-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0340006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-044-856A-5

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 43 ISVQRLASYRRITSSK 58

RESULT 32

US-09-044-855A-5
; Sequence 5, Application US/09044855A
; Patent No. 6100389
; GENERAL INFORMATION:
; APPLICANT: LI, HAODONG
; APPLICANT: RUBEN, STEVEN M
; APPLICANT: SUTTON, GRANGER G III
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A HUMAN CHEMOTACTIC
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,855A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/479,126
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-044-855A-5

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
|||||
Db 43 ISVORLASYYRITSSK 58

RESULT 33
US-08-679-493A-152
Sequence 152, Application US/08679493A
Patent No. 6303295
GENERAL INFORMATION:
APPLICANT: Taylor, Ethan W.
TITLE OF INVENTION: SELENOPROTEINS, CODING SEQUENCES AND METHODS
FILE REFERENCE: 55-95
CURRENT APPLICATION NUMBER: US/08/679,493A
CURRENT FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: 60/001203
PRIOR FILING DATE: 1995-07-14
PRIOR APPLICATION NUMBER: 60/003,112
PRIOR FILING DATE: 1995-09-01
NUMBER OF SEQ ID NOS: 216
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 152
LENGTH: 99
TYPE: PRT
ORGANISM: Homo sapiens
US-08-679-493A-152

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
|||||
Db 43 ISVORLASYYRITSSK 58

RESULT 34
US-08-479-603-19
Sequence 19, Application US/08479603

Patent No. 6320023
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,603
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 27866/32780
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "Hu MCP-1"
US-08-479-603-19

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
|||||
Db 43 ISVORLASYYRITSSK 58

RESULT 35
US-09-419-281-5
Sequence 5, Application US/09419281
Patent No. 6379926
GENERAL INFORMATION:
APPLICANT: KREIDER, BRENT L.
RUBEN, STEVEN M.
OLSEN, HENRIK S.
TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110
;;
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; FILING DATE: 07-Apr-2000
;; CLASSIFICATION: <unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/940,687
;; FILING DATE: 30-SEP-1997
;; APPLICATION NUMBER: 60/027,128
;; FILING DATE: 30-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bieker-Brady, Kristina
;; REGISTRATION NUMBER: 39,109
;; REFERENCE/DOCKET NUMBER: 00786/293002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-428-0200
;; TELEFAX: 617-428-7045
;; TELEX: <Unknown>
;;
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 99 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-545-894-5

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
Db 43 ISVORLASYYRITSSK 58
|||||

RESULT 39
US-09-834-795A-28
; Sequence 28, Application US/09834795A
; Patent No. 6723518
; GENERAL INFORMATION:
; APPLICANT: Lawrence, Papsidero
; APPLICANT: Lyn, Dyster
; APPLICANT: Jana, Frustaci
; TITLE OF INVENTION: Detection and Treatment of Breast Cancer
; FILE REFERENCE: 3380/11127-US3
; CURRENT APPLICATION NUMBER: US/09/834,795A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 09/146,580
; PRIOR FILING DATE: 1998-09-03
; PRIOR APPLICATION NUMBER: 60/071,899
; PRIOR FILING DATE: 1998-01-20
; PRIOR APPLICATION NUMBER: 60/092,155
; PRIOR FILING DATE: 1998-07-09
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-795A-28

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSSK 16
Db 43 ISVORLASYYRITSSK 58
|||||

RESULT 40
US-09-067-447B-19
; Sequence 19, Application US/09067447B
; Patent No. 6737513
; GENERAL INFORMATION:
; APPLICANT: Gray, Patrick W.
; APPLICANT: Chantry, David H.
; APPLICANT: Deeley, Michael C.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE (MDC) AND
; TITLE OF INVENTION: CHEMOKINE ANALOGS AND ASSAY TO IDENTIFY MODULATORS OF MDC
; TITLE OF INVENTION: ACTIVITY
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/067,447B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/939,107
; FILING DATE: 26-SEPT-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/660,542
; FILING DATE: 7-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/558,658
; FILING DATE: 16-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,620
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Gabs, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/34404
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: "Hu MCP-1"
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..76
US-09-067-447B-19

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ISVQLASYRRTSSK 16
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Db 43 ISVQLASYRRTSSK 58

RESULT 41
US-09-517-204-10
; Sequence 10, Application US/09517204
; Patent No. 6780973
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/517,204
; CURRENT FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 08/366,887
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-204-10

Query Match 100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQLASYRRTSSK 16
    |||||
Db 43 ISVQLASYRRTSSK 58

RESULT 42
US-08-437-306-2
; Sequence 2, Application US/08437306
; Patent No. 6787645
; GENERAL INFORMATION:
; APPLICANT: Rollins, Barrett J.
; APPLICANT: Stiles, Charles D.
; APPLICANT: Wong, Gordon G.
; TITLE OF INVENTION: No. 6787645el Human Cytokine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millicia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,306
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/228,931
; FILING DATE: 13-APR-1994

Qy 1 ISVQLASYRRTSSK 16
    |||||
Db 43 ISVQLASYRRTSSK 58

RESULT 43
US-08-479-620-19
; Sequence 19, Application US/08479620
; Patent No. 6790947
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,620
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Gasse, David A.
; REGISTRATION NUMBER: 38,153
; REFERENCE/DOCKET NUMBER: 27866/32628
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: "Hu MCP-1"
US-08-479-620-19

Query Match          100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 44
US-10-054-967-5
; Sequence 5, Application US/10054967
; Patent No. 6815420
; GENERAL INFORMATION:
; APPLICANT: KREIDER, BRENT L.
; RUBEN, STEVEN M.
; OLSEN, HENRIK S.
; TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/054,967
; FILING DATE: 25-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,156
; FILING DATE: 19-DEC-1997
; APPLICATION NUMBER: 60/042,269
; FILING DATE: 31-MAR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0340004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-054-967-5

Query Match          100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 45
US-10-141-965-5
; Sequence 5, Application US/10141965
; Patent No. 6867006
; GENERAL INFORMATION:
; APPLICANT: LI, HAODONG
; RUBEN, STEVEN M
; SUTTON, GRANGER G III
; TITLE OF INVENTION: HUMAN CHEMOTACTIC PROTEIN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/141,965
; FILING DATE: 10-May-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/453,416
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: US 09/044,855
; FILING DATE: 20-MAR-1998
; APPLICATION NUMBER: US 08/479,126
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: 08/424,425
; FILING DATE: 21-APR-1995
; APPLICATION NUMBER: PCT/US94/05384
; FILING DATE: 16-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.034000C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-141-965-5

Query Match          100.0%; Score 73; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 46
PCT-US96-10087-5
; Sequence 5, Application PC/TUS9610087
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Monocyte Chemotactic Protein-4
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPC)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10087
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; FILING DATE: 07-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/479,126
; FILING DATE: 07-JUN-1995
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10087-5

Query Match 100.0%; Score 73; DB 4; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 47
5212073-2
; Patent No. 5212073
; APPLICANT: ROLLINS, BARRETT; STILES, CHARLES; WONG, GORDON G.
; TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/351,008
; FILING DATE: 12-MAY-1989
; SEQ ID NO: 2:
; LENGTH: 99
5212073-2

Query Match 100.0%; Score 73; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISVQRLASYRRITSSK 58

RESULT 48
US-09-133-521-5
; Sequence 5, Application US/09133521
; Patent No. 6281200
; GENERAL INFORMATION:
; APPLICANT: Fife, Kenneth H.
; APPLICANT: Krathwohl, Mitchell D.
; APPLICANT: Hromas, Robert
; APPLICANT: Brown, Daxron R.
; APPLICANT: Broxmeyer, Hal E.
; TITLE OF INVENTION: FUNCTIONAL CHARACTERIZATION OF THE C-C CHEMOKINE-LIKE
; MOLECULES ENCODED BY MOLLUSCUM CONTAGIOSUM VIRUS TYPES 1
; TITLE OF INVENTION: AND 2
; FILE REFERENCE: INDY:034
; CURRENT APPLICATION NUMBER: US/09/133,521
; CURRENT FILING DATE: 1998-08-18
; EARLIER APPLICATION NUMBER: 60/055,532
; EARLIER FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-133-521-5

Query Match 83.6%; Score 61; DB 2; Length 99;
Best Local Similarity 75.0%; Pred. No. 0.001;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 ISVQRLASYRRITSSK 16
Db 43 ISMQLMNYRRVTSSK 58

RESULT 49
US-09-366-887A-20
; Sequence 20, Application US/09366887A
; Patent No. 6403782
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/366,887A
; CURRENT FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-366-887A-20

Query Match 76.7%; Score 56; DB 2; Length 37;
Best Local Similarity 75.0%; Pred. No. 0.0029;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
Db 16 IPLQLLESYRRITSGK 31

RESULT 50
US-09-517-204-20
; Sequence 20, Application US/09517204
; Patent No. 6780973
; GENERAL INFORMATION:
; APPLICANT: LUSTER, ANDREW D.
; APPLICANT: LEDER, PHILIP
; APPLICANT: ROTHENBERG, MARC
; APPLICANT: GARCIA, EDUARDO
; TITLE OF INVENTION: EOTAXIN: AN EOSINOPHIL CHEMOATTRACTANT
; FILE REFERENCE: 00383/025002
; CURRENT APPLICATION NUMBER: US/09/517,204
; CURRENT FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: 08/366,887
; PRIOR FILING DATE: 1999-08-04
; PRIOR APPLICATION NUMBER: 60/000,449
; PRIOR FILING DATE: 1995-06-22
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1995-09-01
; PRIOR APPLICATION NUMBER: 08/522,713
; PRIOR FILING DATE: 1998-06-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-204-20

Query Match 76.7%; Score 56; DB 2; Length 37;
Best Local Similarity 75.0%; Pred. No. 0.0029;
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Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| : ||| ||||| |
Db 16 IPLQRLASYRRITSGK 31

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OM protein - protein search, using sw model

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Perfect score: 73

Sequence: 1 ISVORLASYYRITSSK 16

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA Main.*
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4: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	73	100.0	24	5	US-10-983-453-3
5	73	100.0	26	4	US-10-082-815-4
6	73	100.0	26	4	US-10-243-795-1375
7	73	100.0	26	4	US-10-243-795-1411
8	73	100.0	26	4	US-10-243-795-1412
9	73	100.0	26	5	US-10-983-453-4
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11	73	100.0	35	4	US-10-243-795-1352
12	73	100.0	35	4	US-10-243-795-1353
13	73	100.0	35	4	US-10-243-795-1354
14	73	100.0	35	4	US-10-243-795-1355
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19	73	100.0	35	4	US-10-243-795-1360
20	73	100.0	35	4	US-10-243-795-1361
21	73	100.0	35	4	US-10-243-795-1362
22	73	100.0	35	4	US-10-243-795-1363
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25	73	100.0	35	4	US-10-243-795-1366
26	73	100.0	35	4	US-10-243-795-1367
27	73	100.0	35	4	US-10-243-795-1368

28	73	100.0	35	4	US-10-243-795-1369	GENERAL INFORMATI
29	73	100.0	35	4	US-10-243-795-1370	GENERAL INFORMATI
30	73	100.0	35	4	US-10-243-795-1371	GENERAL INFORMATI
31	73	100.0	35	4	US-10-243-795-1372	GENERAL INFORMATI
32	73	100.0	35	4	US-10-243-795-1373	GENERAL INFORMATI
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34	73	100.0	35	4	US-10-243-795-1413	GENERAL INFORMATI
35	73	100.0	41	4	US-10-243-795-1378	GENERAL INFORMATI
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37	73	100.0	69	4	US-10-339-778-4	Sequence 4, Appli
38	73	100.0	69	4	US-10-276-971-2	Sequence 2, Appli
39	73	100.0	76	3	US-09-195-457-5	Sequence 5, Appli
40	73	100.0	76	3	US-09-792-793A-20	Sequence 20, Appli
41	73	100.0	76	4	US-10-339-778-3	Sequence 3, Appli
42	73	100.0	76	4	US-10-276-971-1	Sequence 1, Appli
43	73	100.0	76	4	US-10-375-209A-20	Sequence 20, Appli
44	73	100.0	76	4	US-10-332-038A-5	Sequence 5, Appli
45	73	100.0	76	4	US-10-668-733-7	Sequence 7, Appli
46	73	100.0	76	4	US-10-668-733-14	Sequence 14, Appli
47	73	100.0	76	4	US-10-393-804A-1	Sequence 1, Appli
48	73	100.0	76	4	US-10-243-795-7	Sequence 7, Appli
49	73	100.0	76	5	US-10-872-198-102	Sequence 102, App
50	73	100.0	76	5	US-10-839-017-8	Sequence 8, Appli
51	73	100.0	76	5	US-10-644-277-149	Sequence 149, App
52	73	100.0	76	5	US-10-332-039A-5	Sequence 5, Appli
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55	73	100.0	76	5	US-10-622-134-5	Sequence 5, Appli
56	73	100.0	76	5	US-10-981-936-42	Sequence 42, Appli
57	73	100.0	76	6	US-11-021-951-102	Sequence 102, App
58	73	100.0	78	4	US-10-803-960-14	Sequence 14, Appli
59	73	100.0	90	4	US-10-424-599-263303	Sequence 263303,
60	73	100.0	98	4	US-10-449-831A-210	Sequence 210, App
61	73	100.0	99	2	US-08-927-939-16	Sequence 16, Appli
62	73	100.0	99	3	US-09-834-795A-28	Sequence 28, Appli
63	73	100.0	99	3	US-09-834-794A-28	Sequence 28, Appli
64	73	100.0	99	4	US-10-057-275-9	Sequence 9, Appli
65	73	100.0	99	4	US-10-033-067-4	Sequence 4, Appli
66	73	100.0	99	4	US-10-141-965-5	Sequence 5, Appli
67	73	100.0	99	4	US-10-146-496-9	Sequence 9, Appli
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71	73	100.0	99	4	US-10-116-275-222	Sequence 222, App
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74	73	100.0	99	5	US-10-733-878-515	Sequence 515, App
75	73	100.0	99	5	US-10-847-824-28	Sequence 28, Appli
76	73	100.0	99	5	US-10-852-335A-141	Sequence 141, App
77	73	100.0	99	5	US-10-852-335A-148	Sequence 148, App
78	73	100.0	99	5	US-10-833-656-1	Sequence 1, Appli
79	73	100.0	99	5	US-10-773-446-130	Sequence 130, App
80	73	100.0	99	5	US-10-818-952-19	Sequence 19, Appli
81	73	100.0	99	6	US-11-035-998-5	Sequence 5, Appli
82	73	100.0	122	4	US-10-339-778-2	Sequence 2, Appli
83	73	100.0	133	4	US-10-449-831A-214	Sequence 214, App
84	73	100.0	325	3	US-09-792-793A-71	Sequence 71, Appli
85	73	100.0	325	4	US-10-375-209A-71	Sequence 71, Appli
86	73	100.0	327	3	US-09-792-793A-72	Sequence 72, Appli
87	73	100.0	327	4	US-10-375-209A-72	Sequence 72, Appli
88	73	100.0	332	3	US-09-792-793A-73	Sequence 73, Appli
89	73	100.0	332	4	US-10-375-209A-73	Sequence 73, Appli
90	69	94.5	23	4	US-10-082-815-13	Sequence 13, Appli
91	69	94.5	23	5	US-10-983-453-13	Sequence 13, Appli
92	68	93.2	23	4	US-10-082-815-14	Sequence 14, Appli
93	68	93.2	23	5	US-10-983-453-14	Sequence 14, Appli
94	67	91.8	44	5	US-10-450-763-41863	Sequence 41863, A
95	63	86.3	19	4	US-10-082-815-16	Sequence 16, Appli
96	63	86.3	19	5	US-10-983-453-16	Sequence 16, Appli
97	63	86.3	23	4	US-10-082-815-11	Sequence 11, Appli
98	63	86.3	23	5	US-10-983-453-11	Sequence 11, Appli
99	62	84.9	103	4	US-10-425-1415-344726	Sequence 344726,
100	59	80.8	23	4	US-10-082-815-12	Sequence 12, Appli

101	59	80.8	23	5	US-10-983-453-12	Sequence 12, Appl	174	47	64.4	137	4	US-10-335-394-2	Sequence 2, Appl
102	58	79.5	23	4	US-10-082-815-5	Sequence 5, Appl	175	47	64.4	151	4	US-10-335-394-7	Sequence 7, Appl
103	58	79.5	23	4	US-10-983-453-5	Sequence 5, Appl	176	47	64.4	325	3	US-09-792-793A-74	Sequence 74, Appl
104	56	76.7	74	3	US-09-792-793A-13	Sequence 13, Appl	177	47	64.4	325	4	US-10-375-209A-74	Sequence 74, Appl
105	56	76.7	74	4	US-10-125-451-20	Sequence 20, Appl	178	47	64.4	327	3	US-09-792-793A-75	Sequence 75, Appl
106	56	76.7	74	4	US-10-125-451-20	Sequence 20, Appl	179	47	64.4	327	4	US-10-375-209A-75	Sequence 75, Appl
107	56	76.7	74	4	US-10-375-209A-13	Sequence 13, Appl	180	47	64.4	332	3	US-09-792-793A-76	Sequence 76, Appl
108	56	76.7	74	4	US-10-646-770-20	Sequence 20, Appl	181	47	64.4	332	4	US-10-375-209A-76	Sequence 76, Appl
109	56	76.7	74	4	US-10-332-038A-3	Sequence 3, Appl	182	47	64.4	348	4	US-10-335-394-51	Sequence 51, Appl
110	56	76.7	74	4	US-10-668-733-8	Sequence 8, Appl	183	47	64.4	359	4	US-10-335-394-16	Sequence 16, Appl
111	56	76.7	74	4	US-10-668-733-11	Sequence 11, Appl	184	47	64.4	361	4	US-10-335-394-14	Sequence 14, Appl
112	56	76.7	74	4	US-10-668-733-15	Sequence 15, Appl	185	47	64.4	471	5	US-10-415-431-1	Sequence 1, Appl
113	56	76.7	74	5	US-10-872-198-101	Sequence 101, App	186	47	64.4	601	4	US-10-335-394-52	Sequence 52, Appl
114	56	76.7	74	5	US-10-332-039A-3	Sequence 3, Appl	187	47	64.4	931	5	US-10-415-431-12	Sequence 12, Appl
115	56	76.7	74	6	US-11-021-951-101	Sequence 101, App	188	46	63.0	70	4	US-10-125-451-17	Sequence 17, Appl
116	56	76.7	97	2	US-08-927-939-25	Sequence 25, Appl	189	46	63.0	70	4	US-10-263-139-17	Sequence 17, Appl
117	56	76.7	97	3	US-09-834-795A-26	Sequence 26, Appl	190	46	63.0	70	4	US-10-646-770-17	Sequence 17, Appl
118	56	76.7	97	3	US-09-834-794A-26	Sequence 26, Appl	191	45	61.6	97	3	US-09-886-119A-21	Sequence 21, Appl
119	56	76.7	97	4	US-10-057-275-2	Sequence 2, Appl	192	45	61.6	97	4	US-10-376-564-21	Sequence 21, Appl
120	56	76.7	97	4	US-10-057-275-5	Sequence 5, Appl	193	45	61.6	156	4	US-10-335-394-4	Sequence 4, Appl
121	56	76.7	97	4	US-10-114-893-52	Sequence 52, Appl	194	45	61.6	171	4	US-10-335-394-9	Sequence 9, Appl
122	56	76.7	97	4	US-10-289-454-242	Sequence 242, App	195	44	60.3	71	3	US-09-537-859-3	Sequence 3, Appl
123	56	76.7	97	4	US-10-050-902-242	Sequence 242, App	196	44	60.3	71	3	US-09-537-859-4	Sequence 4, Appl
124	56	76.7	97	4	US-10-050-898-242	Sequence 242, App	197	44	60.3	71	6	US-11-123-089-4	Sequence 4, Appl
125	56	76.7	97	5	US-10-847-824-26	Sequence 26, Appl	198	44	60.3	74	3	US-09-195-457-6	Sequence 6, Appl
126	56	76.7	323	3	US-09-792-793A-80	Sequence 80, Appl	199	44	60.3	74	5	US-10-622-134-6	Sequence 6, Appl
127	56	76.7	325	3	US-10-375-209A-80	Sequence 80, Appl	200	44	60.3	74	3	US-09-792-793A-21	Sequence 21, Appl
128	56	76.7	325	3	US-09-792-793A-81	Sequence 81, Appl	201	44	60.3	76	3	US-10-001-221A-1	Sequence 1, Appl
129	56	76.7	325	4	US-10-375-209A-81	Sequence 81, Appl	202	44	60.3	76	4	US-10-001-221A-1	Sequence 1, Appl
130	56	76.7	330	3	US-09-792-793A-82	Sequence 82, Appl	203	44	60.3	76	4	US-10-375-209A-21	Sequence 21, Appl
131	56	76.7	330	4	US-10-375-209A-82	Sequence 82, Appl	204	44	60.3	76	4	US-10-398-457-37	Sequence 37, Appl
132	54	74.0	23	4	US-10-082-815-15	Sequence 15, Appl	205	44	60.3	76	5	US-10-839-017-7	Sequence 7, Appl
133	54	74.0	23	5	US-10-983-453-15	Sequence 15, Appl	206	44	60.3	76	5	US-10-818-952-20	Sequence 20, Appl
134	52	71.2	73	3	US-09-195-457-1	Sequence 1, Appl	207	44	60.3	77	2	US-08-927-939-17	Sequence 17, Appl
135	52	71.2	73	3	US-09-195-457-2	Sequence 2, Appl	208	44	60.3	77	3	US-09-834-795A-24	Sequence 24, Appl
136	52	71.2	73	5	US-10-622-134-1	Sequence 1, Appl	209	44	60.3	77	4	US-09-834-794A-24	Sequence 24, Appl
137	52	71.2	73	5	US-10-622-134-2	Sequence 2, Appl	210	44	60.3	77	4	US-10-057-275-10	Sequence 10, Appl
138	52	71.2	82	4	US-10-332-038A-7	Sequence 7, Appl	211	44	60.3	77	5	US-10-293-705-9	Sequence 9, Appl
139	52	71.2	82	5	US-10-332-039A-7	Sequence 7, Appl	212	44	60.3	77	5	US-10-847-824-24	Sequence 24, Appl
140	52	71.2	94	4	US-10-449-831A-208	Sequence 208, App	213	44	60.3	78	4	US-10-001-221A-6	Sequence 6, Appl
141	52	71.2	132	4	US-10-449-831A-212	Sequence 212, App	214	44	60.3	94	4	US-10-001-221A-6	Sequence 6, Appl
142	49	67.1	148	2	US-08-927-939-26	Sequence 26, Appl	215	44	60.3	95	4	US-10-276-774-2198	Sequence 2198, Ap
143	49	67.1	148	4	US-10-764-649-20	Sequence 20, Appl	216	44	60.3	99	3	US-09-886-319A-30	Sequence 30, Appl
144	47	64.4	67	3	US-09-195-457-7	Sequence 7, Appl	217	44	60.3	99	3	US-09-537-859-2	Sequence 2, Appl
145	47	64.4	70	5	US-10-622-134-7	Sequence 7, Appl	218	44	60.3	99	3	US-09-537-859-2	Sequence 2, Appl
146	47	64.4	76	3	US-09-792-793A-22	Sequence 22, Appl	219	44	60.3	99	4	US-10-376-564-30	Sequence 30, Appl
147	47	64.4	76	4	US-10-125-451-19	Sequence 19, Appl	220	44	60.3	99	5	US-10-723-860-2828	Sequence 2828, Ap
148	47	64.4	76	4	US-10-263-139-19	Sequence 19, Appl	221	44	60.3	99	6	US-11-123-089-1	Sequence 1, Appl
149	47	64.4	76	4	US-10-375-209A-22	Sequence 22, Appl	222	44	60.3	99	6	US-11-123-089-2	Sequence 2, Appl
150	47	64.4	76	4	US-10-646-770-19	Sequence 19, Appl	223	44	60.3	109	4	US-09-886-319A-71	Sequence 71, Appl
151	47	64.4	76	4	US-10-332-038A-6	Sequence 6, Appl	224	44	60.3	109	4	US-10-376-564-71	Sequence 71, Appl
152	47	64.4	76	5	US-10-839-017-11	Sequence 11, Appl	225	44	60.3	109	4	US-10-376-564-71	Sequence 71, Appl
153	47	64.4	76	5	US-10-332-039A-6	Sequence 6, Appl	226	44	60.3	109	4	US-10-247-671-169	Sequence 169, App
154	47	64.4	77	3	US-09-792-793A-86	Sequence 86, Appl	227	44	60.3	109	4	US-10-170-385-479	Sequence 479, App
155	47	64.4	77	4	US-10-375-209A-86	Sequence 86, Appl	228	43	58.9	15	2	US-08-927-939-3	Sequence 3, Appl
156	47	64.4	82	4	US-10-803-960-15	Sequence 15, Appl	229	42	57.5	14	4	US-10-082-815-18	Sequence 18, Appl
157	47	64.4	82	4	US-08-927-939-18	Sequence 18, Appl	230	42	57.5	14	5	US-10-983-453-18	Sequence 18, Appl
158	47	64.4	99	2	US-09-834-795A-27	Sequence 27, Appl	231	42	57.5	14	5	US-10-450-763-34016	Sequence 34016, A
159	47	64.4	99	3	US-09-886-319A-22	Sequence 22, Appl	232	41	56.2	18	4	US-10-082-815-17	Sequence 17, Appl
160	47	64.4	99	3	US-09-834-794A-27	Sequence 27, Appl	233	41	56.2	18	4	US-10-082-815-21	Sequence 21, Appl
161	47	64.4	99	4	US-10-125-451-18	Sequence 18, Appl	234	41	56.2	18	5	US-10-983-453-17	Sequence 17, Appl
162	47	64.4	99	4	US-10-263-139-18	Sequence 18, Appl	235	41	56.2	18	5	US-10-983-453-21	Sequence 21, Appl
163	47	64.4	99	4	US-10-376-564-22	Sequence 22, Appl	236	41	56.2	71	3	US-09-195-457-8	Sequence 8, Appl
164	47	64.4	99	4	US-10-170-385-463	Sequence 463, App	237	41	56.2	71	5	US-10-622-134-8	Sequence 8, Appl
165	47	64.4	99	4	US-10-646-770-18	Sequence 18, Appl	238	41	56.2	931	5	US-10-450-763-48926	Sequence 48926, A
166	47	64.4	99	5	US-10-847-824-27	Sequence 27, Appl	239	41	56.2	1908	5	US-10-450-763-48928	Sequence 48928, A
167	47	64.4	99	5	US-10-491-997-144	Sequence 144, App	240	40	54.8	271	4	US-10-424-599-181775	Sequence 181775, A
168	47	64.4	99	5	US-10-287-436A-429	Sequence 429, App	241	39	53.4	186	4	US-10-424-599-257636	Sequence 257636, A
169	47	64.4	99	5	US-10-287-436A-1130	Sequence 1130, App	242	39	53.4	425	4	US-10-424-599-150005	Sequence 150005, A
170	47	64.4	109	4	US-10-818-952-18	Sequence 18, Appl	243	39	53.4	434	4	US-10-424-599-181777	Sequence 181777, A
171	47	64.4	109	4	US-10-057-275-11	Sequence 11, Appl	244	39	53.4	2111	4	US-10-437-963-186073	Sequence 186073, A
172	47	64.4	109	4	US-10-033-067-3	Sequence 3, Appl	245	39	53.4	2498	4	US-10-437-963-186071	Sequence 186071, A
173	47	64.4	109	5	US-10-220-335-311	Sequence 311, App	246	38	52.1	14	4	US-10-082-815-20	Sequence 20, Appl

247	38	52.1	14	5	US-10-983-453-20	Sequence 14, Appl	320	36	49.3	1003	5	US-10-450-763-53380	Sequence 53380, A
248	38	52.1	53	4	US-10-437-963-156780	Sequence 156780,	321	36	49.3	1022	4	US-10-282-122A-55642	Sequence 55642, A
249	38	52.1	82	4	US-10-424-599-231797	Sequence 231797,	322	36	49.3	1134	4	US-10-282-122A-73247	Sequence 73247, A
250	38	52.1	96	4	US-10-425-1101-191161	Sequence 191161,	323	36	49.3	1148	3	US-09-815-242-10134	Sequence 10134, A
251	38	52.1	148	4	US-10-767-701-61944	Sequence 61944, A	324	36	49.3	1148	3	US-09-815-242-13826	Sequence 13826, A
252	38	52.1	179	4	US-10-425-114-43854	Sequence 43854, A	325	36	49.3	1148	4	US-10-282-122A-56525	Sequence 56525, A
253	38	52.1	181	4	US-10-425-115-336200	Sequence 336200,	326	36	49.3	1148	4	US-10-282-122A-59749	Sequence 59749, A
254	38	52.1	200	4	US-10-425-115-336197	Sequence 336197,	327	36	49.3	1148	4	US-10-282-122A-75898	Sequence 75898, A
255	38	52.1	223	4	US-10-017-161-1930	Sequence 1930, Ap	328	36	49.3	1166	4	US-10-282-122A-68505	Sequence 68505, A
256	38	52.1	223	4	US-10-292-798-1582	Sequence 1582, Ap	329	36	49.3	1172	3	US-09-822-268A-2	Sequence 2, Appl
257	38	52.1	266	4	US-10-424-599-248825	Sequence 248825,	330	36	49.3	1172	4	US-10-391-777-2	Sequence 2, Appl
258	38	52.1	311	3	US-09-908-006A-43	Sequence 43, Appl	331	36	49.3	1204	5	US-10-787-726-3	Sequence 3, Appl
259	38	52.1	493	4	US-10-424-599-217880	Sequence 217880,	332	36	49.3	1235	3	US-09-921-159-2	Sequence 2, Appl
260	38	52.1	1026	4	US-10-332-426-6	Sequence 6, Appl	333	36	49.3	1237	5	US-10-343-903-24	Sequence 24, Appl
261	38	52.1	1327	4	US-10-437-963-153470	Sequence 153470,	334	36	49.3	1262	5	US-10-450-763-51033	Sequence 51033, A
262	37	50.7	14	4	US-10-082-815-19	Sequence 19, Appl	335	36	49.3	1326	5	US-10-732-923-1617	Sequence 1617, Ap
263	37	50.7	14	5	US-10-983-453-19	Sequence 19, Appl	336	36	49.3	1330	5	US-10-732-923-1599	Sequence 1599, Ap
264	37	50.7	68	4	US-10-425-115-210351	Sequence 210351,	337	36	49.3	1397	5	US-10-732-923-1596	Sequence 1596, Ap
265	37	50.7	195	4	US-10-767-701-59645	Sequence 59645, A	338	36	49.3	1400	5	US-10-732-923-1597	Sequence 1597, Ap
266	37	50.7	197	4	US-10-282-122A-57389	Sequence 57389, A	339	36	49.3	1413	5	US-10-732-923-1598	Sequence 1598, Ap
267	37	50.7	325	4	US-10-424-599-261253	Sequence 261253,	340	36	49.3	1507	5	US-10-450-763-60702	Sequence 60702, A
268	37	50.7	379	4	US-10-125-692-13	Sequence 13, Appl	341	36	49.3	1585	5	US-10-450-763-36434	Sequence 36434, A
269	37	50.7	379	5	US-10-991-347-13	Sequence 13, Appl	342	36	49.3	1585	5	US-10-450-763-41174	Sequence 41174, A
270	37	50.7	436	5	US-10-946-647-1421	Sequence 1421, Ap	343	36	49.3	1598	5	US-10-450-763-36977	Sequence 36977, A
271	37	50.7	476	4	US-10-425-114-40674	Sequence 40674, A	344	36	49.3	1598	5	US-10-450-763-40014	Sequence 40014, A
272	37	50.7	550	4	US-10-125-692-22	Sequence 22, Appl	345	36	49.3	4292	4	US-10-450-763-34360	Sequence 34360, A
273	37	50.7	550	5	US-10-991-347-22	Sequence 22, Appl	346	36	49.3	4292	4	US-10-080-334-273	Sequence 273, App
274	37	50.7	554	4	US-10-125-692-21	Sequence 21, Appl	347	36	49.3	4292	5	US-10-450-763-47419	Sequence 47419, A
275	37	50.7	554	4	US-10-991-347-21	Sequence 21, Appl	348	36	49.3	4299	4	US-10-080-334-90	Sequence 90, Appl
276	37	50.7	585	5	US-10-946-647-1409	Sequence 1409, Ap	349	36	49.3	4302	4	US-10-080-334-271	Sequence 271, App
277	37	50.7	1078	5	US-10-450-763-52313	Sequence 52313, A	350	36	49.3	4302	4	US-10-080-334-272	Sequence 272, App
278	37	50.7	1265	4	US-10-032-585-7168	Sequence 7168, Ap	351	36	49.3	4302	5	US-10-411-915-171	Sequence 171, App
279	37	50.7	1309	5	US-10-450-763-60725	Sequence 60725, A	352	36	49.3	4303	3	US-09-904-968A-2	Sequence 2, Appl
280	37	50.7	1443	4	US-10-369-493-4119	Sequence 4119, Ap	353	36	49.3	4303	4	US-10-080-334-274	Sequence 274, App
281	36	49.3	44	3	US-09-864-761-46231	Sequence 46231, A	354	36	49.3	4725	5	US-10-450-763-54196	Sequence 54196, A
282	36	49.3	50	4	US-10-424-599-246658	Sequence 246658,	355	36	49.3	4977	5	US-10-450-763-47416	Sequence 47416, A
283	36	49.3	51	4	US-10-425-115-248299	Sequence 248299,	356	36	49.3	6685	3	US-10-450-763-53389	Sequence 53389, A
284	36	49.3	52	4	US-10-424-599-185860	Sequence 185860,	357	35.5	48.6	37	3	US-09-864-761-39501	Sequence 39501, A
285	36	49.3	62	4	US-10-425-115-258463	Sequence 258463,	358	35.5	48.6	75	4	US-09-792-793A-23	Sequence 23, Appl
286	36	49.3	80	4	US-10-424-599-184922	Sequence 184922,	359	35.5	48.6	82	4	US-10-375-209A-23	Sequence 7, Appl
287	36	49.3	93	4	US-10-424-599-254538	Sequence 254538,	360	35.5	48.6	82	4	US-10-803-960-7	Sequence 7, Appl
288	36	49.3	118	3	US-09-731-872-432	Sequence 432, App	361	35.5	48.6	98	2	US-08-927-939-50	Sequence 50, Appl
289	36	49.3	118	3	US-08-876-997-432	Sequence 432, App	362	35.5	48.6	98	2	US-08-927-939-83	Sequence 83, Appl
290	36	49.3	118	5	US-10-643-836-432	Sequence 432, App	363	35.5	48.6	98	3	US-03-261-201A-4	Sequence 4, Appl
291	36	49.3	131	5	US-10-450-763-47322	Sequence 47322, A	364	35.5	48.6	98	3	US-09-834-795A-25	Sequence 25, Appl
292	36	49.3	155	4	US-10-424-599-211127	Sequence 211127, A	365	35.5	48.6	98	3	US-09-872-611A-2	Sequence 2, Appl
293	36	49.3	158	4	US-10-425-114-62150	Sequence 62150, A	366	35.5	48.6	98	3	US-09-834-794A-25	Sequence 25, Appl
294	36	49.3	159	4	US-10-425-114-70777	Sequence 70777, A	367	35.5	48.6	98	4	US-10-164-621-4	Sequence 4, Appl
295	36	49.3	209	4	US-10-029-386-32426	Sequence 32426, A	368	35.5	48.6	98	4	US-10-125-451-4	Sequence 4, Appl
296	36	49.3	217	5	US-10-739-930-6395	Sequence 6395, Ap	369	35.5	48.6	98	4	US-10-283-439-4	Sequence 4, Appl
297	36	49.3	266	4	US-10-425-115-279025	Sequence 279025,	370	35.5	48.6	98	4	US-10-295-027-1221	Sequence 4, Appl
298	36	49.3	281	4	US-10-425-114-38770	Sequence 38770, A	371	35.5	48.6	98	4	US-10-646-770-4	Sequence 4, Appl
299	36	49.3	327	4	US-10-424-599-180549	Sequence 180549,	372	35.5	48.6	98	5	US-10-723-860-3704	Sequence 3704, Ap
300	36	49.3	331	4	US-10-267-502-377	Sequence 377, App	373	35.5	48.6	98	5	US-10-893-995-4	Sequence 4, Appl
301	36	49.3	331	6	US-11-097-143-6393	Sequence 6393, Ap	374	35.5	48.6	98	5	US-10-893-995-4	Sequence 4, Appl
302	36	49.3	345	4	US-10-282-122A-76642	Sequence 76642, A	375	35.5	48.6	98	5	US-10-756-149-5640	Sequence 5640, Ap
303	36	49.3	355	4	US-10-072-012-773	Sequence 773, App	376	35.5	48.6	106	5	US-10-450-763-43931	Sequence 43931, A
304	36	49.3	386	4	US-10-437-963-202924	Sequence 202924,	377	35	47.9	18	4	US-10-082-615-22	Sequence 22, Appl
305	36	49.3	387	4	US-10-424-599-181776	Sequence 181776,	378	35	47.9	18	5	US-10-983-453-22	Sequence 22, Appl
306	36	49.3	394	4	US-10-125-692-14	Sequence 14, Appl	379	35	47.9	77	4	US-10-437-963-153709	Sequence 153709, A
307	36	49.3	394	5	US-10-991-347-14	Sequence 14, Appl	380	35	47.9	83	4	US-10-282-122A-67661	Sequence 67661, A
308	36	49.3	447	5	US-10-450-763-60705	Sequence 60705, A	381	35	47.9	102	4	US-10-425-115-216653	Sequence 216653, A
309	36	49.3	462	4	US-10-072-012-770	Sequence 770, App	382	35	47.9	121	3	US-09-864-408A-7048	Sequence 7048, Ap
310	36	49.3	481	4	US-10-425-115-271756	Sequence 271756,	383	35	47.9	124	4	US-10-437-963-107961	Sequence 107961, A
311	36	49.3	496	4	US-10-072-012-771	Sequence 771, App	384	35	47.9	127	4	US-10-424-599-217879	Sequence 217879, A
312	36	49.3	496	4	US-10-408-765A-2147	Sequence 2147, Ap	385	35	47.9	128	4	US-10-437-963-174540	Sequence 174540, A
313	36	49.3	521	4	US-10-072-012-769	Sequence 769, App	386	35	47.9	141	4	US-10-231-417-604	Sequence 604, App
314	36	49.3	531	5	US-10-739-930-10720	Sequence 10720, A	387	35	47.9	146	4	US-10-425-114-42380	Sequence 42380, A
315	36	49.3	643	4	US-10-276-774-1441	Sequence 1441, Ap	388	35	47.9	205	5	US-10-732-923-10951	Sequence 10951, A
316	36	49.3	664	5	US-10-450-763-34631	Sequence 34631, A	389	35	47.9	209	4	US-10-369-493-18838	Sequence 18838, A
317	36	49.3	664	5	US-10-450-763-35909	Sequence 35909, A	390	35	47.9	219	6	US-11-097-143-34719	Sequence 34719, A
318	36	49.3	789	4	US-10-282-122A-51312	Sequence 51312,	391	35	47.9	239	4	US-10-424-599-214810	Sequence 214810, A
319	36	49.3	905	5	US-10-450-763-35567	Sequence 35567, A	392	35	47.9	260	4	US-10-425-114-53710	Sequence 53710, A

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394	35	47.9	287	4	US-10-125-692-32	Sequence 32, Appl	467	34	46.6	186	4	US-10-767-701-39759	Sequence 39759, A
395	35	47.9	287	5	US-10-991-347-32	Sequence 32, Appl	468	34	46.6	194	4	US-10-038-854-356	Sequence 356, App
396	35	47.9	334	6	US-11-097-143-39003	Sequence 39003, A	469	34	46.6	195	4	US-10-425-115-332905	Sequence 332905, A
397	35	47.9	343	4	US-10-032-585-7164	Sequence 7164, Ap	470	34	46.6	200	4	US-10-425-115-302416	Sequence 302416, A
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411	35	47.9	479	4	US-10-408-765A-1279	Sequence 1279, Ap	484	34	46.6	280	5	US-10-450-763-47733	Sequence 47733, A
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416	35	47.9	505	4	US-10-282-122A-61197	Sequence 61197, A	489	34	46.6	343	4	US-10-156-761-8868	Sequence 8868, Ap
417	35	47.9	507	4	US-10-369-493-3579	Sequence 3579, Ap	490	34	46.6	349	4	US-10-282-122A-67075	Sequence 67075, A
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419	35	47.9	515	4	US-10-425-115-221558	Sequence 221558, A	492	34	46.6	350	4	US-10-104-966-4	Sequence 4, Appl
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422	35	47.9	545	4	US-10-424-599-211220	Sequence 211220, A	495	34	46.6	351	5	US-10-125-692-20	Sequence 20, Appl
423	35	47.9	550	4	US-10-425-114-37544	Sequence 37544, A	496	34	46.6	355	4	US-10-991-347-20	Sequence 20, Appl
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431	35	47.9	808	4	US-10-655-799-38	Sequence 38, Appl	504	34	46.6	421	4	US-10-365-620-70	Sequence 70, Appl
432	35	47.9	811	5	US-10-450-763-59793	Sequence 59793, A	505	34	46.6	421	5	US-10-912-969-72	Sequence 72, Appl
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437	35	47.9	1717	5	US-10-450-763-51031	Sequence 51031, A	510	34	46.6	473	4	US-10-408-765A-2491	Sequence 2491, Ap
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441	34	46.6	30	4	US-10-296-734-468	Sequence 468, App	514	34	46.6	490	4	US-10-125-692-19	Sequence 19, Appl
442	34	46.6	40	4	US-10-425-115-255091	Sequence 255091, A	515	34	46.6	490	4	US-10-767-701-45642	Sequence 45642, A
443	34	46.6	40	4	US-10-425-115-345648	Sequence 345648, A	516	34	46.6	490	5	US-10-991-347-19	Sequence 19, Appl
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446	34	46.6	89	4	US-10-425-115-347133	Sequence 347133, A	519	34	46.6	504	5	US-10-946-847-1399	Sequence 1399, Ap
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448	34	46.6	94	4	US-10-425-115-307564	Sequence 307564, A	521	34	46.6	506	5	US-10-991-347-18	Sequence 18, Appl
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554	34	46.6	990	4	US-10-408-765A-3004	Sequence 3004, Ap	627	33	45.2	174	4	US-10-767-701-34605	Sequence 34605, A
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559	34	46.6	1157	4	US-10-782-096-17	Sequence 17, Appl	632	33	45.2	196	4	US-10-424-599-220215	Sequence 220215,
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568	34	46.6	1935	6	US-11-097-143-6366	Sequence 6366, Ap	641	33	45.2	258	5	US-10-732-923-14336	Sequence 14336, A
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577	34	46.6	2011	3	US-09-917-563-20	Sequence 20, Appl	650	33	45.2	285	3	US-09-898-570-41	Sequence 41, Appl
578	34	46.6	2011	4	US-10-104-966-1	Sequence 1, Appl	651	33	45.2	285	3	US-09-839-446-41	Sequence 42, Appl
579	34	46.6	2011	4	US-10-259-275-20	Sequence 20, Appl	652	33	45.2	285	3	US-09-839-446-42	Sequence 42, Appl
580	34	46.6	2011	4	US-10-184-150-3	Sequence 3, Appl	653	33	45.2	285	3	US-10-085-188-2	Sequence 2, Appl
581	34	46.6	2011	4	US-10-328-987-3	Sequence 3, Appl	654	33	45.2	287	4	US-10-085-188-6	Sequence 6, Appl
582	34	46.6	2011	4	US-10-189-359-14	Sequence 14, Appl	655	33	45.2	287	4	US-10-450-763-34672	Sequence 34672, A
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585	34	46.6	2011	5	US-10-817-591-1	Sequence 1, Appl	658	33	45.2	302	4	US-10-425-115-315906	Sequence 315906,
586	34	46.6	2011	5	US-11-006-313-20	Sequence 20, Appl	659	33	45.2	304	4	US-10-101-454A-602	Sequence 602, App
587	34	46.6	2012	3	US-09-238-076-2	Sequence 2, Appl	660	33	45.2	309	4	US-10-864-252-602	Sequence 602, App
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723	33	45.2	1442	5	US-10-732-923-1603	Sequence 1603, Ap	796	32	43.8	98	4	US-10-425-114-58599	Sequence 58599, A
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740	33	45.2	2828	5	US-10-723-860-554	Sequence 554, App	813	32	43.8	161	4	US-10-424-599-201987	Sequence 201987,
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847	32	43.8	268	3	US-09-764-875-888	Sequence 888, App	920	32	43.8	428	4	US-10-282-122A-78330	Sequence 78330, A
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854	32	43.8	281	6	US-11-097-143-28845	Sequence 28845, A	927	32	43.8	464	3	US-10-357-822-6	Sequence 6, Appl1
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864	32	43.8	308	5	US-10-856-499-644	Sequence 644, App	937	32	43.8	472	5	US-10-925-095-469	Sequence 469, App
865	32	43.8	308	5	US-09-539-24	Sequence 24, Appl	938	32	43.8	472	5	US-10-482-029-172	Sequence 172, App
866	32	43.8	309	3	US-09-864-029-34	Sequence 34, Appl	939	32	43.8	472	5	US-10-521-420-1	Sequence 1, Appl
867	32	43.8	311	3	US-09-886-055-469	Sequence 469, App	940	32	43.8	472	6	US-11-019-829-88	Sequence 88, Appl
868	32	43.8	311	3	US-09-804-291-469	Sequence 469, App	941	32	43.8	479	4	US-10-425-115-195224	Sequence 195224, A
869	32	43.8	311	3	US-09-908-006A-10	Sequence 10, Appl	942	32	43.8	491	4	US-10-369-493-1652	Sequence 1652, Ap
870	32	43.8	311	3	US-09-908-006A-12	Sequence 12, Appl	943	32	43.8	494	5	US-10-756-149-5025	Sequence 5025, Ap
871	32	43.8	311	3	US-09-908-006A-14	Sequence 14, Appl	944	32	43.8	497	5	US-10-739-930-5944	Sequence 5944, Ap
872	32	43.8	311	3	US-09-908-006A-41	Sequence 41, Appl	945	32	43.8	498	4	US-10-272-419-12	Sequence 12, Appl
873	32	43.8	311	3	US-09-908-006A-44	Sequence 44, Appl	946	32	43.8	498	5	US-10-450-763-59721	Sequence 59721, A
874	32	43.8	311	3	US-09-908-006A-14	Sequence 44, Appl	947	32	43.8	498	5	US-10-437-963-152822	Sequence 152822, A
875	32	43.8	311	4	US-10-017-161-162	Sequence 162, App	948	32	43.8	507	4	US-10-437-963-152822	Sequence 152822, A
876	32	43.8	311	4	US-10-292-798-140	Sequence 140, App	949	32	43.8	516	4	US-10-156-761-8798	Sequence 8798, Ap
877	32	43.8	311	4	US-10-297-021-7	Sequence 7, Appl1	950	32	43.8	518	4	US-10-437-963-134815	Sequence 134815, A
878	32	43.8	311	5	US-10-343-650A-516	Sequence 516, App	951	32	43.8	519	4	US-10-369-493-21617	Sequence 21617, A
879	32	43.8	314	3	US-09-819-316-469	Sequence 469, App	952	32	43.8	520	4	US-10-369-493-21617	Sequence 21617, A
880	32	43.8	314	3	US-09-935-428A-3	Sequence 3, Appl1	953	32	43.8	524	4	US-10-424-599-240856	Sequence 240856, A
881	32	43.8	314	4	US-10-112-540-2	Sequence 2, Appl1	954	32	43.8	526	4	US-10-437-963-124505	Sequence 124505, A
882	32	43.8	314	4	US-10-334-245-3	Sequence 3, Appl1	955	32	43.8	527	4	US-10-078-929-106	Sequence 106, App
883	32	43.8	314	4	US-10-682-420-24	Sequence 24, Appl	956	32	43.8	529	4	US-10-437-963-115220	Sequence 115220, A
884	32	43.8	314	4	US-10-409-613-24	Sequence 24, Appl	957	32	43.8	534	4	US-10-424-599-189089	Sequence 189089, A
885	32	43.8	314	4	US-10-442-180-24	Sequence 24, Appl	958	32	43.8	534	4	US-10-424-599-189089	Sequence 189089, A
886	32	43.8	314	5	US-10-653-849-3	Sequence 3, Appl1	959	32	43.8	537	4	US-10-156-761-12817	Sequence 12817, A
887	32	43.8	314	5	US-10-718-266-24	Sequence 24, Appl	960	32	43.8	542	4	US-10-302-551-17	Sequence 17, Appl
888	32	43.8	314	5	US-10-637-011-24	Sequence 24, Appl	961	32	43.8	545	4	US-10-369-493-1404	Sequence 1404, Ap
889	32	43.8	314	5	US-10-840-879-2	Sequence 2, Appl1	962	32	43.8	545	6	US-11-0451-467A-694	Sequence 694, App
890	32	43.8	314	6	US-11-007-798-24	Sequence 24, Appl	963	32	43.8	547	4	US-10-156-761-12541	Sequence 12541, A
891	32	43.8	317	4	US-10-424-599-179149	Sequence 179149, A	964	32	43.8	548	4	US-10-425-114-54439	Sequence 54439, A
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893	32	43.8	320	4	US-10-369-493-32018	Sequence 32018, A	966	32	43.8	551	4	US-10-437-963-158474	Sequence 158474, A
894	32	43.8	323	4	US-10-282-122A-55722	Sequence 55722, A	967	32	43.8	553	4	US-10-425-115-378342	Sequence 378342, A
895	32	43.8	323	4	US-10-425-115-265866	Sequence 265866, A	968	32	43.8	554	4	US-10-312-187-13	Sequence 13, Appl
896	32	43.8	326	4	US-10-320-797-3093	Sequence 3093, Ap	969	32	43.8	566	4	US-10-682-420-18	Sequence 18, Appl
897	32	43.8	326	4	US-10-425-114-40948	Sequence 40948, A	970	32	43.8	566	4	US-10-409-613-18	Sequence 18, Appl
898	32	43.8	328	4	US-10-282-122A-45285	Sequence 45285, A	971	32	43.8	566	5	US-10-442-180-18	Sequence 18, Appl
899	32	43.8	328	4	US-10-437-963-107630	Sequence 107630, A	972	32	43.8	566	5	US-10-718-266-18	Sequence 18, Appl
900	32	43.8	332	4	US-10-389-647-393	Sequence 393, App	973	32	43.8	566	5	US-10-775-337-18	Sequence 18, Appl
901	32	43.8	332	4	US-10-425-114-37788	Sequence 37788, A	974	32	43.8	566	5	US-10-637-011-18	Sequence 18, Appl
902	32	43.8	333	4	US-10-437-963-203691	Sequence 203691, A	975	32	43.8	567	6	US-11-007-798-18	Sequence 18, Appl
903	32	43.8	344	3	US-09-975-719-108	Sequence 108, App	976	32	43.8	567	4	US-10-287-274-374	Sequence 374, App

977 32 43.8 567 4 US-10-282-122A-42670 Sequence 42670, A
978 32 43.8 567 4 US-10-425-114-59051 Sequence 69051, A
979 32 43.8 570 4 US-10-425-115-265868 Sequence 265868,
980 32 43.8 589 4 US-10-094-749-1841 Sequence 1841, Ap
981 32 43.8 592 4 US-10-425-115-305838 Sequence 305838,
982 32 43.8 623 4 US-10-464-939-12 Sequence 12, Appl
983 32 43.8 623 4 US-10-424-599-145986 Sequence 145986,
984 32 43.8 623 6 US-11-097-143-2028 Sequence 2028, Ap
985 32 43.8 626 4 US-10-424-599-268358 Sequence 268358,
986 32 43.8 643 5 US-10-736-868-2 Sequence 2, Appl
987 32 43.8 645 4 US-10-369-493-5619 Sequence 5619, Ap
988 32 43.8 664 3 US-09-388-316-18 Sequence 18, Appl
989 32 43.8 664 4 US-10-357-822-18 Sequence 18, Appl
990 32 43.8 680 4 US-10-102-143-19 Sequence 19, Appl
991 32 43.8 703 4 US-10-437-963-104263 Sequence 104263,
992 32 43.8 708 6 US-11-097-143-16377 Sequence 16377, A
993 32 43.8 710 4 US-10-094-749-2315 Sequence 2315, Ap
994 32 43.8 710 4 US-10-408-765A-2496 Sequence 2496, Ap
995 32 43.8 754 4 US-10-381-906-198 Sequence 198, App
996 32 43.8 757 4 US-10-389-566-516 Sequence 516, App
997 32 43.8 757 4 US-10-607-726-5 Sequence 6, Appl
998 32 43.8 767 4 US-10-032-585-7329 Sequence 7329, Ap
999 32 43.8 777 5 US-10-363-285-1 Sequence 1, Appl
1000 32 43.8 802 4 US-10-259-194A-216 Sequence 216, App

ALIGNMENTS

RESULT 1
US-10-082-815-10
; Sequence 10, Application US/10082815
; Publication No. US20020182650A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, James C.
; APPLICANT: Sworin, Michael
; TITLE OF INVENTION: INHIBITORS OF BINDING BETWEEN PROTEINS
; FILE REFERENCE: 2791.1003-007
; CURRENT APPLICATION NUMBER: US/10/082,815
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: PCT/US00/23346
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/150,230
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/150,318
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/152,421
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment of Monocyte Chemoattractant Protein-1
US-10-082-815-10

Query Match 100.0%; Score 73; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
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Db 8 ISVORLASYYRRTSSK 23

RESULT 2
US-10-983-453-10
; Sequence 10, Application US/10983453
; Publication No. US20050221347A1
; GENERAL INFORMATION:

; APPLICANT: Sworin, Michael
; APPLICANT: Jensen, James C.
; TITLE OF INVENTION: Inhibitors of Binding Between Proteins
; FILE REFERENCE: 2791.1003-008
; CURRENT APPLICATION NUMBER: US/10/983,453
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 10/082,815
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/23346
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/150,230
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/150,318
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/152,421
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Fragment of Monocyte Chemoattractant Protein-1
US-10-983-453-10

Query Match 100.0%; Score 73; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
|||
Db 8 ISVORLASYYRRTSSK 23

RESULT 3
US-10-082-815-3
; Sequence 3, Application US/10082815
; Publication No. US20020182650A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, James C.
; APPLICANT: Sworin, Michael
; TITLE OF INVENTION: INHIBITORS OF BINDING BETWEEN PROTEINS
; FILE REFERENCE: 2791.1003-007
; CURRENT APPLICATION NUMBER: US/10/082,815
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: PCT/US00/23346
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/150,230
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/150,318
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/152,421
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fragment of Monocyte Chemoattractant Protein-1
US-10-082-815-3

Query Match 100.0%; Score 73; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
|||
Db 9 ISVORLASYYRRTSSK 24

RESULT 4
US-10-983-453-3
; Sequence 3, Application US/10983453
; Publication No. US20050221347A1
; GENERAL INFORMATION:
; APPLICANT: Sworin, Michael
; APPLICANT: Jensen, James C.
; TITLE OF INVENTION: Inhibitors of Binding Between Proteins
; TITLE OF INVENTION: and Macromolecular Ligands
; FILE REFERENCE: 2791.1003-008
; CURRENT APPLICATION NUMBER: US/10/983,453
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 10/082,815
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/23346
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/150,230
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/150,318
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/152,421
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-983-453-3

Query Match 100.0%; Score 73; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | | | |
Db 9 ISVQRLASYRRITSSK 24

RESULT 5
US-10-082-815-4
; Sequence 4, Application US/10082815
; Publication No. US20020182650A1
; GENERAL INFORMATION:
; APPLICANT: Jensen, James C.
; APPLICANT: Sworin, Michael
; TITLE OF INVENTION: INHIBITORS OF BINDING BETWEEN PROTEINS
; TITLE OF INVENTION: AND MACROMOLECULAR LIGANDS
; FILE REFERENCE: 2791.1003-007
; CURRENT APPLICATION NUMBER: US/10/082,815
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: PCT/US00/23346
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/150,230
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/150,318
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/152,421
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide cyclized fragments of Monocyte
; OTHER INFORMATION: Chemottractant protein-1
; OTHER INFORMATION: Disulfide bond between cysteines at positions 2
; OTHER INFORMATION: and 26
US-10-082-815-4

Query Match 100.0%; Score 73; DB 4; Length 26;

Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | | | |
Db 10 ISVQRLASYRRITSSK 25
RESULT 6
US-10-243-795-1375
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1375

Query Match 100.0%; Score 73; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | | | |
Db 10 ISVQRLASYRRITSSK 25

RESULT 7
US-10-243-795-1411
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1411

Query Match 100.0%; Score 73; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | | | |
Db 10 ISVQRLASYRRITSSK 25

RESULT 8
US-10-243-795-1412
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1412

Query Match 100.0%; Score 73; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16

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Db      10 ISVQRLASYRRITSSK 25
|||||
RESULT 9
US-10-983-453-4
; Sequence 4, Application US/10983453
; Publication No. US20050221347A1
; GENERAL INFORMATION:
; APPLICANT: Sworin, Michael
; TITLE OF INVENTION: Inhibitors of Binding Between Proteins
; TITLE OF INVENTION: and Macromolecular Ligands
; FILE REFERENCE: 2791.1003-008
; CURRENT APPLICATION NUMBER: US/10/983,453
; CURRENT FILING DATE: 2004-11-08
; PRIOR APPLICATION NUMBER: 10/082,815
; PRIOR FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: PCT/US00/23346
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 60/150,230
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/150,318
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: 60/152,421
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-983-453-4

Query Match      100.0%; Score 73; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
|||||
Db      10 ISVQRLASYRRITSSK 25
|||||

RESULT 10
US-10-243-795-1351
; Sequence 1351, Application US/10243795
; Publication No. US20040197303A1
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1351
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1351

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
|||||
Db      20 ISVQRLASYRRITSSK 35
|||||

RESULT 11
US-10-243-795-1352
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1352

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
|||||
Db      20 ISVQRLASYRRITSSK 35
|||||

RESULT 12
US-10-243-795-1353
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1353

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
|||||
Db      20 ISVQRLASYRRITSSK 35
|||||

RESULT 13
US-10-243-795-1354
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1354

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
|||||
Db      20 ISVQRLASYRRITSSK 35
|||||

RESULT 14
US-10-243-795-1355
; GENERAL INFORMATION:
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; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1355

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 15
US-10-243-795-1356
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1356

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 16
US-10-243-795-1357
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1357

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 17
US-10-243-795-1358
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
```

```
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1358

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 18
US-10-243-795-1359
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1359

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 19
US-10-243-795-1360
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1360

Query Match          100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
   |||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 20
US-10-243-795-1361
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
```

```
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1361

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 21
US-10-243-795-1362
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1362

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 22
US-10-243-795-1363
; Sequence 1363, Application US/10243795
; Publication No. US20040197303A1
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1363
; LENGTH: 35
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1363

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 23
US-10-243-795-1364
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
```

```
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1364

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 24
US-10-243-795-1365
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1365

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 25
US-10-243-795-1366
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1366

Query Match      100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ISVQRLASYRRITSSK 16
      |||||
Db      20 ISVQRLASYRRITSSK 35

RESULT 26
US-10-243-795-1367
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
```


; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1367

Query Match 100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASYYRRTSSK 35

RESULT 27
US-10-243-795-1368
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1368

Query Match 100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASYYRRTSSK 35

RESULT 28
US-10-243-795-1369
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1369

Query Match 100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASYYRRTSSK 35

RESULT 29
US-10-243-795-1370
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1370

Query Match 100.0%; Score 73; DB 4; Length 35;

Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASYYRRTSSK 35

RESULT 30
US-10-243-795-1371
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1371

Query Match 100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASYYRRTSSK 35

RESULT 31
US-10-243-795-1372
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1372

Query Match 100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASYYRRTSSK 35

RESULT 32
US-10-243-795-1373
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1373

Query Match 100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16

Db 20 ISVORLASYYRRITSSK 35
|||||

RESULT 33

US-10-243-795-1374
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1374

Query Match 100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRITSSK 16
|||||
Db 20 ISVORLASYYRRITSSK 35
|||||

RESULT 34

US-10-243-795-1413
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1413

Query Match 100.0%; Score 73; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRITSSK 16
|||||
Db 20 ISVORLASYYRRITSSK 35
|||||

RESULT 35

US-10-243-795-1378
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1378

Query Match 100.0%; Score 73; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRITSSK 16
|||||
Db 8 ISVORLASYYRRITSSK 23
|||||

RESULT 36

US-10-243-795-1416
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.00003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; FEATURE:
; OTHER INFORMATION: c-term may be amidated
US-10-243-795-1416

Query Match 100.0%; Score 73; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRITSSK 16
|||||
Db 8 ISVORLASYYRRITSSK 23
|||||

RESULT 37

US-10-339-778-4
; Sequence 4, Application US/10339778
; Publication No. US20030129214A1
; GENERAL INFORMATION:
; APPLICANT: Bornstein, P.
; TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDIC
; FILE REFERENCE: UWOTL-1-20275
; CURRENT APPLICATION NUMBER: US/10/339,778
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,560
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(69)
; OTHER INFORMATION: MCP-1 truncation
US-10-339-778-4

Query Match 100.0%; Score 73; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRITSSK 16
|||||
Db 13 ISVORLASYYRRITSSK 28
|||||

RESULT 38

US-10-276-971-2
; Sequence 2, Application US/10276971
; Publication No. US20030162737A1
; GENERAL INFORMATION:
; APPLICANT: Egashira Kensuke
; APPLICANT: Yoshikazu Yonemitsu
; APPLICANT: Katsuo Sueishi
; APPLICANT: Yasuhiro Ikeda
; APPLICANT: Yoshiyuki Inada
; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
; FILE REFERENCE: 2733 USOP
; CURRENT APPLICATION NUMBER: US/10/276,971
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 4

; SEQ ID NO 2
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Human
US-10-276-971-2

Query Match 100.0%; Score 73; DB 4; Length 69;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 13 ISVORLASYYRRTSSK 28

RESULT 39

US-09-195-457-5
; Sequence 5, Application US/09195457
; Patent No. US20020081623A1
; GENERAL INFORMATION:
; APPLICANT: WILLIAMS, TIMOTHY J.
; APPLICANT: JOSE, PETER J.
; APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
; APPLICANT: HSUAN, JOHN J.
; TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
; FILE REFERENCE: 550-33
; CURRENT APPLICATION NUMBER: US/09/195.457
; CURRENT FILING DATE: 1998-11-18
; PRIOR APPLICATION NUMBER: 08/470,323
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: PCT/GB94/02006
; PRIOR FILING DATE: 1994-09-14
; PRIOR APPLICATION NUMBER: GB 9318984.3
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: GB 94086902.2
; PRIOR FILING DATE: 1994-04-29
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 5
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-09-195-457-5

Query Match 100.0%; Score 73; DB 3; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASYYRRTSSK 35

RESULT 40

US-09-792-793A-20
; Sequence 20, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
; APPLICANT: McDonald, John R.
; APPLICANT: Coggin, Philip
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
; TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
; FILE REFERENCE: 25020-601D
; CURRENT APPLICATION NUMBER: US/09/792.793A
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: homo sapien
; FEATURE:
; OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-09-792-793A-20

Query Match 100.0%; Score 73; DB 3; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASYYRRTSSK 35

RESULT 41

US-10-339-778-3
; Sequence 3, Application US/10339778
; Publication No. US20030129214A1
; GENERAL INFORMATION:
; APPLICANT: Bornstein, P.
; APPLICANT: Kyriakides, T.
; TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDIC
; TITLE OF INVENTION: DEVICE
; FILE REFERENCE: UWOTL-1-20275
; CURRENT APPLICATION NUMBER: US/10/339,778
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,560
; PRIOR FILING DATE: 2002-01-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-339-778-3

Query Match 100.0%; Score 73; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASYYRRTSSK 35

RESULT 42

US-10-276-971-1
; Sequence 1, Application US/10276971
; Publication No. US20030162737A1
; GENERAL INFORMATION:
; APPLICANT: Egashira Kensuke
; APPLICANT: Yoshikazu Yonemitsu
; APPLICANT: Katsuo Sueishi
; APPLICANT: Yasuhiro Ikeda
; APPLICANT: Yoshiyuki Inada
; TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
; FILE REFERENCE: 2733 US0P
; CURRENT APPLICATION NUMBER: US/10/276,971
; CURRENT FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Human
US-10-276-971-1

Query Match 100.0%; Score 73; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRRTSSK 16
| | | | | | | | | | | | | | | | | |
Db 20 ISVORLASYYRRTSSK 35

RESULT 43

US-10-375-209A-20

US-10-393-804A-1

Query Match 100.0%; Score 73; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 48

US-10-243-795-7
; Sequence 7, Application US/10243795
; Publication No. US20040197303A1
; GENERAL INFORMATION:
; APPLICANT: CHEMOKINE THERAPEUTICS CORP.
; TITLE OF INVENTION: DESIGN OF CHEMOKINE ANALOGS FOR THE TREATMENT OF HUMAN DISEASES
; FILE REFERENCE: 59296.0003
; CURRENT APPLICATION NUMBER: US/10/243,795
; CURRENT FILING DATE: 2002-09-13
; NUMBER OF SEQ ID NOS: 1640
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-243-795-7

Query Match 100.0%; Score 73; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 49

US-10-872-198-102
; Sequence 102, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMEIER
; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.0002U4
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 102
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-102

Query Match 100.0%; Score 73; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 20 ISVQRLASYRRITSSK 35

RESULT 50

US-10-839-017-8
; Sequence 8, Application US/10839017
; Publication No. US20050058635A1
; GENERAL INFORMATION:
; APPLICANT: DEMUTH, HANS-ULRICH
; APPLICANT: HOFFMANN, TORSTEN
; APPLICANT: NIESTROJ, ANDRE J.
; APPLICANT: SCHILLING, STEPHAN
; TITLE OF INVENTION: USE OF EFFECTORS OF GLUTAMINYL CYCLASE
; FILE REFERENCE: 20488-53
; CURRENT APPLICATION NUMBER: US/10/839,017
; CURRENT FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,043
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/512,038
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/468,014
; PRIOR FILING DATE: 2003-05-05
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-839-017-8

Query Match 100.0%; Score 73; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
|||||
Db 20 ISVQRLASYRRITSSK 35

Search completed: February 6, 2006, 14:33:50
Job time : 189 secs

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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:42:04 ; Search time 21.9909 Seconds
(without alignments)
1518.479 Million cell updates/sec

Title: US-10-644-277-149

Perfect score: 405

Sequence: 1 QPDALNAPVTCCYNFTNRKI.....QKWQDSMDHLDKQTQPKT 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	76	2 AAR28660	Aar28660 MCF. 3/20
2	405	100.0	76	2 AAR87680	Aar87680 Monocyte
3	405	100.0	76	3 AAY69030	Aay69030 Amino aci
4	405	100.0	76	5 AAO20010	Aao20010 Human che
5	405	100.0	76	5 AAO14143	Aao14143 Human MCP
6	405	100.0	76	5 AAM53048	Aam53048 Human mon
7	405	100.0	76	7 ADC89673	Adc89673 Human mat
8	405	100.0	76	7 ADD14998	Add14998 Human mon
9	405	100.0	76	7 ADE80852	Ad80852 huMCP1 ch
10	405	100.0	76	7 ADE06777	Ad806777 Human MCP
11	405	100.0	76	8 ADK52443	Adk52443 Human MCP
12	405	100.0	76	8 ADM70376	Adm70376 Human MCP
13	405	100.0	76	8 ADS19898	Adsi9898 Modified
14	405	100.0	76	8 ADS19905	Adsi9905 Human che
15	405	100.0	76	8 ADS75929	Adsi75929 Monocyte
16	405	100.0	76	8 ADR70694	Adr70694 Macrophag
17	405	100.0	76	8 ADR70705	Adr70705 Macrophag
18	405	100.0	76	8 ADR70702	Adr70702 Macrophag
19	405	100.0	76	8 ADR70703	Adr70703 Macrophag
20	405	100.0	76	8 ADR70691	Adr70691 Human mac
21	405	100.0	76	8 ADR70696	Adr70696 Macrophag
22	405	100.0	76	8 ADR70704	Adr70704 Macrophag
23	405	100.0	76	8 ADR70695	Adr70695 Macrophag
24	405	100.0	76	8 ADR70700	Adr70700 Macrophag

25	405	100.0	76	8 ADR70693	Adr70693 Macrophag
26	405	100.0	76	8 ADR70698	Adr70698 Macrophag
27	405	100.0	76	8 ADR70706	Adr70706 Macrophag
28	405	100.0	76	8 ADR70697	Adr70697 Macrophag
29	405	100.0	76	8 ADR70699	Adr70699 Macrophag
30	405	100.0	76	8 ADR70701	Adr70701 Macrophag
31	405	100.0	76	8 ADU24450	Adu24450 Novel glu
32	405	100.0	76	8 ADU46724	Adu46724 CCL2, sub
33	405	100.0	76	9 ADV90272	Adv90272 Proteasee-
34	405	100.0	76	9 ADV91968	Adv91968 Human mat
35	405	100.0	76	9 ADZ58557	Adz58557 Mature hu
36	405	100.0	76	9 ADZ71380	Adz71380 N-termina
37	405	100.0	76	9 AEA16549	Aea16549 Human mon
38	405	100.0	76	9 AEB92582	Aeb92582 Glutaminyl
39	405	100.0	98	8 ADJ36261	Adj36261 Self-coal
40	405	100.0	99	1 AAP95387	Aap95387 Human mon
41	405	100.0	99	2 AAR28663	Aar28663 MCF. 3/20
42	405	100.0	99	2 AAR73914	Aar73914 Human mon
43	405	100.0	99	2 AAR70800	Aar70800 Chemoattr
44	405	100.0	99	2 AAW40174	Aaw40174 Macrophag
45	405	100.0	99	2 AAY26176	Aay26176 Monocyte

ALIGNMENTS

RESULT 1

AAR28660
XX AAR28660 standard; protein; 76 AA.
AC AAR28660;
XX
XX 25-MAR-2003 (revised)
DT 24-MAR-1993 (first entry)
XX
XX MCF.
XX Plasmid; monocyte chemotactic factor; MCF; translation; termination;
KW terminator; initiation; ribosome binding site; RBS; promoter; tryptophan;
KW repressor.
XX Synthetic.
OS
XX WO9219737-A1.
XX
XX PD 12-NOV-1992.
XX
XX PF 27-APR-1992; 92WO-JP000550.
XX
XX PR 09-MAY-1991; 91JP-00135950.
XX (DAIN) DAINIPPON PHARM CO LTD.
XX Yamagishi J, Matsuo N, Fukui T, Yamada M;
XX WPI; 1992-398864/48.
DR N-PSDB; AAQ30745, AAQ30746.
XX Prodn. of polypeptide(s) having monocyte chemotactic activity - using
expression plasmids with E. coli elements and specific E.coli strains.
XX Claim 1; Page 48 + Page 36; 56pp; English.
XX An expression plasmid, pHM483, for producing MCF(76) consisting of 76
amino acids was constructed. The prod. can be used for e.g. treating
bacterial infectious diseases. (Updated on 25-MAR-2003 to correct PN
field.)
XX
XX SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 QPDAINAPVTCNFTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 1 QPDAINAPVTCNFTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
QY 61 QDSMDHLDKQTPTPKT 76
DB 61 QDSMDHLDKQTPTPKT 76

RESULT 2
AAR87680
ID AAR87680 standard; protein; 76 AA.
XX
AC AAR87680;
XX
DT 05-MAR-1996 (first entry)
DE Monocyte chemotactic activating factor for use as wound remedy.
XX monocyte chemotactic activating factor; MCAF; wound remedy.
XX Homo sapiens.
XX WO9507710-A1.
XX 23-MAR-1995.
XX 13-SEP-1994; 94WO-JP001512.
XX 13-SEP-1993; 93JP-00227385.
XX (TORA ) TORAY IND INC.
XX Matsushina K, Naruto M;
XX WPI; 1995-131181/17.
XX Wound treatment using monocyte chemotactic factor - has potent
PT therapeutic effect on skin wounds and ulcers.
XX Disclosure; Page 12; 22pp; Japanese.
XX The invention relates to a new remedy for curing wounds which, instead of
CC comprising a growth factor, comprises a monocyte chemotactic activating
CC factor (MCAF) or its variants or derivatives. The factor has potent
CC effect on skin wounds and ulcers. The present sequence is human MCAF, the
CC activity of which is exemplified as the new remedy
XX
SQ Sequence 76 AA;
Query Match 100.0%; Score 405; DB 2; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCNFTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 1 QPDAINAPVTCNFTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
QY 61 QDSMDHLDKQTPTPKT 76
DB 61 QDSMDHLDKQTPTPKT 76

RESULT 3
AAY69030
ID AAY69030 standard; protein; 76 AA.
XX
AC AAY69030;
XX
DT 30-MAY-2000 (first entry)
DE Amino acid sequence of chemokine receptor ligand MCP-1.
```

```
XX Chemokine receptor; ligand; inflammatory response; immune effector cell;
KW secondary tissue damage; central nervous system injury; MCP-1;
KW CNS inflammatory disease; neurodegenerative disorder; heart disease;
KW inflammatory eye disease; inflammatory bowel disease;
KW inflammatory joint disease; inflammatory kidney; renal disease;
KW inflammatory lung disease; inflammatory nasal disease;
KW inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer.
XX
OS Homo sapiens.
XX WO200004926-A2.
XX 03-FEB-2000.
XX 21-JUL-1999; 99WO-CA000659.
XX 22-JUL-1998; 98US-00120523.
XX (OSPR-) OSPREY PHARM LTD.
XX McDonald JR, Coggins PJ;
XX WPI; 2000-182542/16.
XX A new therapeutic agent comprising a conjugate for treating secondary
PT tissue damage and other disease conditions like Alzheimer's disease,
PT stroke, Parkinson's disease and atherosclerosis.
XX Disclosure; Page 60; 204pp; English.
XX The present sequence represents a chemokine receptor ligand. The present
CC ligand can be incorporated into the conjugates of the invention. The
CC specification describes a conjugate, comprising a targeted agent and a
CC chemokine receptor ligand. The conjugate binds to a chemokine receptor
CC resulting in internalisation of the targeted agent in cells bearing the
CC receptor. The conjugates are used for formulating a medicament or for
CC treating disorders associated with inflammatory responses resulting from
CC activation, proliferation and migration of immune effector cells. The
CC disorders or disease states comprise secondary tissue damage such as
CC central nervous system (CNS) injury, CNS inflammatory diseases,
CC neurodegenerative disorders, heart disease, inflammatory eye diseases,
CC inflammatory bowel diseases, inflammatory joint diseases, inflammatory
CC kidney or renal diseases, inflammatory lung diseases, inflammatory nasal
CC diseases, inflammatory thyroid disease such as thyroiditis, or cytokine-
CC regulated cancers
XX
SQ Sequence 76 AA;
Query Match 100.0%; Score 405; DB 3; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCNFTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 1 QPDAINAPVTCNFTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
QY 61 QDSMDHLDKQTPTPKT 76
DB 61 QDSMDHLDKQTPTPKT 76

RESULT 4
AAO20010
ID AAO20010 standard; protein; 76 AA.
XX
AC AAO20010;
XX
DT 11-JUN-2002 (first entry)
DE Human chemokine MCP-1 protein.
XX Human; chemokine; anti-HIV; antiasthmatic; antiarthritic; antirheumatic;
```


KW antiarteriosclerotic; dermatological; antiinflammatory; antiallergic;
 KW immunosuppressive; polymer-modified bioactive synthetic chemokine; HIV;
 KW AIDS; asthma; allergic rhinitis; atopic dermatitis; rheumatoid arthritis;
 KW atheroma; atherosclerosis; organ transplant rejection; MCP-1.
 XX Homo sapiens.
 XX OS
 XX WO200204015-A1.
 XX PN
 XX 17-JAN-2002.
 XX PD
 XX PF
 XX 12-JUL-2001; 2001WO-US021933.
 XX PR
 XX 12-JUL-2000; 2000US-0217683P.
 XX PA (GRYP-) GRYPHON SCI.
 XX PI Kochendoerfer G, Botti P, Bradburne JA, Chen S, Cressman S;
 XX WIPI; 2002-268857/31.
 XX DR
 XX The present invention relates to polymer-modified bioactive synthetic chemokines useful in the treatment of various diseases or disorders e.g. asthma.
 XX PT
 XX Claim 8; Fig 10A; 176pp; English.
 XX PS
 XX The invention relates to polymer-modified bioactive synthetic chemokines and to methods for their production and use. The compounds and methods of the backbone of the invention are useful in the analysis and treatment of various diseases states e.g. HIV and AIDS related disorders, asthma, allergic rhinitis, atopic dermatitis, atheroma/atherosclerosis, organ transplant rejection, and rheumatoid arthritis. This sequence represents the human chemokine MCP-1 protein of the invention
 XX CC
 XX Sequence 76 AA;
 XX SQ
 Query Match 100.0%; Score 405; DB 5; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.3e-42;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPDAINAPVTCYNTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
 DB 1 QPDAINAPVTCYNTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
 QY 61 QDSMDHLDKQTQPKT 76
 DB 61 QDSMDHLDKQTQPKT 76
 RESULT 5
 AAO14143
 ID AAO14143 standard; protein; 76 AA.
 XX
 XX AAO14143;
 XX AC
 XX 25-APR-2002 (first entry)
 XX DT
 XX Human MCP-1 protein.
 XX DE
 XX Human; chemokine receptor modulator; chemokine; HIV infection; AIDS;
 KW asthma; allergic rhinitis; atopic dermatitis; atheroma; antiinflammatory;
 KW antiasthmatic; antiallergic; dermatological; antiarteriosclerotic;
 KW antirheumatic; antiarthritic; anti-HIV; immunosuppressive; MCP-1;
 KW atherosclerosis; organ transplant rejection; rheumatoid arthritis.
 XX OS
 XX Homo sapiens.
 XX WO200204499-A1.
 XX PN
 XX 17-JAN-2002.
 XX PD
 XX PF
 XX 12-JUL-2001; 2001WO-US021934.

PR 12-JUL-2000; 2000US-0217683P.
 XX (GRYP-) GRYPHON SCI.
 XX PI Offord R, Gaertner H, Hartley O;
 XX WIPI; 2002-171703/22.
 XX DR
 XX Chemokine receptor modulator useful for treating e.g. asthma, allergic rhinitis comprises a chemically modified carboxyl-terminus and/or amino terminus analogs.
 XX PT
 XX Example 3; Fig 2; 86pp; English.
 XX PS
 XX The present invention relates to chemokine receptor modulators, which comprise a chemokine polypeptide chain modified at N-terminus with an aliphatic chain and at least one amino acid derivatives and/or modified at its C-terminus with an aliphatic chain or polycyclic. The modulators can be used to treat diseases such as HIV infection, AIDS, asthma, allergic rhinitis, atopic dermatitis, atheroma, atherosclerosis, organ transplant rejection and rheumatoid arthritis. The present sequence is the human MCP-1 protein
 XX CC
 XX Sequence 76 AA;
 XX SQ
 Query Match 100.0%; Score 405; DB 5; Length 76;
 Best Local Similarity 100.0%; Pred. No. 1.3e-42;
 Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QPDAINAPVTCYNTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
 DB 1 QPDAINAPVTCYNTNRKISVORLASRYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
 QY 61 QDSMDHLDKQTQPKT 76
 DB 61 QDSMDHLDKQTQPKT 76
 RESULT 6
 AAM53048
 ID AAM53048 standard; protein; 76 AA.
 XX
 XX AAM53048;
 XX AC
 XX 26-MAR-2002 (first entry)
 XX DT
 XX Human monocyte chemoattractant protein-1 (MCP-1).
 XX DE
 XX Human; monocyte chemoattractant protein-1; MCP-1; C-C chemokine family; pulmonary hypertension; primary; hypotensive.
 KW
 KW Homo sapiens.
 XX OS
 XX Key Location/Qualifiers
 XX FT Misc-difference 2..8
 XX FT /note= "These residues are deleted in a specifically claimed human MCP-1 mutant, 7ND-MCP-1 (AAM53049)"
 XX PN WO200189582-A1.
 XX 29-NOV-2001.
 XX PD
 XX 25-MAY-2001; 2001WO-JP004381.
 XX PF
 XX 26-MAY-2000; 2000JP-00161145.
 XX PR
 XX (TAKE) TAKEDA CHEM IND LTD.
 XX PA (EGAS/) EGASHIRA K.
 XX PI Egashira K, Yonemitsu Y, Sueishi K, Ikeda Y, Inada Y;
 XX WIPI; 2002-083059/11.
 XX DR N-PSDB; ABA02497.

XX preventives and remedies for pulmonary hypertension containing mutant of
PT MCP-1 antagonistic inhibitory type or its salt, encoded DNA or
PT neutralization antibody.
XX
PS Disclosure; Page 31; 39pp; Japanese.
XX
XX The invention relates to preventives and remedies for pulmonary
CC hypertension, comprising an antagonistic inhibitory mutant of monocyte
CC chemoattractant protein-1 (MCP-1), DNA encoding the mutant MCP-1, or a
CC neutralising antibody against MCP-1. MCP-1 is a member of the C-C
CC chemokine family. The preventives and remedies have hypotensive activity
CC and can be used in the prevention and treatment of pulmonary hypertension
CC particularly pulmonary primary hypertension. The present sequence
CC represents wild-type human MCP-1
XX
SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76
DB 61 QDSMDHLDKQTQTPKT 76

RESULT 7
ADC89673
ID ADC89673 standard; protein; 76 AA.
XX
AC ADC89673;
XX
DT 01-JAN-2004 (first entry)
XX
DE Human mature MCP-1 SEQ ID NO:4.
XX
XX human; MCP-1; monocyte chemoattractant protein; MCP; immunosuppressive;
KW antiinflammatory; cytostatic; antimicrobial; vasotropic; gene therapy;
KW MCP-2; MCP-3; MCP-4; Eotaxin; leukocyte migration; leukocyte activation;
KW vascular disorder; cancer; inflammation; autoimmune disease; infection.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX WO2003084993-A1.
XX
PD 16-OCT-2003.
XX
XX 09-APR-2003; 2003WO-EP050097.
XX
XX 10-APR-2002; 2002US-0371442P.
XX
XX (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
XX
XX Proudfoot A, Kosco-Vilbois M, Handel T;
XX WPI; 2003-804294/75.
XX
XX New antagonists of MCP proteins, useful in preparing a composition for
PT treating or preventing diseases related to excessive leukocyte migration
PT and activation e.g. vascular, inflammatory or autoimmune disease, cancer
PT or infection.
XX
XX Example 3; SEQ ID NO 4; 63pp; English.
XX
XX The invention relates to novel antagonists of MCP proteins comprising
CC mutants of MCP proteins in which the following combinations of residues,
CC numbered on the sequence of human mature MCP-1, are substituted to

CC Alanine, Glycine, Serine, Threonine, Proline, Aspartic Acid, Asparagine,
CC Glutamic Acid or Glutamine: 18 and 19; 18 and/or 19, together with 58; 18
CC and/or 19, together with 66; 18 and/or 19, together with 58 and 66; and
CC 18 and/or 19, together with 24, 44, 49 and/or 75. A protein of the
CC invention has immunosuppressive, antiinflammatory, cytostatic,
CC antimicrobial, and vasotropic activity. The protein may have a use in
CC gene therapy, and in a vaccine. The MCP proteins are human MCP-1, human
CC MCP-2, human MCP-3, human MCP-4 or human Eotaxin. The MCP antagonists are
CC useful in preparing a composition for treating or preventing diseases
CC related to excessive leukocyte migration and activation, e.g., vascular
CC disorders, cancer, inflammatory or autoimmune disease or infection. The
CC present sequence is used in the exemplification of the invention.
XX

SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;

Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

DB 1 QPDAINAPVTCYNTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60

QY 61 QDSMDHLDKQTQTPKT 76

DB 61 QDSMDHLDKQTQTPKT 76

RESULT 8

ADD14998

ID ADD14998 standard; protein; 76 AA.

XX

AC ADD14998;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human monocyte chemoattractant protein-1 (MCP-1) mature protein.

XX

XX antiinflammatory; MCP-1 Antagonist; biocompatibility; medical device;

KW monocyte chemoattractant protein 1; MCP-1; MCP-1 antagonist;

KW chronic inflammation; fibrous encapsulation; human.

XX

OS Homo sapiens.

XX

XX US2003129214-A1.

PN

XX 10-JUL-2003.

PD

XX 09-JAN-2003; 2003US-00339778.

XX

XX 10-JAN-2002; 2002US-0347560P.

XX

XX (UNIW) UNIV WASHINGTON.

XX

XX Bornstein P, Kyriakides T;

XX

XX WPI; 2003-787133/74.

DR

XX N-PSDB; ADD14996.

XX

XX Enhancing biocompatibility of a medical device implanted in a portion of

PT a living body by contacting the portion of the body that is in contact

PT with the implanted device with monocyte chemoattractant protein 1 (MCP-1)

PT antagonist.

XX

XX Disclosure; SEQ ID NO 3; 18pp; English.

XX

XX The invention describes a method of enhancing (M1) the biocompatibility

CC of a medical device implanted within a portion of a living body

CC comprising contacting a portion of the living body in contact with the

CC device with a monocyte chemoattractant protein 1 (MCP-1) antagonist to

CC inhibit chronic inflammation induced by the presence of the medical

CC device or fibrous encapsulation of the medical device. The method is

CC useful for enhancing the biocompatibility of a medical device implanted

CC in a portion of a living body by inhibiting chronic inflammation or
CC formation of fibrous capsules around the device. This is the amino acid
CC sequence of human monocyte chemoattractant protein-1 (MCP-1) mature
CC protein.
XX
SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTPTPKT 76

Db 61 QDSMDHLDKQTPTPKT 76

RESULT 9

ADE80852
ID ADE80852 standard; peptide; 76 AA.

XX AC ADE80852;

DT 29-JAN-2004 (first entry)

XX huMCP1 chemokine.

XX Nuclear targeting peptide; nuclear targeting domain; ESKine; PESKY;
XX chemokine; cancer; cytostatic; huMCP1; chemokine.

XX Unidentified.

XX WO2003082920-A1.

XX 09-OCT-2003.

XX 02-APR-2003; 2003WO-GB001472.

XX 02-APR-2002; 2002GB-00007624.

XX (CANC-) CANCER RES TECHNOLOGY LTD.

XX Graham G;

XX WPI; 2003-788341/74.

XX New nuclear targeting peptide comprising a nuclear targeting domain
PT isolated from a chemokine, useful for preparing a medicament for treating
PT cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma.

XX Disclosure; Fig 11; 66pp; English.

XX The present invention relates to a nuclear targeting peptide (ADE80826)
CC comprising a nuclear targeting domain isolated from the C-terminal
CC sequence of the ESKine and PESKY chemokines. The nuclear targeting domain
CC allows the protein to translocate to the cell nucleus. The nuclear
CC targeting peptide is useful in preparing a medicament for treating
CC cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma. The
CC present sequence is a chemokine sequence, used in a sequence alignment in
CC the invention.
XX
SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Db 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTPTPKT 76

Db 61 QDSMDHLDKQTPTPKT 76

RESULT 10

ADE06777
ID ADE06777 standard; protein; 76 AA.

XX AC ADE06777;

DT 29-JAN-2004 (first entry)

XX Human MCP-1 SEQ ID NO:1.

XX human; MCP-1; monocyte chemoattractant protein-1; immunosuppressive;
XX cardiant; neuroprotective; antimicrobial; cytostatic; gene therapy;
XX immune disorder; cardiovascular disorder; neurological disorder;
XX infectious disorder; malignant disorder.

XX Homo sapiens.

XX WO2003083059-A2.

XX 09-OCT-2003.

XX 24-MAR-2003; 2003WO-US009056.

XX 26-MAR-2002; 2002US-0367932P.

XX (CENZ) CENTOCOR INC.

XX Heavner GA, Das A;

XX WPI; 2003-804039/75.

XX New monocyte chemoattractant protein-1 (MCP-1) mutein nucleic acid,
PT useful for diagnosing or treating a MCP-1 mutein-related condition, e.g.
PT immune, cardiovascular, neurologic or infectious or malignant disorders.

XX Claim 1; SEQ ID NO 1; 81pp; English.

XX The invention relates to a novel monocyte chemoattractant protein-1 (MCP-
CC 1) mutant nucleic acid. A protein of the invention has immunosuppressive,
CC cardiant, neuroprotective, antimicrobial, and cytostatic activity. A
CC polynucleotide of the invention may have a use in gene therapy. The
CC protein, nucleic acid, composition and method are useful for diagnosing
CC or treating a MCP-1 mutein-related condition, e.g. immune,
CC cardiovascular, neurologic or infectious or malignant disorders. The
CC present sequence represents human MCP-1.

XX Sequence 76 AA;

Query Match 100.0%; Score 405; DB 7; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Db 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTPTPKT 76

Db 61 QDSMDHLDKQTPTPKT 76

RESULT 11

ADK52443
ID ADK52443 standard; protein; 76 AA.

XX AC ADK52443;

XX

DT 20-MAY-2004 (first entry)
XX Human MCP-1 peptide.
DE
XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis; ds;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN WO2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas JM, Haak-Frendescho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
XX WPI; 2004-203794/19.
DR
XX New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
XX Example 1; SEQ ID NO 149; 154pp; English.
PS
XX The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents human MCP-1 peptide.
XX
SQ Sequence 76 AA;
Query Match 100.0%; Score 405; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCYNYFTNRKISVQRLASVYRRTSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 1 QPDAINAPVTCYNYFTNRKISVQRLASVYRRTSSKCPKEAVIFKTIIVAKEICADPKQKW 60
QY 61 QDSMDHLDKQTTPKT 76
DB 61 QDSMDHLDKQTTPKT 76
RESULT 12
ID ADM70376 standard; protein; 76 AA.
XX
AC ADM70376;
XX
XX 17-JUN-2004 (first entry)
DT
XX Human MCP-1, SEQ ID 7.
DE
XX Chemokine analog; Chemokine; interleukin-8; IL-8;
KW

KW Interferon inducible Protein-10; IP-10; CXCL 10;
KW Macrophage Inflammatory Protein-1-alpha; MIP-1-alpha; RANTES; CCL5;
KW I-309; Monocyte Chemoattractant Protein-1; MCP-1; CCL28;
KW autoimmune disease; cancer; chronic inflammation; cardiovascular disease;
KW infectious disease; inflammatory condition; graft rejection;
KW bacterial infection; viral infection; vascular condition;
KW atherosclerosis; restenosis; systemic lupus erythematosus;
KW ischaemia-reperfusion; sepsis; tumorigenesis; angiogenesis; Cytostatic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis; ds;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN WO2004024088-A2.
XX
PD 25-MAR-2004.
XX
PF 11-SEP-2003; 2003WO-US028745.
XX
PR 13-SEP-2002; 2002US-00243795.
XX
XX (CHEM-) CHEMOKINE THERAPEUTICS CORP.
XX
XX Merzouk A, Wong D, Salari H;
PI
XX WPI; 2004-329387/30.
DR
XX Compound useful for treating cancer and cardiovascular disease, comprises
PT structure of chemokine analogs such as interleukin-8 and interferon
PT inducible protein-10.
XX
XX Disclosure; SEQ ID NO 7; 271pp; English.
PS
XX The present invention relates to chemokine analogs (I, ADM70378-
CC ADM72006), including interleukin (IL)-8 analogs, Interferon inducible
CC Protein-10 (IP-10 or CXCL 10) analogs, Macrophage Inflammatory Protein-1-
CC alpha (MIP-1-alpha or CCL3) analogs, RANTES (Regulated upon Activation,
CC Normal T-cell Expressed, and Presumably Secreted or CCL5) analogs, I-309
CC analogs, Monocyte Chemoattractant Protein-1 (MCP-1) analogs and CCL28
CC analogs. (I) are useful for treating a disease or disorder by
CC administering (I) to a patient. The disease or disorder is chosen from
CC autoimmune diseases, cancer, chronic inflammation, cardiovascular disease
CC or infectious disease. The administration increases the hemocrit, assist
CC in mobilizing stem cells, in vaccine production or in gene therapy. (I)
CC are also useful for modulating the activity of chemokine receptor, which
CC involves contacting the chemokine receptor with (I) for mobilizing
CC intracellular calcium in a patient, which involves administering (I) to a
CC haematopoietic cells in a patient undergoing treatment with cytotoxic
CC agent, by administering (I) to the patient, where the survival of white
CC blood cells or leukocytes is increased. (I) are also useful for
CC maintaining cells capable of divisions in a quiescent state cells in a
CC patient undergoing treatment with a cytotoxic agent, by administering (I)
CC to the patient, and for mobilizing leukocytes e.g. neutrophils in a
CC patient by administering (I) to the patient. (I) are also useful for
CC treating or preventing inflammatory conditions, graft rejection,
CC bacterial infection, viral infection, vascular conditions (e.g.
CC atherosclerosis, restenosis, systemic lupus erythematosus, stem cell
CC reperfusion), sepsis, tumorigenesis, and angiogenesis, used to
CC mobilization, vaccine production and blood cell recovery following
CC chemotherapy. The present sequence is human chemokine MCP-1, used to
CC illustrate the invention. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 76 AA;
Query Match 100.0%; Score 405; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QPDAINAPVTCYNYFTNRKISVQRLASVYRRTSSKCPKEAVIFKTIIVAKEICADPKQKW 60
DB 1 QPDAINAPVTCYNYFTNRKISVQRLASVYRRTSSKCPKEAVIFKTIIVAKEICADPKQKW 60
QY 61 QDSMDHLDKQTTPKT 76
DB 61 QDSMDHLDKQTTPKT 76
RESULT 12
ID ADM70376 standard; protein; 76 AA.
XX
AC ADM70376;
XX
XX 17-JUN-2004 (first entry)
DT
XX Human MCP-1, SEQ ID 7.
DE
XX Chemokine analog; Chemokine; interleukin-8; IL-8;
KW

Db 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60

Qy 61 QDSMDHLDKQTQTPKT 76
|||||

Db 61 QDSMDHLDKQTQTPKT 76

RESULT 13

ADSI19898

ID ADSI19898 standard; protein; 76 AA.

XX AC ADSI19898;

XX DT 18-NOV-2004 (first entry)

XX DE Modified human chemokine CCL2/MCP-1 polypeptide SEQ ID NO: 7.

XX KW human; chemokine; CCL2; receptor-binding; labeled chemokine;

XX KW chemokine receptor assay; MCP-1.

XX OS Homo sapiens.

OS Synthetic.

FH Key Location/Qualifiers

XX Modified-site 75

FT /note= "biotinylated"

FT

XX WO2004026893-A2.

XX 01-APR-2004.

XX 23-SEP-2003; 2003WO-EP010698.

XX 23-SEP-2002; 2002US-0412866P.

XX (RMFD-) RMF DICTAGENE SA.

XX Demotz S, Moulon C, Strong A, Vizzavona J, Cousin P, Raymond C;
Roggero M;

XX WPI; 2004-295377/27.

XX Producing detectably labeled chemokines retaining the receptor-binding
PT specificity of unlabeled chemokines comprises introducing by chemical
PT synthesis a modified moiety at selected amino acid positions in the
PT chemokines.

XX Example 3; Page 46; 53pp; English.

XX The present invention relates to a method of producing a detectably
CC labeled polypeptide retaining the receptor-binding specificity of the
CC unlabeled polypeptide, which comprises introducing by chemical synthesis
CC a modified moiety at one or more selected amino acid positions in the
CC polypeptide. The methods are useful for detecting chemokine receptors or
CC for producing labeled chemokines having improved chemokine biological
CC activity. The labeled chemokine molecules may be used in a variety of
CC therapeutic and diagnostic applications, including in chemokine receptor
CC assays or high-throughput screening assays. The present sequence is a
CC modified peptide as described in the invention.

XX SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
|||||

Db 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
|||||

Qy 61 QDSMDHLDKQTQTPKT 76
|||||

Db 61 QDSMDHLDKQTQTPKT 76

RESULT 15

ADSI75929

ID ADSI75929 standard; protein; 76 AA.

XX AC ADSI75929;

XX DT 16-DEC-2004 (first entry)

XX

RESULT 14

ADSI19905

ID ADSI19905 standard; protein; 76 AA.

XX AC ADSI19905;

XX DT 18-NOV-2004 (first entry)

XX DE Human chemokine CCL2.

XX KW human; chemokine; CCL2; receptor-binding; labeled chemokine;

XX KW chemokine receptor assay.

XX OS Homo sapiens.

XX WO2004026893-A2.

XX 01-APR-2004.

XX 23-SEP-2003; 2003WO-EP010698.

XX 23-SEP-2002; 2002US-0412866P.

XX (RMFD-) RMF DICTAGENE SA.

XX Demotz S, Moulon C, Strong A, Vizzavona J, Cousin P, Raymond C;
Roggero M;

XX WPI; 2004-295377/27.

XX Producing detectably labeled chemokines retaining the receptor-binding
PT specificity of unlabeled chemokines comprises introducing by chemical
PT synthesis a modified moiety at selected amino acid positions in the
PT chemokines.

XX Disclosure; Page 49-50; 53pp; English.

XX The present invention relates to a method of producing a detectably
CC labeled polypeptide retaining the receptor-binding specificity of the
CC unlabeled polypeptide, which comprises introducing by chemical synthesis
CC a modified moiety at one or more selected amino acid positions in the
CC polypeptide. The methods are useful for detecting chemokine receptors or
CC for producing labeled chemokines having improved chemokine biological
CC activity. The labeled chemokine molecules may be used in a variety of
CC therapeutic and diagnostic applications, including in chemokine receptor
CC assays or high-throughput screening assays. The present sequence is a
CC modified peptide as described in the invention.

XX SQ Sequence 76 AA;

Query Match 100.0%; Score 405; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
|||||

Db 1 QPDAINAPVTCYNTNRKISVQRLASYRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
|||||

Qy 61 QDSMDHLDKQTQTPKT 76
|||||

Db 61 QDSMDHLDKQTQTPKT 76

RESULT 15

ADSI75929

ID ADSI75929 standard; protein; 76 AA.

XX AC ADSI75929;

XX DT 16-DEC-2004 (first entry)

XX

DE Monocyte chemoattractant protein 1 C-terminal fragment.
XX cytostatic; prostate cancer; monocyte chemoattractant protein-1; MCP-1.
KW Homo sapiens.
XX
OS
XX
PN WO2004080273-A2.
XX
PD 23-SEP-2004.
XX
XX 14-MAR-2004; 2004WO-IL000240.
XX
XX 12-MAR-2003; 2003US-0453514P.
PR 12-MAR-2003; 2003US-0453515P.
PR 28-NOV-2003; 2003US-0525135P.
PR 05-JAN-2004; 2004US-0534111P.
XX
XX (RAPP-) RAPPAPORT FAMILY INST RES IN MEDICAL SCI.
PA
XX Karin N;
PI
XX WPI; 2004-690440/67.
DR N-PSDB; ADS75928.
XX
XX Treating prostate cancer, involves administering agent capable of
PT reducing activity and/or expression of monocyte chemoattractant protein-1
PT or its effector to subject, thus treating prostate cancer in subject.
XX
XX Example; SEQ ID NO 8; 78pp; English.
XX
XX The invention relates to a method of treating (M1) prostate cancer, by
CC administering an agent capable of reducing activity and/or expression of
CC monocyte chemoattractant protein-1 (MCP-1) or its effector to a subject,
CC thus treating the prostate cancer in the subject. (M1) is useful for
CC treating prostate cancer. An antibody (I) to MCP-1 is useful for
CC manufacturing a medicament for the treatment of prostate cancer. This
CC sequence corresponds to the C-terminal fragment of the MCP-1 protein.
XX
SQ Sequence 76 AA;
Query Match 100.0%; Score 405; DB 8; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.3e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QPDAINAPVTCYNFTNRKISVQRLASYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 1 QPDAINAPVTCYNFTNRKISVQRLASYRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Qy 61 QDSMDHLDKQTPTKT 76
Db 61 QDSMDHLDKQTPTKT 76
Search completed: February 3, 2006, 09:50:53
Job time : 23.9909 secs

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OM protein - protein search, using sw model

Run on: February 6, 2006, 14:30:54 ; Search time 16 Seconds

(Without alignments)
11.718 Million cell updates/sec

Title: US-10-644-277-149_COPY_20_35

Perfect score: 73

Sequence: 1 ISVORLASVRRITSSK 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 88029 seqs, 11718060 residues

Total number of hits satisfying chosen parameters: 88029

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA New:*

1: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB pep.*
5: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB pep.*
7: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB pep.*
8: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	65	7	US-11-043-788-9
2	73	100.0	99	7	US-11-043-788-8
3	56	76.7	74	6	US-10-509-292-1
4	56	76.7	97	6	US-10-995-561-900
5	46	63.0	73	6	US-10-329-472-7
6	38	52.1	44	6	US-10-957-887B-309
7	38	52.1	818	6	US-10-501-675-9
8	37	50.7	550	7	US-11-052-554A-200
9	36	49.3	1680	6	US-10-517-939-362
10	35	47.9	495	6	US-10-821-234-1154
11	35	47.9	808	7	US-11-110-082-38
12	34	46.6	3011	6	US-10-985-205-3
13	34	46.6	3194	7	US-11-052-554A-90
14	33	45.2	317	6	US-10-497-135-8
15	33	45.2	318	6	US-10-497-135-7
16	33	45.2	500	6	US-10-517-151-4
17	33	45.2	548	7	US-11-152-697-3
18	33	45.2	2828	7	US-11-080-931-54
19	33	45.2	2828	7	US-11-186-284-49
20	32	43.8	43	6	US-10-957-887B-215
21	32	43.8	43	6	US-10-957-887B-225
22	32	43.8	311	7	US-11-156-084-358
23	32	43.8	314	7	US-11-217-562-3
24	32	43.8	432	6	US-10-454-437-140
25	32	43.8	432	7	US-11-055-822-184
					Sequence 9, Appli
					Sequence 8, Appli
					Sequence 1, Appli
					Sequence 900, App
					Sequence 7, Appli
					Sequence 309, App
					Sequence 9, Appli
					Sequence 200, App
					Sequence 362, App
					Sequence 1154, Ap
					Sequence 38, Appli
					Sequence 3, Appli
					Sequence 90, Appli
					Sequence 8, Appli
					Sequence 4, Appli
					Sequence 3, Appli
					Sequence 54, Appli
					Sequence 49, Appli
					Sequence 215, App
					Sequence 225, App
					Sequence 358, App
					Sequence 3, Appli
					Sequence 184, App

472	7	US-11-127-877-39	Sequence 39, Appl
496	6	US-11-182-016-33	Sequence 33, Appl
566	6	US-10-467-962B-37	Sequence 37, Appl
43	6	US-10-957-887B-222	Sequence 222, App
43	6	US-10-957-887B-233	Sequence 233, App
43	6	US-10-957-887B-236	Sequence 236, App
110	6	US-10-793-626-894	Sequence 894, App
254	7	US-11-054-515-1584	Sequence 1584, Ap
334	7	US-11-129-143-103	Sequence 103, App
374	7	US-11-196-976-4	Sequence 4, Appli
375	6	US-11-103-957-95	Sequence 95, Appl
386	6	US-10-467-657-7076	Sequence 7076, Ap
432	6	US-10-821-234-1463	Sequence 1463, Ap
465	7	US-11-024-959-287	Sequence 287, App
465	7	US-11-024-959-288	Sequence 288, App
545	7	US-11-065-943-65	Sequence 65, Appl
545	7	US-11-065-943-67	Sequence 67, Appl
545	7	US-11-065-943-69	Sequence 69, Appl
545	7	US-11-065-943-73	Sequence 73, Appl
545	7	US-11-065-943-75	Sequence 75, Appl
545	7	US-11-065-943-77	Sequence 77, Appl
545	7	US-11-065-943-79	Sequence 79, Appl
545	7	US-11-065-943-81	Sequence 81, Appl
545	7	US-11-065-943-83	Sequence 83, Appl
545	7	US-11-065-943-85	Sequence 85, Appl
545	7	US-11-065-943-87	Sequence 87, Appl
545	7	US-11-065-943-89	Sequence 89, Appl
545	7	US-11-065-943-91	Sequence 91, Appl
545	7	US-11-065-943-93	Sequence 93, Appl
545	7	US-11-065-943-95	Sequence 95, Appl
545	7	US-11-065-943-97	Sequence 97, Appl
545	7	US-11-065-943-99	Sequence 99, Appl
554	6	US-10-850-816-2	Sequence 2, Appli
554	6	US-10-850-816-4	Sequence 4, Appli
554	6	US-10-850-816-6	Sequence 6, Appli
562	7	US-11-065-943-20	Sequence 20, Appl
562	7	US-11-065-943-22	Sequence 22, Appl
562	7	US-11-065-943-26	Sequence 26, Appl
562	7	US-11-065-943-28	Sequence 28, Appl
562	7	US-11-065-943-30	Sequence 30, Appl
562	7	US-11-065-943-32	Sequence 32, Appl
562	7	US-11-065-943-34	Sequence 34, Appl
562	7	US-11-065-943-36	Sequence 36, Appl
562	7	US-11-065-943-38	Sequence 38, Appl
711	7	US-11-087-100-18	Sequence 18, Appl
711	7	US-11-087-084-18	Sequence 18, Appl
711	7	US-11-087-085-18	Sequence 18, Appl
832	7	US-11-065-943-100	Sequence 100, App
832	7	US-11-007-797A-11	Sequence 11, Appl
832	7	US-11-007-642B-11	Sequence 11, Appl
834	6	US-10-928-446A-188	Sequence 188, App
834	6	US-10-928-446A-192	Sequence 192, App
834	6	US-10-928-446A-194	Sequence 194, App
834	6	US-10-928-446A-196	Sequence 196, App
834	6	US-10-928-446A-198	Sequence 198, App
834	6	US-10-928-446A-200	Sequence 200, App
834	6	US-10-928-446A-202	Sequence 202, App
913	7	US-11-024-959-365	Sequence 365, App
918	6	US-10-878-556A-82	Sequence 82, Appl
942	6	US-10-928-446A-190	Sequence 190, App
947	6	US-10-928-446A-182	Sequence 182, App
950	6	US-10-928-446A-184	Sequence 184, App
955	6	US-10-928-446A-186	Sequence 186, App
2910	7	US-11-087-100-2	Sequence 2, Appli
2910	7	US-11-087-084-2	Sequence 2, Appli
2910	7	US-11-087-085-2	Sequence 2, Appli
40	6	US-10-957-887B-283	Sequence 283, App
82	6	US-10-821-234-1503	Sequence 1503, Ap
131	6	US-11-152-366-277	Sequence 277, App
131	6	US-10-467-657-7950	Sequence 7950, Ap
211	6	US-10-821-234-1541	Sequence 1541, Ap
211	6	US-11-214-199-10	Sequence 10, Appl
260	6	US-10-055-877-166	Sequence 166, App

99	30	41.1	293	6	US-10-454-437-320	Sequence 320, App	172	29	39.7	1216	7	US-11-115-639-44	Sequence 44, Appl
100	30	41.1	309	7	US-11-156-084-266	Sequence 266, App	173	29	39.7	1216	7	US-11-115-639-45	Sequence 45, Appl
101	30	41.1	359	7	US-11-152-366-38	Sequence 38, Appl	174	29	39.7	1227	6	US-10-793-626-96	Sequence 96, Appl
102	30	41.1	459	6	US-10-512-376-6	Sequence 6, Appli	175	29	39.7	1247	6	US-10-055-877-10	Sequence 10, Appl
103	30	41.1	473	7	US-11-124-368A-325	Sequence 325, App	176	29	39.7	1508	7	US-11-043-889-47	Sequence 47, Appl
104	30	41.1	474	7	US-11-043-889-16	Sequence 16, Appl	177	29	39.7	3003	6	US-10-453-372-1080	Sequence 1080, Ap
105	30	41.1	481	6	US-10-512-376-5	Sequence 5, Appli	178	29	39.7	3361	6	US-10-453-372-1082	Sequence 1082, Ap
106	30	41.1	485	6	US-11-052-554A-36	Sequence 36, Appl	179	29	39.7	4655	6	US-10-995-561-556	Sequence 556, App
107	30	41.1	501	7	US-11-124-368A-324	Sequence 324, App	180	28.5	39.0	279	7	US-11-056-408-13	Sequence 13, Appl
108	30	41.1	545	7	US-11-065-943-71	Sequence 71, Appl	181	28	38.4	29	7	US-11-196-670-50	Sequence 50, Appl
109	30	41.1	593	7	US-11-169-041-239	Sequence 239, App	182	28	38.4	108	6	US-10-793-626-1636	Sequence 1636, Ap
110	30	41.1	669	6	US-10-878-556A-87	Sequence 87, Appl	183	28	38.4	175	6	US-11-098-662-124	Sequence 124, App
111	30	41.1	980	7	US-11-064-246-10	Sequence 10, Appl	184	28	38.4	176	6	US-10-965-694-27	Sequence 27, Appl
112	30	41.1	980	7	US-11-169-041-141	Sequence 141, App	185	28	38.4	176	7	US-11-098-662-122	Sequence 122, App
113	30	41.1	3803	6	US-10-995-561-771	Sequence 773, App	186	28	38.4	176	7	US-11-098-662-134	Sequence 134, App
114	30	41.1	3960	6	US-10-995-561-771	Sequence 771, App	187	28	38.4	177	7	US-11-098-662-120	Sequence 120, App
115	30	41.1	5335	6	US-10-995-561-777	Sequence 777, App	188	28	38.4	178	7	US-11-098-662-118	Sequence 118, App
116	30	41.1	5406	6	US-10-995-561-774	Sequence 774, App	189	28	38.4	179	7	US-11-098-662-114	Sequence 114, App
117	30	41.1	5415	6	US-10-995-561-779	Sequence 779, App	190	28	38.4	180	7	US-11-098-662-114	Sequence 114, App
118	30	41.1	5464	6	US-10-995-561-775	Sequence 775, App	191	28	38.4	181	7	US-11-098-662-32	Sequence 32, Appl
119	29.5	40.4	713	7	US-11-190-799-2	Sequence 2, Appli	192	28	38.4	181	7	US-11-098-662-42	Sequence 42, Appl
120	29.5	40.4	713	7	US-11-103-957-97	Sequence 97, Appl	193	28	38.4	181	7	US-11-098-662-46	Sequence 46, Appl
121	29.5	40.4	922	6	US-10-517-939-38	Sequence 38, Appl	194	28	38.4	181	7	US-11-098-662-50	Sequence 50, Appl
122	29.5	40.4	1473	7	US-11-019-711-112	Sequence 112, App	195	28	38.4	181	7	US-11-098-662-54	Sequence 54, Appl
123	29	39.7	43	6	US-10-957-887B-212	Sequence 212, App	196	28	38.4	181	7	US-11-098-662-58	Sequence 58, Appl
124	29	39.7	43	6	US-10-895-064-1491	Sequence 1491, Ap	197	28	38.4	181	7	US-11-098-662-62	Sequence 62, Appl
125	29	39.7	125	7	US-11-082-389-46	Sequence 46, Appl	198	28	38.4	181	7	US-11-098-662-66	Sequence 66, Appl
126	29	39.7	168	7	US-11-044-111-27	Sequence 27, Appl	199	28	38.4	181	7	US-11-098-662-70	Sequence 70, Appl
127	29	39.7	210	6	US-10-467-657-698	Sequence 698, App	200	28	38.4	181	7	US-11-098-662-74	Sequence 74, Appl
128	29	39.7	250	6	US-10-821-234-987	Sequence 987, App	201	28	38.4	181	7	US-11-098-662-78	Sequence 78, Appl
129	29	39.7	261	6	US-10-055-877-164	Sequence 164, App	202	28	38.4	181	7	US-11-098-662-82	Sequence 82, Appl
130	29	39.7	261	6	US-10-055-877-165	Sequence 165, App	203	28	38.4	182	7	US-11-098-662-84	Sequence 84, Appl
131	29	39.7	262	6	US-10-055-877-16	Sequence 16, Appl	204	28	38.4	182	7	US-11-098-662-88	Sequence 88, Appl
132	29	39.7	262	6	US-10-055-877-18	Sequence 18, Appl	205	28	38.4	182	7	US-11-098-662-44	Sequence 44, Appl
133	29	39.7	272	6	US-10-793-626-3198	Sequence 3198, Ap	206	28	38.4	182	7	US-11-098-662-48	Sequence 48, Appl
134	29	39.7	299	6	US-10-858-730-17	Sequence 17, Appl	207	28	38.4	182	7	US-11-098-662-52	Sequence 52, Appl
135	29	39.7	312	7	US-11-217-562-4	Sequence 4, Appli	208	28	38.4	182	7	US-11-098-662-56	Sequence 56, Appl
136	29	39.7	318	6	US-10-055-877-222	Sequence 222, App	209	28	38.4	182	7	US-11-098-662-60	Sequence 60, Appl
137	29	39.7	318	6	US-10-055-877-326	Sequence 326, App	210	28	38.4	182	7	US-11-098-662-64	Sequence 64, Appl
138	29	39.7	325	6	US-10-888-730-14	Sequence 14, Appl	211	28	38.4	182	7	US-11-098-662-68	Sequence 68, Appl
139	29	39.7	362	6	US-10-467-657-2872	Sequence 2872, Ap	212	28	38.4	182	7	US-11-098-662-72	Sequence 72, Appl
140	29	39.7	366	6	US-10-510-386-42	Sequence 42, Appl	213	28	38.4	182	7	US-11-098-662-76	Sequence 76, Appl
141	29	39.7	400	7	US-11-127-877-55	Sequence 55, Appl	214	28	38.4	182	7	US-11-098-662-80	Sequence 80, Appl
142	29	39.7	422	7	US-11-055-822-560	Sequence 560, App	215	28	38.4	182	7	US-11-098-662-84	Sequence 84, Appl
143	29	39.7	422	7	US-11-055-822-562	Sequence 562, App	216	28	38.4	182	7	US-11-098-662-88	Sequence 88, Appl
144	29	39.7	445	7	US-11-115-564-1	Sequence 1, Appli	217	28	38.4	182	7	US-11-098-662-112	Sequence 112, App
145	29	39.7	445	7	US-11-115-564-2	Sequence 2, Appli	218	28	38.4	182	7	US-11-098-662-128	Sequence 128, App
146	29	39.7	445	7	US-11-115-564-3	Sequence 3, Appli	219	28	38.4	182	7	US-11-098-662-132	Sequence 132, App
147	29	39.7	446	6	US-10-714-887-214	Sequence 214, App	220	28	38.4	183	7	US-11-098-662-126	Sequence 126, App
148	29	39.7	448	6	US-10-967-537A-16	Sequence 16, Appl	221	28	38.4	183	7	US-11-098-662-130	Sequence 130, App
149	29	39.7	459	7	US-11-112-882-23	Sequence 23, App	222	28	38.4	185	7	US-11-098-662-136	Sequence 136, App
150	29	39.7	466	7	US-11-110-082-33	Sequence 33, Appl	223	28	38.4	196	6	US-10-467-657-3296	Sequence 3296, Ap
151	29	39.7	467	6	US-10-793-626-2652	Sequence 2652, Ap	224	28	38.4	200	7	US-11-098-662-4	Sequence 4, Appli
152	29	39.7	476	6	US-11-055-822-942	Sequence 942, App	225	28	38.4	200	7	US-11-098-662-20	Sequence 20, Appl
153	29	39.7	476	6	US-11-055-822-962	Sequence 962, App	226	28	38.4	228	6	US-10-670-009-2	Sequence 2, Appli
154	29	39.7	503	6	US-10-793-626-1810	Sequence 1810, App	227	28	38.4	249	7	US-11-010-239-107	Sequence 107, App
155	29	39.7	525	7	US-11-112-882-27	Sequence 27, Appl	228	28	38.4	251	6	US-10-821-234-898	Sequence 898, App
156	29	39.7	633	6	US-10-453-372-1072	Sequence 1072, Ap	229	28	38.4	262	6	US-10-055-877-162	Sequence 162, App
157	29	39.7	633	6	US-10-453-372-1078	Sequence 1078, Ap	230	28	38.4	291	7	US-11-078-735-30	Sequence 30, Appl
158	29	39.7	642	6	US-10-131-826A-370	Sequence 370, App	231	28	38.4	291	7	US-11-050-346-24	Sequence 24, Appl
159	29	39.7	745	6	US-10-532-153-15	Sequence 15, Appl	232	28	38.4	312	7	US-11-156-084-167	Sequence 167, App
160	29	39.7	778	6	US-10-821-234-1276	Sequence 1276, Ap	233	28	38.4	330	6	US-11-156-084-359	Sequence 359, App
161	29	39.7	790	6	US-10-763-712A-75	Sequence 75, Appl	234	28	38.4	330	6	US-10-485-517-415	Sequence 415, App
162	29	39.7	959	6	US-10-453-372-1074	Sequence 1074, Ap	235	28	38.4	331	7	US-11-078-735-33	Sequence 33, Appl
163	29	39.7	1021	6	US-10-453-372-1076	Sequence 1076, Ap	236	28	38.4	331	7	US-11-050-346-27	Sequence 27, Appl
164	29	39.7	1025	6	US-10-453-372-1068	Sequence 1068, Ap	237	28	38.4	332	7	US-11-078-735-51	Sequence 51, Appl
165	29	39.7	1025	6	US-10-453-372-1070	Sequence 1070, Ap	238	28	38.4	332	7	US-11-103-077-24	Sequence 24, Appl
166	29	39.7	1063	6	US-10-453-372-1066	Sequence 1066, Ap	239	28	38.4	369	7	US-11-078-735-38	Sequence 38, Appl
167	29	39.7	1070	7	US-11-000-463-721	Sequence 721, App	240	28	38.4	369	7	US-11-050-346-32	Sequence 32, Appl
168	29	39.7	1188	7	US-11-115-639-42	Sequence 42, Appl	241	28	38.4	385	6	US-10-714-887-220	Sequence 220, App
169	29	39.7	1188	7	US-11-115-639-43	Sequence 43, Appl	242	28	38.4	385	6	US-10-995-561-838	Sequence 838, App
170	29	39.7	1194	7	US-11-000-463-249	Sequence 249, App	243	28	38.4	386	6	US-10-995-561-837	Sequence 837, App
171	29	39.7	1197	6	US-10-055-877-8	Sequence 8, Appli	244	28	38.4	389	6		

245	28	38.4	419	6	US-10-537-075-9	Sequence 9, Appli	318	27	37.0	146	7	US-11-176-830-672	Sequence 672, App
246	28	38.4	456	6	US-10-763-712A-44	Sequence 44, Appl	319	27	37.0	146	7	US-11-176-830-673	Sequence 673, App
247	28	38.4	456	6	US-10-966-483-34	Sequence 34, Appl	320	27	37.0	146	7	US-11-176-830-674	Sequence 674, App
248	28	38.4	456	6	US-11-021-441-18	Sequence 18, Appl	321	27	37.0	146	7	US-11-176-830-675	Sequence 675, App
249	28	38.4	479	6	US-10-966-483-36	Sequence 36, Appl	322	27	37.0	146	7	US-11-176-830-676	Sequence 676, App
250	28	38.4	479	6	US-11-021-441-20	Sequence 20, Appl	323	27	37.0	146	7	US-11-176-830-677	Sequence 677, App
251	28	38.4	480	6	US-10-878-556A-198	Sequence 198, Appl	324	27	37.0	146	7	US-11-176-830-678	Sequence 678, App
252	28	38.4	480	6	US-10-521-162-40	Sequence 40, Appl	325	27	37.0	146	7	US-11-176-830-679	Sequence 679, App
253	28	38.4	484	7	US-11-078-735-43	Sequence 43, Appl	326	27	37.0	146	7	US-11-176-830-680	Sequence 680, App
254	28	38.4	484	7	US-11-050-346-37	Sequence 37, Appl	327	27	37.0	146	7	US-11-176-830-681	Sequence 681, App
255	28	38.4	490	6	US-10-966-483-42	Sequence 42, Appl	328	27	37.0	146	7	US-11-176-830-682	Sequence 682, App
256	28	38.4	490	7	US-11-021-441-26	Sequence 26, Appl	329	27	37.0	146	7	US-11-176-830-683	Sequence 683, App
257	28	38.4	497	6	US-10-966-483-38	Sequence 38, Appl	330	27	37.0	153	7	US-11-155-288-12	Sequence 12, Appl
258	28	38.4	497	6	US-10-966-483-40	Sequence 40, Appl	331	27	37.0	153	7	US-11-166-412-231	Sequence 231, App
259	28	38.4	497	7	US-11-021-441-22	Sequence 22, Appl	332	27	37.0	160	7	US-10-453-372-838	Sequence 838, App
260	28	38.4	497	7	US-11-021-441-24	Sequence 24, Appl	333	27	37.0	172	6	US-10-793-626-1266	Sequence 1266, Ap
261	28	38.4	503	6	US-10-878-556A-2	Sequence 2, Appli	334	27	37.0	178	6	US-10-521-162-7	Sequence 7, Appli
262	28	38.4	531	7	US-11-010-239-32	Sequence 32, Appl	335	27	37.0	178	6	US-10-453-372-846	Sequence 846, App
263	28	38.4	532	6	US-10-821-234-1071	Sequence 1071, Ap	336	27	37.0	185	6	US-10-821-234-1384	Sequence 1384, Ap
264	28	38.4	541	7	US-11-024-959-463	Sequence 463, App	337	27	37.0	197	6	US-10-714-887-98	Sequence 98, Appl
265	28	38.4	542	7	US-11-074-176-30	Sequence 30, Appl	338	27	37.0	199	7	US-11-052-554A-84	Sequence 84, Appl
266	28	38.4	551	7	US-11-143-984A-32	Sequence 32, Appl	339	27	37.0	212	7	US-11-214-199-4	Sequence 4, Appli
267	28	38.4	687	6	US-10-821-234-1197	Sequence 1197, Ap	340	27	37.0	212	7	US-11-214-199-12	Sequence 12, Appl
268	28	38.4	723	6	US-10-131-826A-346	Sequence 346, App	341	27	37.0	213	6	US-10-467-657-8566	Sequence 8566, Ap
269	28	38.4	723	7	US-11-078-735-17	Sequence 17, Appl	342	27	37.0	222	6	US-10-453-372-844	Sequence 844, App
270	28	38.4	723	7	US-11-050-346-62	Sequence 62, Appl	343	27	37.0	222	7	US-11-076-164-10	Sequence 10, Appl
271	28	38.4	723	7	US-11-103-077-17	Sequence 17, Appl	344	27	37.0	223	6	US-10-793-626-2884	Sequence 2884, Ap
272	28	38.4	775	6	US-10-795-201-1	Sequence 1, Appli	345	27	37.0	232	6	US-10-714-887-90	Sequence 90, Appl
273	28	38.4	787	7	US-11-175-690-251	Sequence 251, App	346	27	37.0	238	7	US-11-010-239-101	Sequence 101, App
274	28	38.4	864	7	US-11-050-346-10	Sequence 10, Appl	347	27	37.0	233	6	US-10-714-887-100	Sequence 100, App
275	28	38.4	864	7	US-11-103-077-29	Sequence 29, Appl	348	27	37.0	233	7	US-11-179-977-20	Sequence 20, Appl
276	28	38.4	882	7	US-11-169-041-137	Sequence 137, App	349	27	37.0	248	7	US-11-166-412-230	Sequence 230, App
277	28	38.4	944	7	US-11-057-058-68	Sequence 68, Appl	350	27	37.0	249	7	US-11-113-424-30	Sequence 30, Appl
278	28	38.4	976	6	US-10-966-483-2	Sequence 2, Appli	351	27	37.0	252	6	US-10-763-712A-114	Sequence 114, App
279	28	38.4	976	7	US-11-233-796-2	Sequence 20, Appl	352	27	37.0	252	7	US-11-166-412-229	Sequence 229, App
280	28	38.4	1035	6	US-10-966-483-20	Sequence 20, Appl	353	27	37.0	254	7	US-11-067-323-430	Sequence 430, App
281	28	38.4	1035	7	US-11-021-411-4	Sequence 4, Appli	354	27	37.0	254	7	US-11-067-323-432	Sequence 432, App
282	28	38.4	1050	6	US-10-770-726-47	Sequence 47, Appl	355	27	37.0	273	7	US-11-113-424-74	Sequence 74, Appl
283	28	38.4	1206	6	US-10-763-712A-18	Sequence 18, Appl	356	27	37.0	273	7	US-11-113-424-75	Sequence 75, Appl
284	28	38.4	1206	6	US-10-763-712A-99	Sequence 99, Appl	357	27	37.0	277	6	US-10-793-626-2086	Sequence 2086, Ap
285	28	38.4	1213	7	US-11-074-176-256	Sequence 256, App	358	27	37.0	283	6	US-10-453-372-850	Sequence 850, App
286	28	38.4	1343	7	US-11-115-639-37	Sequence 37, Appl	359	27	37.0	289	6	US-10-467-657-2452	Sequence 2452, Ap
287	28	38.4	1343	7	US-11-115-639-38	Sequence 38, Appl	360	27	37.0	290	6	US-10-453-372-836	Sequence 836, App
288	28	38.4	1343	7	US-11-115-639-39	Sequence 39, Appl	361	27	37.0	290	6	US-10-453-372-842	Sequence 842, App
289	28	38.4	1343	7	US-11-115-639-40	Sequence 40, Appl	362	27	37.0	290	6	US-10-453-372-848	Sequence 848, App
290	28	38.4	1343	7	US-11-115-639-41	Sequence 41, Appl	363	27	37.0	290	7	US-11-113-424-77	Sequence 77, Appl
291	28	38.4	1344	7	US-11-091-643-20	Sequence 20, Appl	364	27	37.0	290	7	US-11-113-424-78	Sequence 78, Appl
292	28	38.4	1504	7	US-11-019-711-98	Sequence 98, Appl	365	27	37.0	295	6	US-10-453-372-840	Sequence 840, App
293	28	38.4	1532	6	US-10-821-234-914	Sequence 914, App	366	27	37.0	312	7	US-11-008-570-42	Sequence 42, Appl
294	28	38.4	1562	6	US-10-467-657-2704	Sequence 2704, Ap	367	27	37.0	313	7	US-11-166-412-228	Sequence 228, App
295	28	38.4	1572	7	US-11-143-980-46	Sequence 46, Appl	368	27	37.0	326	6	US-10-873-528-33	Sequence 33, Appl
296	28	38.4	1881	7	US-11-040-472-8	Sequence 8, Appli	369	27	37.0	348	7	US-10-467-657-8350	Sequence 8350, Ap
297	28	38.4	1905	6	US-10-877-346-44	Sequence 44, Appl	370	27	37.0	375	7	US-11-196-976-2	Sequence 2, Appli
298	27	37.0	43	6	US-10-957-887B-68	Sequence 68, Appl	371	27	37.0	394	6	US-10-821-234-1194	Sequence 1194, Ap
299	27	37.0	45	6	US-10-957-887B-297	Sequence 297, App	372	27	37.0	397	6	US-10-858-730-29	Sequence 29, Appl
300	27	37.0	49	6	US-10-467-657-3762	Sequence 3762, Ap	373	27	37.0	397	7	US-11-192-219-47	Sequence 47, Appl
301	27	37.0	67	6	US-10-995-561-707	Sequence 707, App	374	27	37.0	405	6	US-10-467-657-4964	Sequence 4964, Ap
302	27	37.0	92	5	US-09-978-360A-776	Sequence 776, App	375	27	37.0	421	6	US-10-793-626-144	Sequence 144, App
303	27	37.0	95	6	US-10-467-657-6530	Sequence 6530, Ap	376	27	37.0	430	7	US-11-126-313-35	Sequence 35, Appl
304	27	37.0	110	5	US-09-978-360A-616	Sequence 616, App	377	27	37.0	430	7	US-11-126-313-36	Sequence 36, Appl
305	27	37.0	117	6	US-10-821-234-1362	Sequence 1362, Ap	378	27	37.0	445	6	US-10-793-626-1294	Sequence 1294, Ap
306	27	37.0	138	6	US-10-467-657-2928	Sequence 2928, Ap	379	27	37.0	453	6	US-10-793-626-804	Sequence 804, App
307	27	37.0	146	6	US-10-519-390-19	Sequence 19, Appl	380	27	37.0	460	7	US-11-076-163-5	Sequence 5, Appli
308	27	37.0	146	7	US-11-176-830-211	Sequence 211, App	381	27	37.0	460	7	US-11-166-412-68	Sequence 68, Appl
309	27	37.0	146	7	US-11-176-830-663	Sequence 663, App	382	27	37.0	461	6	US-10-858-730-62	Sequence 62, Appl
310	27	37.0	146	7	US-11-176-830-664	Sequence 664, App	383	27	37.0	465	7	US-11-186-284-197	Sequence 197, App
311	27	37.0	146	7	US-11-176-830-665	Sequence 665, App	384	27	37.0	473	6	US-10-467-657-298	Sequence 298, App
312	27	37.0	146	7	US-11-176-830-666	Sequence 666, App	385	27	37.0	473	6	US-10-467-657-6328	Sequence 6328, Ap
313	27	37.0	146	7	US-11-176-830-667	Sequence 667, App	386	27	37.0	482	6	US-10-793-626-24	Sequence 24, Appl
314	27	37.0	146	7	US-11-176-830-668	Sequence 668, App	387	27	37.0	487	7	US-11-124-368A-308	Sequence 308, App
315	27	37.0	146	7	US-11-176-830-669	Sequence 669, App	388	27	37.0	487	7	US-11-124-368A-309	Sequence 309, App
316	27	37.0	146	7	US-11-176-830-670	Sequence 670, App	389	27	37.0	514	6	US-10-878-556A-32	Sequence 32, Appl
317	27	37.0	146	7	US-11-176-830-671	Sequence 671, App	390	27	37.0	526	7	US-11-124-368A-310	Sequence 310, App

391	27	37.0	537	7	US-11-123-442-47	Sequence 47, Appl	464	26	35.6	184	6	US-10-620-787-13	Sequence 13, Appl
392	27	37.0	545	7	US-11-065-943-63	Sequence 63, Appl	465	26	35.6	184	6	US-10-620-787-14	Sequence 14, Appl
393	27	37.0	548	6	US-10-467-657-6000	Sequence 6000, Ap	466	26	35.6	199	6	US-10-467-657-8058	Sequence 8058, Ap
394	27	37.0	549	6	US-10-467-657-4612	Sequence 4612, Ap	467	26	35.6	211	7	US-11-124-368A-175	Sequence 175, App
395	27	37.0	549	6	US-10-467-657-7190	Sequence 7190, Ap	468	26	35.6	211	7	US-11-124-368A-176	Sequence 176, App
396	27	37.0	549	6	US-10-521-162-4	Sequence 4, Appl	469	26	35.6	216	6	US-10-821-234-1033	Sequence 1033, Ap
397	27	37.0	559	6	US-10-821-234-1352	Sequence 1352, Ap	470	26	35.6	229	6	US-10-793-626-62	Sequence 62, Appl
398	27	37.0	637	6	US-10-821-234-961	Sequence 961, App	471	26	35.6	229	6	US-10-821-234-894	Sequence 894, App
399	27	37.0	637	7	US-11-154-324-4	Sequence 4, Appl	472	26	35.6	232	6	US-11-052-826A-186	Sequence 186, App
400	27	37.0	641	7	US-11-094-519A-29	Sequence 29, Appl	473	26	35.6	242	6	US-10-131-826A-244	Sequence 244, App
401	27	37.0	712	6	US-10-521-162-12	Sequence 12, Appl	474	26	35.6	247	7	US-11-113-424-76	Sequence 76, Appl
402	27	37.0	720	6	US-10-063-703-38	Sequence 38, Appl	475	26	35.6	254	7	US-11-067-323-724	Sequence 724, App
403	27	37.0	720	6	US-11-102-240-38	Sequence 38, Appl	476	26	35.6	254	7	US-11-067-323-1013	Sequence 1013, Ap
404	27	37.0	737	6	US-10-467-657-3452	Sequence 3452, Ap	477	26	35.6	263	7	US-11-082-389-66	Sequence 66, Appl
405	27	37.0	748	6	US-10-821-234-888	Sequence 888, App	478	26	35.6	264	6	US-10-873-528-70	Sequence 70, Appl
406	27	37.0	751	7	US-11-114-906-8	Sequence 8, Appl	479	26	35.6	264	7	US-11-055-822-550	Sequence 550, App
407	27	37.0	764	7	US-11-114-906-6	Sequence 6, Appl	480	26	35.6	264	7	US-11-055-822-596	Sequence 596, App
408	27	37.0	768	7	US-11-114-906-2	Sequence 12, Appl	481	26	35.6	265	6	US-10-793-626-1976	Sequence 1976, Ap
409	27	37.0	769	6	US-10-485-517-401	Sequence 401, App	482	26	35.6	266	6	US-10-467-657-5258	Sequence 5258, Ap
410	27	37.0	838	7	US-11-114-906-40	Sequence 40, Appl	483	26	35.6	278	6	US-10-793-626-2344	Sequence 2344, Ap
411	27	37.0	851	7	US-11-114-906-38	Sequence 38, Appl	484	26	35.6	280	7	US-11-170-653-66	Sequence 66, Appl
412	27	37.0	862	7	US-11-182-016-35	Sequence 35, Appl	485	26	35.6	302	7	US-11-112-882-2	Sequence 2, Appl
413	27	37.0	864	7	US-11-114-906-4	Sequence 4, Appl	486	26	35.6	308	7	US-11-156-084-304	Sequence 304, App
414	27	37.0	870	7	US-11-114-906-2	Sequence 2, Appl	487	26	35.6	312	7	US-11-008-570-41	Sequence 41, Appl
415	27	37.0	943	7	US-11-024-959-487	Sequence 487, App	488	26	35.6	313	6	US-10-723-207-4	Sequence 4, Appl
416	27	37.0	951	7	US-11-114-906-36	Sequence 36, Appl	489	26	35.6	313	7	US-11-095-093-2	Sequence 2, Appl
417	27	37.0	953	7	US-11-037-243-66	Sequence 66, Appl	490	26	35.6	318	7	US-11-127-877-38	Sequence 38, Appl
418	27	37.0	957	7	US-11-114-906-34	Sequence 34, Appl	491	26	35.6	318	7	US-11-012-522-11	Sequence 11, Appl
419	27	37.0	1075	7	US-11-089-551A-23	Sequence 23, Appl	492	26	35.6	320	7	US-11-012-522-17	Sequence 17, Appl
420	27	37.0	1138	6	US-10-509-422-4	Sequence 4, Appl	493	26	35.6	324	6	US-11-226-701-6	Sequence 6, Appl
421	27	37.0	1168	6	US-11-059-422-2	Sequence 2, Appl	494	26	35.6	328	6	US-10-793-626-1286	Sequence 1286, Ap
422	27	37.0	1300	7	US-11-052-554A-125	Sequence 125, App	495	26	35.6	329	6	US-11-156-084-124	Sequence 124, App
423	27	37.0	1436	6	US-10-453-372-1094	Sequence 1094, Ap	496	26	35.6	329	7	US-10-467-657-182	Sequence 182, App
424	27	37.0	1588	6	US-10-453-372-2892	Sequence 280, App	497	26	35.6	335	7	US-11-229-371-121	Sequence 121, App
425	27	37.0	1593	6	US-10-453-372-1092	Sequence 1092, Ap	498	26	35.6	336	6	US-11-012-522-17	Sequence 17, Appl
426	27	37.0	1627	7	US-11-052-554A-124	Sequence 124, App	499	26	35.6	343	6	US-10-467-657-159	Sequence 159, App
427	27	37.0	1728	7	US-11-019-711-72	Sequence 72, Appl	500	26	35.6	348	6	US-11-129-143-58	Sequence 58, Appl
428	27	37.0	1873	7	US-11-126-313-29	Sequence 29, Appl	501	26	35.6	359	6	US-11-082-389-64	Sequence 64, Appl
429	27	37.0	2221	7	US-11-126-313-30	Sequence 30, Appl	502	26	35.6	361	7	US-11-013-247A-7	Sequence 7, Appl
430	27	37.0	2591	6	US-10-453-372-718	Sequence 718, App	503	26	35.6	362	7	US-11-052-547A-77	Sequence 77, Appl
431	27	37.0	2602	6	US-10-453-372-716	Sequence 716, App	504	26	35.6	362	7	US-11-052-547A-77	Sequence 204, App
432	27	37.0	2617	6	US-10-453-372-666	Sequence 666, App	505	26	35.6	362	7	US-11-186-807-4	Sequence 4, Appl
433	27	37.0	2617	6	US-10-453-372-732	Sequence 732, App	506	26	35.6	363	7	US-11-013-247A-6	Sequence 6, Appl
434	27	37.0	2617	6	US-10-453-372-734	Sequence 734, App	507	26	35.6	364	7	US-10-467-657-4118	Sequence 4118, Ap
435	27	37.0	2617	6	US-10-453-372-736	Sequence 736, App	508	26	35.6	383	6	US-10-467-657-1038	Sequence 1038, Ap
436	27	37.0	2617	6	US-10-453-372-738	Sequence 738, App	509	26	35.6	393	6	US-11-052-554A-308	Sequence 308, App
437	27	37.0	2617	6	US-10-453-372-740	Sequence 740, App	510	26	35.6	413	6	US-11-156-084-40	Sequence 40, Appl
438	27	37.0	2617	6	US-10-453-372-742	Sequence 742, App	511	26	35.6	422	7	US-11-171-531-1	Sequence 1, Appl
439	27	37.0	2617	6	US-10-453-372-744	Sequence 744, App	512	26	35.6	422	7	US-11-127-877-51	Sequence 51, Appl
440	27	37.0	2617	6	US-10-453-372-746	Sequence 746, App	513	26	35.6	427	7	US-11-156-084-43	Sequence 43, Appl
441	27	37.0	2617	6	US-10-453-372-748	Sequence 748, App	514	26	35.6	447	7	US-11-013-247A-5	Sequence 5, Appl
442	27	37.0	2617	6	US-10-453-372-750	Sequence 750, App	515	26	35.6	448	7	US-10-714-887-212	Sequence 212, App
443	27	37.0	7102	7	US-11-143-980-48	Sequence 48, Appl	516	26	35.6	455	6	US-11-156-084-242	Sequence 242, App
444	26.5	36.3	77	7	US-11-113-424-190	Sequence 190, App	517	26	35.6	459	7	US-11-169-041-173	Sequence 173, App
445	26.5	36.3	381	6	US-10-689-742-172	Sequence 172, App	518	26	35.6	461	6	US-10-131-826A-454	Sequence 454, App
446	26.5	36.3	713	6	US-10-467-657-1012	Sequence 1012, Ap	519	26	35.6	463	6	US-10-501-411A-341	Sequence 341, App
447	26.5	36.3	713	7	US-11-190-799-4	Sequence 4, Appl	520	26	35.6	463	6	US-11-156-084-32	Sequence 32, Appl
448	26	35.6	20	6	US-10-485-788A-568	Sequence 568, App	521	26	35.6	463	7	US-11-156-084-41	Sequence 41, Appl
449	26	35.6	29	7	US-11-196-670-51	Sequence 51, Appl	522	26	35.6	463	7	US-11-156-084-42	Sequence 42, Appl
450	26	35.6	40	6	US-10-957-887B-271	Sequence 271, App	523	26	35.6	463	7	US-11-156-084-242	Sequence 242, App
451	26	35.6	74	6	US-10-467-657-1976	Sequence 1976, Ap	524	26	35.6	463	7	US-11-169-041-173	Sequence 173, App
452	26	35.6	100	7	US-11-127-877-567	Sequence 567, App	525	26	35.6	466	7	US-11-127-877-50	Sequence 50, Appl
453	26	35.6	110	6	US-10-793-626-200	Sequence 200, App	526	26	35.6	466	7	US-11-156-084-42	Sequence 42, Appl
454	26	35.6	114	6	US-10-467-657-124	Sequence 124, App	527	26	35.6	466	6	US-10-467-657-86	Sequence 86, Appl
455	26	35.6	114	6	US-10-467-657-1414	Sequence 1414, Ap	528	26	35.6	472	6	US-10-467-657-6324	Sequence 6324, Ap
456	26	35.6	114	6	US-10-467-657-3162	Sequence 3162, Ap	529	26	35.6	472	6	US-10-714-887-4	Sequence 4, Appl
457	26	35.6	114	6	US-10-467-657-3754	Sequence 3754, Ap	530	26	35.6	483	6	US-10-467-657-2894	Sequence 2894, Ap
458	26	35.6	114	6	US-10-467-657-8674	Sequence 8674, Ap	531	26	35.6	483	6	US-10-770-726-81	Sequence 81, Appl
459	26	35.6	119	7	US-11-084-508-23	Sequence 23, Appl	532	26	35.6	495	6	US-11-013-247A-2	Sequence 2, Appl
460	26	35.6	135	7	US-11-019-711-82	Sequence 82, Appl	533	26	35.6	501	7	US-11-226-701-4	Sequence 4, Appl
461	26	35.6	135	7	US-11-019-711-83	Sequence 83, Appl	534	26	35.6	502	7	US-11-052-554A-119	Sequence 119, App
462	26	35.6	146	6	US-10-835-615-797	Sequence 797, App	535	26	35.6	510	7	US-11-045-802-36	Sequence 36, Appl
463	26	35.6	154	7	US-11-055-822-894	Sequence 894, App	536	26	35.6	516	7		

537	26	35.6	528	6	US-10-793-626-1930	Sequence 1930, Ap	610	26	35.6	3144	7	US-11-055-035-1	Sequence 1, Appli
538	26	35.6	529	7	US-11-013-247A-17	Sequence 17, Appl	611	26	35.6	3333	6	US-10-766-317-4	Sequence 4, Appli
539	26	35.6	540	7	US-11-045-802-35	Sequence 35, Appl	612	26	35.6	4384	6	US-10-821-234-1120	Sequence 1120, Ap
540	26	35.6	562	7	US-11-065-943-24	Sequence 24, Appl	613	25.5	34.9	140	6	US-10-821-234-1347	Sequence 1347, Ap
541	26	35.6	562	7	US-11-166-892-10	Sequence 10, Appl	614	25.5	34.9	331	6	US-10-131-826A-184	Sequence 184, App
542	26	35.6	565	7	US-11-045-802-34	Sequence 34, Appl	615	25.5	34.9	803	6	US-10-513-759-2	Sequence 2, Appli
543	26	35.6	575	6	US-10-467-657-1456	Sequence 1456, Ap	616	25	34.2	6	US-10-895-064-158	Sequence 158, App	
544	26	35.6	579	7	US-11-045-802-32	Sequence 32, Appl	617	25	34.2	14	6	US-10-857-620A-1	Sequence 1, Appli
545	26	35.6	579	7	US-11-045-802-33	Sequence 33, Appl	618	25	34.2	18	6	US-10-485-788A-838	Sequence 838, App
546	26	35.6	581	7	US-11-045-802-30	Sequence 30, Appl	619	25	34.2	18	7	US-11-024-251-9	Sequence 9, Appli
547	26	35.6	583	6	US-10-763-712A-38	Sequence 38, Appl	620	25	34.2	23	7	US-11-060-005-18	Sequence 18, Appl
548	26	35.6	584	7	US-11-045-802-31	Sequence 31, Appl	621	25	34.2	30	7	US-11-145-861-387	Sequence 387, App
549	26	35.6	585	7	US-11-127-877-63	Sequence 63, Appl	622	25	34.2	31	6	US-10-982-727-89	Sequence 89, Appl
550	26	35.6	587	7	US-11-205-109-27	Sequence 27, Appl	623	25	34.2	42	7	US-11-067-425A-77	Sequence 77, Appl
551	26	35.6	592	6	US-10-467-962B-95	Sequence 95, Appl	624	25	34.2	42	7	US-11-067-425A-78	Sequence 78, Appl
552	26	35.6	592	6	US-10-524-647-112	Sequence 112, App	625	25	34.2	42	7	US-11-067-425A-79	Sequence 79, Appl
553	26	35.6	597	6	US-10-055-877-303	Sequence 303, App	626	25	34.2	42	7	US-11-067-425A-80	Sequence 80, Appl
554	26	35.6	597	6	US-11-045-802-28	Sequence 28, Appl	627	25	34.2	43	6	US-10-957-887B-231	Sequence 231, App
555	26	35.6	600	6	US-10-878-556A-43	Sequence 43, Appl	628	25	34.2	44	6	US-10-957-887B-61	Sequence 61, Appl
556	26	35.6	626	6	US-10-467-657-1772	Sequence 1772, Ap	629	25	34.2	45	6	US-10-467-657-7602	Sequence 7602, Ap
557	26	35.6	655	7	US-11-045-802-29	Sequence 29, Appl	630	25	34.2	49	6	US-10-467-657-5052	Sequence 5052, Ap
558	26	35.6	659	6	US-10-467-657-6006	Sequence 6006, Ap	631	25	34.2	50	6	US-10-895-064-2746	Sequence 2746, Ap
559	26	35.6	661	7	US-11-019-711-107	Sequence 107, App	632	25	34.2	60	6	US-10-502-972-11	Sequence 11, Appl
560	26	35.6	692	7	US-11-045-802-26	Sequence 26, Appl	633	25	34.2	98	6	US-10-821-234-1161	Sequence 1161, Ap
561	26	35.6	710	7	US-11-043-802-2	Sequence 2, Appli	634	25	34.2	108	5	US-09-978-360A-440	Sequence 440, App
562	26	35.6	710	7	US-11-045-802-19	Sequence 19, Appl	635	25	34.2	133	6	US-10-467-657-5098	Sequence 5098, Ap
563	26	35.6	710	7	US-11-045-802-20	Sequence 20, Appl	636	25	34.2	133	7	US-11-149-462-5	Sequence 5, Appli
564	26	35.6	710	7	US-11-045-802-21	Sequence 21, Appl	637	25	34.2	135	7	US-11-019-711-56	Sequence 56, Appl
565	26	35.6	710	7	US-11-045-802-22	Sequence 22, Appl	638	25	34.2	135	7	US-11-019-711-84	Sequence 84, Appl
566	26	35.6	710	7	US-11-045-802-23	Sequence 23, Appl	639	25	34.2	153	6	US-10-821-234-1086	Sequence 1086, Ap
567	26	35.6	710	7	US-11-045-802-24	Sequence 24, Appl	640	25	34.2	159	6	US-10-467-657-2736	Sequence 2736, Ap
568	26	35.6	712	6	US-10-995-561-984	Sequence 984, App	641	25	34.2	166	6	US-10-467-657-1080	Sequence 1080, Ap
569	26	35.6	729	7	US-11-130-821-4	Sequence 4, Appli	642	25	34.2	182	6	US-10-661-966-6	Sequence 6, Appli
570	26	35.6	731	7	US-11-130-821-3	Sequence 3, Appli	643	25	34.2	192	7	US-11-175-690-336	Sequence 336, App
571	26	35.6	732	7	US-11-078-189-14	Sequence 14, Appl	644	25	34.2	192	7	US-11-175-690-337	Sequence 337, App
572	26	35.6	763	7	US-11-013-247A-35	Sequence 35, Appl	645	25	34.2	205	6	US-10-793-626-240	Sequence 240, App
573	26	35.6	769	6	US-10-995-561-985	Sequence 985, App	646	25	34.2	207	7	US-11-129-104-98	Sequence 98, Appl
574	26	35.6	769	6	US-10-995-561-986	Sequence 986, App	647	25	34.2	209	6	US-10-467-657-6890	Sequence 6890, Ap
575	26	35.6	769	6	US-11-107-028-5	Sequence 5, Appli	648	25	34.2	218	6	US-10-821-234-1595	Sequence 1595, Ap
576	26	35.6	773	7	US-11-010-239-63	Sequence 63, Appl	649	25	34.2	219	6	US-10-793-626-2206	Sequence 2206, Ap
577	26	35.6	816	7	US-11-143-980-67	Sequence 67, Appl	650	25	34.2	220	6	US-10-661-966-5	Sequence 5, Appli
578	26	35.6	828	6	US-10-995-561-983	Sequence 983, App	651	25	34.2	225	6	US-10-793-626-1452	Sequence 1452, Ap
579	26	35.6	834	6	US-10-131-826A-148	Sequence 148, App	652	25	34.2	226	6	US-10-793-626-1734	Sequence 1734, Ap
580	26	35.6	834	6	US-11-052-554A-212	Sequence 212, App	653	25	34.2	226	6	US-10-670-009-6	Sequence 6, Appli
581	26	35.6	841	6	US-10-624-932-6	Sequence 6, Appli	654	25	34.2	229	7	US-11-055-822-798	Sequence 798, App
582	26	35.6	841	6	US-10-624-932-8	Sequence 8, Appli	655	25	34.2	233	6	US-10-878-556A-147	Sequence 147, App
583	26	35.6	847	7	US-11-124-368A-234	Sequence 234, App	656	25	34.2	239	6	US-10-895-064-1311	Sequence 1311, Ap
584	26	35.6	854	6	US-10-511-657-4	Sequence 4, Appli	657	25	34.2	245	6	US-10-467-657-8582	Sequence 8582, Ap
585	26	35.6	892	7	US-11-082-389-396	Sequence 396, App	658	25	34.2	247	6	US-10-510-386-242	Sequence 242, App
586	26	35.6	918	6	US-10-995-561-981	Sequence 981, App	659	25	34.2	249	6	US-10-821-234-1596	Sequence 1596, Ap
587	26	35.6	961	6	US-10-831-997-4	Sequence 4, Appli	660	25	34.2	252	6	US-10-995-561-601	Sequence 601, App
588	26	35.6	970	6	US-10-467-657-5524	Sequence 5524, Ap	661	25	34.2	257	6	US-10-793-626-3244	Sequence 3244, Ap
589	26	35.6	1019	6	US-10-995-561-982	Sequence 982, App	662	25	34.2	257	6	US-10-467-657-720	Sequence 720, App
590	26	35.6	1023	6	US-10-995-561-968	Sequence 968, App	663	25	34.2	257	7	US-11-156-084-290	Sequence 290, App
591	26	35.6	1076	6	US-10-995-561-968	Sequence 968, App	664	25	34.2	261	7	US-11-169-041-190	Sequence 190, App
592	26	35.6	1165	7	US-10-467-657-5708	Sequence 5708, Ap	665	25	34.2	262	6	US-10-793-626-876	Sequence 876, App
593	26	35.6	1390	7	US-11-197-380-6	Sequence 6, Appli	666	25	34.2	267	7	US-11-165-067A-3	Sequence 3, Appli
594	26	35.6	1430	6	US-11-063-343-35	Sequence 35, Appl	667	25	34.2	269	5	US-09-978-360A-529	Sequence 529, App
595	26	35.6	1433	7	US-11-094-519A-40	Sequence 40, Appl	668	25	34.2	277	6	US-10-510-386-96	Sequence 96, Appl
596	26	35.6	1445	7	US-11-169-041-181	Sequence 181, App	669	25	34.2	277	6	US-10-454-437-8	Sequence 8, Appli
597	26	35.6	1463	7	US-11-080-991-22	Sequence 22, Appl	670	25	34.2	277	7	US-11-055-822-608	Sequence 608, App
598	26	35.6	1581	7	US-11-090-439-24	Sequence 24, Appl	671	25	34.2	278	7	US-11-009-658-8	Sequence 8, Appli
599	26	35.6	1581	7	US-11-090-439-26	Sequence 26, Appl	672	25	34.2	281	7	US-11-144-833-14	Sequence 14, Appl
600	26	35.6	1588	6	US-10-995-561-527	Sequence 527, App	673	25	34.2	288	6	US-10-793-626-1118	Sequence 1118, Ap
601	26	35.6	1713	6	US-10-766-317-2	Sequence 2, Appli	674	25	34.2	292	6	US-10-527-500-9	Sequence 9, Appli
602	26	35.6	1724	6	US-10-766-317-6	Sequence 6, Appli	675	25	34.2	293	6	US-10-467-657-6664	Sequence 6664, Ap
603	26	35.6	1992	7	US-11-013-759-3	Sequence 3, Appli	676	25	34.2	296	6	US-10-467-657-2944	Sequence 2944, Ap
604	26	35.6	1992	7	US-11-013-759-13	Sequence 13, Appl	677	25	34.2	300	6	US-10-793-626-1900	Sequence 1900, Ap
605	26	35.6	2047	7	US-11-013-759-4	Sequence 4, Appli	678	25	34.2	302	7	US-11-165-226-127	Sequence 127, App
606	26	35.6	2047	7	US-11-013-759-7	Sequence 7, Appli	679	25	34.2	310	7	US-11-169-041-163	Sequence 163, App
607	26	35.6	2233	6	US-10-873-528-2	Sequence 2, Appli	680	25	34.2	311	6	US-10-793-626-1260	Sequence 1260, Ap
608	26	35.6	2471	7	US-11-050-346-60	Sequence 60, Appl	681	25	34.2	313	6	US-10-995-561-972	Sequence 972, App
609	26	35.6	2902	7	US-11-052-554A-91	Sequence 91, Appl	682	25	34.2	314	7	US-11-008-570-43	Sequence 43, Appl

683	25	34.2	318	6	US-10-467-657-7760	Sequence 7760, Ap	756	25	34.2	542	6	US-10-524-647-12	Sequence 12, Appl
684	25	34.2	318	7	US-11-058-924-8	Sequence 8, Appli	757	25	34.2	542	7	US-11-152-747-6	Sequence 6, Appli
685	25	34.2	323	7	US-11-185-067A-13	Sequence 13, Appl	758	25	34.2	544	7	US-11-166-609-18	Sequence 18, Appl
686	25	34.2	323	6	US-10-793-626-1076	Sequence 1076, Ap	759	25	34.2	546	7	US-11-166-609-2	Sequence 2, Appli
687	25	34.2	327	6	US-10-821-234-884	Sequence 884, App	760	25	34.2	548	7	US-11-114-906-14	Sequence 14, Appl
688	25	34.2	329	7	US-11-194-246-299	Sequence 299, App	761	25	34.2	548	7	US-11-159-902-4	Sequence 4, Appli
689	25	34.2	335	6	US-10-995-561-970	Sequence 970, App	762	25	34.2	554	7	US-11-082-389-78	Sequence 78, Appl
690	25	34.2	335	7	US-11-129-143-106	Sequence 106, App	763	25	34.2	567	6	US-10-503-051-5	Sequence 5, Appli
691	25	34.2	337	6	US-10-485-517-234	Sequence 234, App	764	25	34.2	568	6	US-10-997-247-4	Sequence 4, Appli
692	25	34.2	338	6	US-10-520-820-6	Sequence 6, Appli	765	25	34.2	572	6	US-10-878-556A-47	Sequence 1358, Ap
693	25	34.2	345	6	US-10-995-561-971	Sequence 971, App	766	25	34.2	583	6	US-10-793-626-1358	Sequence 42, Appl
694	25	34.2	346	7	US-11-012-522-13	Sequence 13, Appl	767	25	34.2	585	6	US-10-878-556A-42	Sequence 3, Appli
695	25	34.2	353	6	US-10-875-716-10	Sequence 10, Appl	768	25	34.2	600	6	US-10-606-302-3	Sequence 4656, Ap
696	25	34.2	355	6	US-10-503-051-2	Sequence 2, Appli	769	25	34.2	611	6	US-10-467-657-4656	Sequence 4, Appli
697	25	34.2	366	5	US-09-978-360A-421	Sequence 421, App	770	25	34.2	618	6	US-10-523-912-4	Sequence 56, Appl
698	25	34.2	366	7	US-11-000-463-897	Sequence 897, App	771	25	34.2	621	6	US-10-632-150-56	Sequence 56, Appl
699	25	34.2	368	6	US-10-467-657-4756	Sequence 4756, Ap	772	25	34.2	621	7	US-11-073-457-56	Sequence 56, Appl
700	25	34.2	380	7	US-11-144-833-12	Sequence 12, Appl	773	25	34.2	621	7	US-11-073-460-56	Sequence 56, Appl
701	25	34.2	380	7	US-11-144-833-13	Sequence 13, Appl	774	25	34.2	628	7	US-11-094-519A-28	Sequence 28, Appl
702	25	34.2	383	7	US-11-159-516A-2	Sequence 2, Appli	775	25	34.2	631	6	US-10-467-657-5452	Sequence 5452, Ap
703	25	34.2	383	7	US-11-159-516A-29	Sequence 29, Appl	776	25	34.2	631	6	US-10-467-657-7396	Sequence 7396, Ap
704	25	34.2	384	6	US-10-467-657-508	Sequence 508, App	777	25	34.2	631	6	US-10-813-646-22	Sequence 22, Appl
705	25	34.2	389	6	US-10-513-118-2	Sequence 2, Appli	778	25	34.2	640	7	US-11-034-519A-44	Sequence 44, Appl
706	25	34.2	398	7	US-11-110-011-4	Sequence 1115, Ap	779	25	34.2	640	7	US-11-205-109-9	Sequence 9, Appli
707	25	34.2	400	7	US-11-108-172-1115	Sequence 1115, Ap	780	25	34.2	644	6	US-10-763-712A-36	Sequence 36, Appl
708	25	34.2	400	7	US-11-000-463-425	Sequence 425, App	781	25	34.2	648	6	US-10-793-626-568	Sequence 568, App
709	25	34.2	406	6	US-10-131-826A-82	Sequence 82, Appl	782	25	34.2	648	7	US-10-793-626-568	Sequence 12, Appl
710	25	34.2	406	6	US-10-131-826A-430	Sequence 430, App	783	25	34.2	648	7	US-11-114-906-12	Sequence 10, Appl
711	25	34.2	406	6	US-10-467-657-1048	Sequence 1048, Ap	784	25	34.2	654	7	US-11-114-906-10	Sequence 10, Appl
712	25	34.2	406	6	US-10-878-556A-11	Sequence 11, Appl	785	25	34.2	657	7	US-11-080-991-48	Sequence 48, Appl
713	25	34.2	406	7	US-11-108-841-1	Sequence 1, Appli	786	25	34.2	661	6	US-10-453-372-642	Sequence 642, App
714	25	34.2	406	7	US-11-108-841-3	Sequence 3, Appli	787	25	34.2	664	7	US-11-080-991-40	Sequence 40, Appl
715	25	34.2	410	6	US-10-821-234-912	Sequence 912, App	788	25	34.2	685	6	US-10-661-966-3	Sequence 3, Appli
716	25	34.2	416	6	US-10-793-626-2	Sequence 2, Appli	789	25	34.2	688	7	US-11-165-326-124	Sequence 124, App
717	25	34.2	422	6	US-10-524-647-122	Sequence 122, App	790	25	34.2	695	6	US-10-453-372-648	Sequence 648, App
718	25	34.2	424	6	US-10-793-626-1046	Sequence 1046, Ap	791	25	34.2	700	6	US-10-935-561-922	Sequence 922, App
719	25	34.2	424	6	US-10-467-657-2678	Sequence 2678, Ap	792	25	34.2	706	6	US-10-935-561-924	Sequence 924, App
720	25	34.2	429	6	US-10-967-457-74	Sequence 74, Appl	793	25	34.2	709	7	US-11-024-959-269	Sequence 269, App
721	25	34.2	429	7	US-11-000-463-302	Sequence 302, App	794	25	34.2	710	7	US-11-165-067A-9	Sequence 9, Appli
722	25	34.2	429	7	US-11-000-463-774	Sequence 774, App	795	25	34.2	710	7	US-11-089-551A-33	Sequence 33, Appl
723	25	34.2	429	7	US-11-205-109-32	Sequence 32, Appl	796	25	34.2	736	6	US-11-078-189-11	Sequence 11, Appl
724	25	34.2	431	7	US-11-060-920-4	Sequence 4, Appli	797	25	34.2	752	6	US-10-793-626-1138	Sequence 1138, Ap
725	25	34.2	432	6	US-10-793-626-2942	Sequence 2942, Ap	798	25	34.2	752	6	US-10-485-517-173	Sequence 173, App
726	25	34.2	434	6	US-10-821-234-1553	Sequence 1553, Ap	799	25	34.2	757	6	US-10-055-877-157	Sequence 157, App
727	25	34.2	440	6	US-10-063-703-134	Sequence 134, App	800	25	34.2	758	6	US-10-467-962B-12	Sequence 12, Appl
728	25	34.2	440	6	US-10-063-703-134	Sequence 134, App	801	25	34.2	765	6	US-10-661-966-10	Sequence 10, Appl
729	25	34.2	447	6	US-10-102-240-134	Sequence 134, App	802	25	34.2	765	6	US-10-661-966-15	Sequence 15, Appl
730	25	34.2	451	6	US-10-770-726-79	Sequence 79, Appl	803	25	34.2	765	7	US-11-144-630-69	Sequence 69, Appl
731	25	34.2	458	6	US-10-878-556A-28	Sequence 28, Appl	804	25	34.2	774	7	US-11-000-463-459	Sequence 459, App
732	25	34.2	460	6	US-10-990-276-1	Sequence 1, Appli	805	25	34.2	775	6	US-10-453-372-656	Sequence 656, App
733	25	34.2	468	7	US-10-336-263A-6	Sequence 182, App	806	25	34.2	776	6	US-11-114-906-24	Sequence 24, Appl
734	25	34.2	471	6	US-11-069-642-5	Sequence 6, Appli	807	25	34.2	777	6	US-10-821-234-1658	Sequence 1658, Ap
735	25	34.2	473	7	US-10-131-826A-528	Sequence 528, App	808	25	34.2	783	6	US-10-661-966-2	Sequence 2, Appli
736	25	34.2	487	6	US-10-793-626-2770	Sequence 2770, Ap	809	25	34.2	783	7	US-11-186-284-59	Sequence 59, Appl
737	25	34.2	491	6	US-10-793-626-2770	Sequence 2770, Ap	810	25	34.2	789	7	US-11-108-172-1127	Sequence 1127, Ap
738	25	34.2	492	6	US-10-467-962B-51	Sequence 51, Appl	811	25	34.2	792	7	US-11-095-561-925	Sequence 925, App
739	25	34.2	495	6	US-10-873-528-99	Sequence 99, Appl	812	25	34.2	793	6	US-11-175-690-249	Sequence 249, App
740	25	34.2	496	6	US-10-793-626-1386	Sequence 1386, Ap	813	25	34.2	801	7	US-11-175-690-250	Sequence 250, App
741	25	34.2	500	7	US-11-110-082-31	Sequence 31, Appl	814	25	34.2	801	7	US-11-175-690-250	Sequence 250, App
742	25	34.2	504	7	US-11-055-822-136	Sequence 136, App	815	25	34.2	804	6	US-10-453-372-650	Sequence 650, App
743	25	34.2	504	7	US-11-055-822-136	Sequence 136, App	816	25	34.2	825	6	US-10-453-372-644	Sequence 644, App
744	25	34.2	510	6	US-10-485-517-320	Sequence 320, App	817	25	34.2	833	7	US-11-159-902-2	Sequence 2, Appli
745	25	34.2	518	7	US-11-166-609-13	Sequence 13, Appl	818	25	34.2	834	6	US-10-453-372-658	Sequence 658, App
746	25	34.2	519	6	US-10-821-234-1373	Sequence 1373, Ap	819	25	34.2	838	7	US-11-052-554A-42	Sequence 42, Appl
747	25	34.2	520	7	US-11-112-882-26	Sequence 26, Appl	820	25	34.2	840	7	US-11-052-554A-40	Sequence 40, Appl
748	25	34.2	524	7	US-11-054-281-34	Sequence 34, Appl	821	25	34.2	844	6	US-10-763-712A-48	Sequence 48, Appl
749	25	34.2	524	7	US-11-054-281-121	Sequence 121, App	822	25	34.2	847	6	US-10-453-372-652	Sequence 652, App
750	25	34.2	526	6	US-10-467-657-6754	Sequence 6754, App	823	25	34.2	857	6	US-10-878-556A-36	Sequence 36, Appl
751	25	34.2	527	7	US-11-069-642-21	Sequence 21, Appl	824	25	34.2	858	6	US-10-878-556A-36	Sequence 36, Appl
752	25	34.2	529	6	US-10-467-657-3958	Sequence 3958, Ap	825	25	34.2	863	7	US-11-114-906-30	Sequence 30, Appl
753	25	34.2	531	6	US-10-517-939-70	Sequence 70, Appl	826	25	34.2	876	7	US-11-114-906-30	Sequence 30, Appl
754	25	34.2	535	7	US-11-114-906-16	Sequence 16, Appl	827	25	34.2	877	6	US-10-821-234-960	Sequence 960, App
755	25	34.2	538	7	US-11-166-609-21	Sequence 21, Appl	828	25	34.2	889	7	US-11-114-906-18	Sequence 18, Appl

829	25	34.2	905	6	US-10-453-372-638	Sequence 638, App	902	24.5	33.6	302	7	US-11-156-084-351	Sequence 351, App
830	25	34.2	905	6	US-10-453-372-662	Sequence 662, App	903	24.5	33.6	334	6	US-10-895-064-24	Sequence 24, Appl
831	25	34.2	905	6	US-10-453-372-664	Sequence 664, App	904	24.5	33.6	334	6	US-10-895-064-25	Sequence 25, Appl
832	25	34.2	917	7	US-11-169-041-145	Sequence 145, App	905	24.5	33.6	334	6	US-10-895-064-26	Sequence 26, Appl
833	25	34.2	963	6	US-10-995-561-923	Sequence 923, App	906	24.5	33.6	351	7	US-11-067-884-4	Sequence 4, Appl
834	25	34.2	963	6	US-10-453-372-660	Sequence 660, App	907	24.5	33.6	352	7	US-11-052-554A-220	Sequence 220, App
835	25	34.2	976	7	US-11-114-906-28	Sequence 28, Appl	908	24.5	33.6	401	7	US-11-055-832-336	Sequence 336, App
836	25	34.2	982	7	US-11-114-906-26	Sequence 26, Appl	909	24.5	33.6	416	6	US-10-467-657-5060	Sequence 5060, Ap
837	25	34.2	983	7	US-11-113-424-59	Sequence 59, Appl	910	24.5	33.6	490	6	US-10-467-657-7280	Sequence 7280, Ap
838	25	34.2	984	7	US-11-113-424-60	Sequence 60, Appl	911	24.5	33.6	490	6	US-10-467-657-8158	Sequence 8158, Ap
839	25	34.2	985	7	US-11-113-424-61	Sequence 61, Appl	912	24.5	33.6	862	7	US-11-128-420-11	Sequence 11, Appl
840	25	34.2	986	6	US-10-821-234-1310	Sequence 1310, Ap	913	24.5	33.6	862	7	US-11-007-428-2	Sequence 2, Appl
841	25	34.2	998	6	US-10-510-524-1	Sequence 1, Appl	914	24.5	33.6	862	7	US-11-183-294-16	Sequence 16, Appl
842	25	34.2	1012	6	US-10-453-372-646	Sequence 646, App	915	24.5	33.6	914	6	US-10-312-954-2	Sequence 2, Appl
843	25	34.2	1015	6	US-10-467-657-180	Sequence 180, App	916	24.5	33.6	1141	6	US-10-995-561-1009	Sequence 1009, Ap
844	25	34.2	1015	6	US-10-467-657-3764	Sequence 3764, Ap	917	24.5	33.6	1141	6	US-10-995-561-1010	Sequence 1010, Ap
845	25	34.2	1035	7	US-11-113-424-20	Sequence 20, Appl	918	24.5	33.6	1405	6	US-10-995-561-529	Sequence 529, Ap
846	25	34.2	1042	7	US-11-037-243-74	Sequence 74, Appl	919	24.5	33.6	1406	6	US-10-995-561-530	Sequence 530, App
847	25	34.2	1045	7	US-11-113-424-54	Sequence 54, Appl	920	24.5	33.6	1436	6	US-10-995-561-531	Sequence 531, App
848	25	34.2	1052	7	US-11-113-424-22	Sequence 22, Appl	921	24	32.9	10	6	US-10-857-620A-2	Sequence 2, Appl
849	25	34.2	1061	7	US-11-059-814-18	Sequence 18, Appl	922	24	32.9	13	7	US-11-097-749-12	Sequence 12, Appl
850	25	34.2	1094	6	US-10-821-234-1097	Sequence 1097, Ap	923	24	32.9	18	7	US-11-033-039-1230	Sequence 1230, Ap
851	25	34.2	1099	6	US-10-873-528-11	Sequence 11, Appl	924	24	32.9	20	6	US-10-982-727-90	Sequence 90, Appl
852	25	34.2	1122	7	US-11-191-374-3	Sequence 3, Appl	925	24	32.9	21	6	US-10-509-787A-109	Sequence 109, App
853	25	34.2	1122	7	US-11-191-375-3	Sequence 3, Appl	926	24	32.9	21	7	US-11-033-039-1221	Sequence 1221, Ap
854	25	34.2	1122	7	US-11-191-588-3	Sequence 3, Appl	927	24	32.9	28	7	US-11-019-834A-21	Sequence 21, Appl
855	25	34.2	1138	7	US-11-012-762-28	Sequence 28, Appl	928	24	32.9	30	7	US-11-145-703-232	Sequence 30, App
856	25	34.2	1183	7	US-11-115-639-13	Sequence 13, Appl	929	24	32.9	42	7	US-11-067-425A-76	Sequence 76, Appl
857	25	34.2	1183	7	US-11-115-639-15	Sequence 15, Appl	930	24	32.9	47	6	US-10-467-657-8562	Sequence 8562, Ap
858	25	34.2	1183	7	US-11-115-639-16	Sequence 16, Appl	931	24	32.9	48	6	US-10-467-657-4314	Sequence 4314, Ap
859	25	34.2	1183	7	US-11-115-639-17	Sequence 17, Appl	932	24	32.9	54	7	US-11-150-054A-32	Sequence 32, Appl
860	25	34.2	1183	7	US-11-115-639-18	Sequence 18, Appl	933	24	32.9	58	6	US-10-667-235-210	Sequence 210, App
861	25	34.2	1189	6	US-11-074-176-134	Sequence 134, App	934	24	32.9	60	6	US-10-467-657-2482	Sequence 2482, Ap
862	25	34.2	1198	6	US-10-451-375-4	Sequence 4, Appl	935	24	32.9	60	6	US-10-467-657-5628	Sequence 5628, Ap
863	25	34.2	1210	6	US-11-108-172-692	Sequence 692, App	936	24	32.9	60	6	US-10-467-657-8328	Sequence 8328, Ap
864	25	34.2	1234	6	US-10-467-657-4224	Sequence 4224, Ap	937	24	32.9	60	6	US-10-467-657-8330	Sequence 8330, Ap
865	25	34.2	1254	6	US-10-528-031-47	Sequence 47, Appl	938	24	32.9	60	6	US-10-897-981-2	Sequence 2, Appl
866	25	34.2	1295	6	US-11-091-928-2	Sequence 2, Appl	939	24	32.9	68	6	US-10-895-064-2719	Sequence 2719, Ap
867	25	34.2	1296	6	US-10-615-668-3	Sequence 3, Appl	940	24	32.9	70	6	US-10-895-064-2548	Sequence 2548, Ap
868	25	34.2	1340	7	US-11-070-575-6	Sequence 6, Appl	941	24	32.9	74	6	US-10-467-657-4254	Sequence 4254, Ap
869	25	34.2	1346	7	US-11-060-005-2	Sequence 2, Appl	942	24	32.9	78	6	US-10-467-657-3012	Sequence 3012, Ap
870	25	34.2	1362	6	US-10-895-064-420	Sequence 420, App	943	24	32.9	79	6	US-10-467-657-8136	Sequence 8136, Ap
871	25	34.2	1377	6	US-10-821-234-1070	Sequence 1070, Ap	944	24	32.9	82	6	US-10-467-657-2530	Sequence 2530, Ap
872	25	34.2	1403	7	US-11-091-928-1	Sequence 1, Appl	945	24	32.9	86	6	US-10-895-064-2906	Sequence 2906, Ap
873	25	34.2	1404	6	US-10-878-556A-169	Sequence 169, App	946	24	32.9	92	7	US-11-008-727-6	Sequence 6, Appl
874	25	34.2	1476	7	US-11-019-711-114	Sequence 114, App	947	24	32.9	92	7	US-11-058-542-1	Sequence 1, Appl
875	25	34.2	1548	7	US-11-108-172-1095	Sequence 1095, Ap	948	24	32.9	94	6	US-10-467-657-7290	Sequence 7290, Ap
876	25	34.2	1588	7	US-11-043-889-37	Sequence 37, Appl	949	24	32.9	96	6	US-10-467-657-320	Sequence 320, App
877	25	34.2	1596	7	US-11-060-005-4	Sequence 4, Appl	950	24	32.9	97	7	US-11-034-569-2	Sequence 2, Appl
878	25	34.2	1604	7	US-11-037-243-73	Sequence 73, Appl	951	24	32.9	98	7	US-11-097-749-59	Sequence 59, Appl
879	25	34.2	1627	6	US-10-821-234-1283	Sequence 1283, Ap	952	24	32.9	99	6	US-10-467-657-6714	Sequence 6714, Ap
880	25	34.2	1751	6	US-11-103-957-45	Sequence 45, Appl	953	24	32.9	99	6	US-10-467-657-7862	Sequence 7862, Ap
881	25	34.2	1933	6	US-10-523-912-2	Sequence 2, Appl	954	24	32.9	103	6	US-10-986-501-125	Sequence 125, App
882	25	34.2	2312	7	US-11-126-313-34	Sequence 34, Appl	955	24	32.9	110	6	US-10-467-657-282	Sequence 282, App
883	25	34.2	2326	7	US-11-126-313-37	Sequence 37, Appl	956	24	32.9	110	6	US-10-467-657-5260	Sequence 5260, Ap
884	25	34.2	2333	7	US-11-096-281-13	Sequence 13, Appl	957	24	32.9	114	7	US-11-019-711-42	Sequence 42, Appl
885	25	34.2	2339	7	US-11-096-281-11	Sequence 11, Appl	958	24	32.9	116	6	US-10-821-234-1625	Sequence 1625, Ap
886	25	34.2	2376	7	US-11-096-051-4	Sequence 4, Appl	959	24	32.9	122	6	US-10-793-626-102	Sequence 102, App
887	25	34.2	2505	7	US-11-126-313-33	Sequence 33, Appl	960	24	32.9	124	7	US-11-145-861-403	Sequence 403, App
888	25	34.2	2671	6	US-10-876-787-6	Sequence 6, Appl	961	24	32.9	128	7	US-11-194-246-425	Sequence 425, App
889	25	34.2	2715	7	US-11-096-051-2	Sequence 2, Appl	962	24	32.9	133	6	US-10-667-295-221	Sequence 221, App
890	25	34.2	2721	7	US-11-113-424-51	Sequence 51, Appl	963	24	32.9	134	6	US-10-793-626-2256	Sequence 2256, Ap
891	25	34.2	2721	7	US-11-096-051-10	Sequence 10, Appl	964	24	32.9	136	6	US-10-873-528-10	Sequence 10, Appl
892	25	34.2	2725	7	US-11-096-051-8	Sequence 8, Appl	965	24	32.9	137	6	US-10-454-437-338	Sequence 338, App
893	25	34.2	2765	6	US-10-877-346-62	Sequence 62, Appl	966	24	32.9	145	7	US-11-055-822-164	Sequence 164, App
894	25	34.2	2801	7	US-11-124-368A-305	Sequence 305, App	967	24	32.9	147	6	US-10-793-626-2238	Sequence 2238, Ap
895	25	34.2	2896	7	US-11-124-368A-306	Sequence 306, App	968	24	32.9	148	7	US-11-037-749-54	Sequence 54, Appl
896	25	34.2	3256	7	US-11-124-368A-304	Sequence 304, App	969	24	32.9	150	6	US-10-793-626-328	Sequence 328, App
897	25	34.2	5024	6	US-10-793-626-2964	Sequence 2964, Ap	970	24	32.9	152	6	US-10-467-657-2668	Sequence 2668, Ap
898	25	34.2	5179	7	US-11-108-172-1068	Sequence 1068, Ap	971	24	32.9	153	6	US-10-821-234-893	Sequence 893, App
899	25	34.2	7968	7	US-11-143-980-49	Sequence 49, Appl	972	24	32.9	153	6	US-10-467-657-7674	Sequence 7674, Ap
900	25	34.2	8695	7	US-11-205-109-15	Sequence 15, Appl	973	24	32.9	153	6	US-10-467-657-8432	Sequence 8432, Ap
901	24.5	33.6	2603	6	US-10-793-626-1784	Sequence 1784, Ap	974	24	32.9	153	7	US-11-145-703-34	Sequence 34, Appl

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975 24 32.9 157 6 US-10-793-626-3268 Sequence 3268, Ap
976 24 32.9 158 6 US-10-821-234-1294 Sequence 1294, Ap
977 24 32.9 160 6 US-10-821-234-1422 Sequence 1422, Ap
978 24 32.9 166 7 US-11-176-830-1098 Sequence 1098, Ap
979 24 32.9 166 7 US-11-196-067-294 Sequence 294, Ap
980 24 32.9 168 7 US-11-097-749-58 Sequence 58, Appl
981 24 32.9 169 7 US-11-186-284-53 Sequence 53, Appl
982 24 32.9 169 7 US-11-182-908-21 Sequence 21, Appl
983 24 32.9 176 6 US-10-821-234-1336 Sequence 1336, Ap
984 24 32.9 177 6 US-10-798-579A-28 Sequence 28, Appl
985 24 32.9 179 6 US-10-714-887-88 Sequence 88, Appl
986 24 32.9 179 7 US-11-194-246-413 Sequence 413, Ap
987 24 32.9 186 6 US-10-467-657-7854 Sequence 7854, Ap
988 24 32.9 186 7 US-11-150-845-36 Sequence 36, Appl
989 24 32.9 186 7 US-11-182-016-40 Sequence 40, Appl
990 24 32.9 188 6 US-10-793-626-3272 Sequence 3272, Ap
991 24 32.9 190 7 US-11-055-822-442 Sequence 442, Ap
992 24 32.9 190 7 US-11-182-016-39 Sequence 39, Appl
993 24 32.9 194 7 US-11-194-246-301 Sequence 301, Ap
994 24 32.9 196 6 US-10-821-234-982 Sequence 982, Ap
995 24 32.9 197 7 US-11-037-749-52 Sequence 52, Appl
996 24 32.9 197 7 US-11-097-749-53 Sequence 53, Appl
997 24 32.9 197 7 US-11-097-749-55 Sequence 55, Appl
998 24 32.9 197 7 US-11-097-749-56 Sequence 56, Appl
999 24 32.9 197 7 US-11-097-749-57 Sequence 57, Appl
1000 24 32.9 198 6 US-10-793-626-990 Sequence 990, Ap
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ALIGNMENTS

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RESULT 1
US-11-043-788-9
; Sequence 9, Application US/11043788
; Publication No. US20060014166A1
; GENERAL INFORMATION:
; APPLICANT: Comugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1006
; CURRENT APPLICATION NUMBER: US/11/043,788
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO 9
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-043-788-9
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Query Match 100.0%; Score 73; DB 7; Length 65;
Best Local Similarity 100.0%; Pred. No. 5.1e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 ISVQLASYYRRTSSK 16
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Db 43 ISVQLASYYRRTSSK 58
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RESULT 2
US-11-043-788-8
; Sequence 8, Application US/11043788
; Publication No. US20060014166A1
; GENERAL INFORMATION:
; APPLICANT: Comugen Ltd
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
; FILE REFERENCE: 1847.1006
; CURRENT APPLICATION NUMBER: US/11/043,788
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 506
; SEQ ID NO 8
; LENGTH: 99
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-11-043-788-8
Query Match 100.0%; Score 73; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ISVQLASYYRRTSSK 16
| | | | | | | | | | | | | | | |
Db 43 ISVQLASYYRRTSSK 58
| | | | | | | | | | | | | | | |
RESULT 3
US-10-509-292-1
; Sequence 1, Application US/10509292
; Publication No. US20050287159A1
; GENERAL INFORMATION:
; APPLICANT: Merckia Pharma LLC
; TITLE OF INVENTION: Methods and Compositions for Treating and Preventing Botaxin
; FILE REFERENCE: MERPH.001
; CURRENT APPLICATION NUMBER: US/10/509,292
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/367,591
; PRIOR FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-509-292-1
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Query Match 76.7%; Score 56; DB 6; Length 74;
Best Local Similarity 75.0%; Pred. No. 0.00077;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 ISVQLASYYRRTSSK 16
| | | | | | | | | | | | | | | |
Db 18 IPLQLRSYRRTISGK 33
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RESULT 4
US-10-995-561-900
; Sequence 900, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 900
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-900
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Query Match 76.7%; Score 56; DB 6; Length 97;
Best Local Similarity 75.0%; Pred. No. 0.001;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 1 ISVQLASYYRRTSSK 16
| | | | | | | | | | | | | | | |
Db 41 IPLQLRSYRRTISGK 56
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RESULT 5
US-10-329-472-7
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; Sequence 7, Application US/10329472
; Publication No. US20050244888A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human Chemokine Beta-9
; FILE REFERENCE: PFI31P2D1
; CURRENT APPLICATION NUMBER: US/10/329,472
; CURRENT FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: US 08/793,381
; PRIOR FILING DATE: 1997-05-19
; PRIOR APPLICATION NUMBER: PCT/US95/06260
; PRIOR FILING DATE: 1996-02-29
; PRIOR APPLICATION NUMBER: US 08/294,251
; PRIOR FILING DATE: 1994-08-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (54)..(54)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (55)..(55)
; OTHER INFORMATION: Xaa equals any amino acid
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (70)..(70)
; OTHER INFORMATION: Xaa equals any amino acid
; ;
US-10-329-472-7

Query Match 63.0%; Score 46; DB 6; Length 73;
Best Local Similarity 68.8%; Pred. No. 0.052;
Matches 11; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
| | | | | | | | | | | | | | | | | |
Db 17 ISFQALKSYKIITSSK 32

RESULT 6
US-10-957-887B-309
; Sequence 309, Application US/10957887B
; Publication No. US20050272677A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Robert H. E.
; APPLICANT: Leenhouts, Cornelius J.
; APPLICANT: Hektor, Harm
; APPLICANT: van Esch, Johannes H.
; APPLICANT: Heeres, Andre
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
; FILE REFERENCE: 2183-6668US
; CURRENT APPLICATION NUMBER: US/10/957,887B
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/NL/00256
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 309
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Xylella fastidiosa
US-10-957-887B-309

Query Match 52.1%; Score 38; DB 6; Length 44;
Best Local Similarity 43.8%; Pred. No. 0.08;
Matches 7; Conservative 6; Mismatches 3; Indels 3; Gaps 0;

Qy 1 ISVQRLASYRRITSSK 16
: : | | | : | : | : | : | : | : |

Db 18 VAPQDLAAWNRLTASK 33

RESULT 7
US-10-501-675-9
; Sequence 9, Application US/10501675
; Publication No. US20050282161A1
; GENERAL INFORMATION:
; APPLICANT: TANABE SEIYAKU CO., LTD.
; TITLE OF INVENTION: A Novel Phospholipase A2 and the gene thereof.
; FILE REFERENCE: 03-004-PCT
; CURRENT APPLICATION NUMBER: US/10/501,675
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: JP2002-008435
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 818
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-675-9

Query Match 52.1%; Score 38; DB 6; Length 818;
Best Local Similarity 80.0%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SVQRLASYRR 11
| : | | | | | | | | | | | |
Db 401 SPERLASYRR 410

RESULT 8
US-11-052-554A-200
; Sequence 200, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 200
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Shigella flexneri 2a str. 2457T
US-11-052-554A-200

Query Match 50.7%; Score 37; DB 7; Length 550;
Best Local Similarity 53.3%; Pred. No. 21;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
| : | | | | | | | | | | | |
Db 28 SIERLSSGLRINSK 42

RESULT 9
US-10-517-939-362
; Sequence 362, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
; APPLICANT: Steer, Brian
; APPLICANT: Callen, Walter
; APPLICANT: Healey, Shaun
; APPLICANT: Hazlewood, Geoff

```

; APPLICANT: Wu, Di
; APPLICANT: Blum, David
; APPLICANT: Esteghalian, Alireza
; TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THEM
; FILE REFERENCE: 564462007901
; CURRENT APPLICATION NUMBER: US/10/517,939
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/US03/19153
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/389,299
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 362
; LENGTH: 1680
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Obtained from an environmental sample.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1) .. (26)
; US-10-517-939-362

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Query Match      49.3%; Score 36; DB 6; Length 1680;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches      8; Conservative      2; Mismatches      6; Indels      0; Gaps      0;

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Qy 1 ISVQLASYRRITSSK 16
db 989 IGVORGGSYRFVACGR 1004

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RESULT 10
US-10-821-234-1154
; Sequence 1154, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampaia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1154
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1154

```

Query Match	47.9%	Score 35;	DB 6;	Length 495;
Best Local Similarity	70.0%	Pred. No. 43;		
Matches	7: Conservative	2: Mismatches	1: Indels	0: Gaps

Qy	2	SVQRLASYRR	11
Db	33	SSQRVSSYRR	42

RESULT 11
US-11-110-082-38
; Sequence 38, Application US/11110082
; Publication No. US2005026558A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Hall, Claire

```

; APPLICANT: Norriss, Michael Geoffrey
; APPLICANT: Saulesbury, Keith Martin
; TITLE OF INVENTION: Compositions Isolated from Forage
; TITLE OF INVENTION: Grasses and methods for their use

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Query Match	47.9%	Score 35;	DB 7;	Length 808;
Best Local Similarity	46.2%	Pred. No. 73;		
Matches 6;	Conservative	5;	Mismatches	2;
			Indels	0;
			Gaps	0;

Qy 3 VQRLASYRRITSS 15
||| :||: :||:
Db 744 VQRCSSFKSVTSN 756

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RESULT 12
US-10-985-205-3
; Sequence 3, Application US/10985205
; Publication No. US20050266400A1
; GENERAL INFORMATION:
; APPLICANT: Dumonceaux, Julie
; APPLICANT: Cormier, Emmanuel G.
; APPLICANT: Gardner, Jason P.
; APPLICANT: Dragic, Tatjana
; TITLE OF INVENTION: NOVEL SEQUENCES ENCODING HEPATITIS C VIRUS GLYCOPROTEINS
; FILE REFERENCE: 71242-A/JPW/AJD
; CURRENT APPLICATION NUMBER: US/10/985,205
; CURRENT FILING DATE: 2004-11-09
; PRIOR APPLICATION NUMBER: US 60/519,536
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3011
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-985-205-3

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Query Match	46.6%	Score 34;	DB 6;	Length 3011;
Best Local Similarity	70.0%;	Pred. No. 4.6e+02;		
Matches	7;	Conservative	2;	Mismatches 1;
Matches	7;	Conservative	2;	Indels 0;
Matches	7;	Conservative	2;	Gaps 0;

QY 4 QRLASYRRIT 13
:|||||:|
Db 454 ERLASCRRLT 463

RESULT 13
US-11-052-554A-90
Sequence 90, Application US/11052554A
Publication No. US20050298866A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07

; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 90
; LENGTH: 3194
; TYPE: PRT
; ORGANISM: Helicobacter pylori J99
US-11-052-554A-90

Query Match 46.6%; Score 34; DB 7; Length 3194;
Best Local Similarity 87.5%; Pred. No. 4.9e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 YRRITSSK 16
| | | | |
Db 2972 YRRITSSK 2979

RESULT 14
US-10-497-135-8
; Sequence 8, Application US/10497135
; Publication No. US20050272132A1
; GENERAL INFORMATION:
; APPLICANT: Biotica Technology Ltd
; APPLICANT: Gregory, Matthew A
; APPLICANT: Gaisser, Sabine
; APPLICANT: Petkovic, Hrvoje
; APPLICANT: Moss, Steven
; TITLE OF INVENTION: Production of Polyketides and Other Natural Products
; FILE REFERENCE: 4408-P03444US00
; CURRENT APPLICATION NUMBER: US/10/497,135
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: PCT/GB03/003230
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: GB0216509.0
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: GB0224922.5
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Streptomyces hygroscopicus
US-10-497-135-8

Query Match 45.2%; Score 33; DB 6; Length 317;
Best Local Similarity 63.6%; Pred. No. 61;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 QRLASYRRITS 14
| | | | |
Db 210 QRLAMRRITT 220

RESULT 15
US-10-497-135-7
; Sequence 7, Application US/10497135
; Publication No. US20050272132A1
; GENERAL INFORMATION:
; APPLICANT: Biotica Technology Ltd
; APPLICANT: Gaisser, Sabine
; APPLICANT: Petkovic, Hrvoje
; APPLICANT: Moss, Steven
; TITLE OF INVENTION: Production of Polyketides and Other Natural Products
; FILE REFERENCE: 4408-P03444US00
; CURRENT APPLICATION NUMBER: US/10/497,135
; CURRENT FILING DATE: 2004-05-26
; PRIOR APPLICATION NUMBER: PCT/GB03/003230

; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: GB0216509.0
; PRIOR FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: GB0224922.5
; PRIOR FILING DATE: 2002-10-25
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Streptomyces hygroscopicus
US-10-497-135-7

Query Match 45.2%; Score 33; DB 6; Length 318;
Best Local Similarity 63.6%; Pred. No. 62;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 QRLASYRRITS 14
| | | | |
Db 211 QRLAMRRITT 221

RESULT 16
US-10-517-151-4
; Sequence 4, Application US/10517151
; Publication No. US20060019252A1
; GENERAL INFORMATION:
; APPLICANT: Nakamura, Yusuke
; APPLICANT: Furukawa, Yoichi
; APPLICANT: Oncotherapy Science, Inc.
; APPLICANT: The University of Tokyo
; TITLE OF INVENTION: Genes and Polypeptides Relating to Hepatocellular or
; FILE REFERENCE: 082379-000400US
; CURRENT APPLICATION NUMBER: US/10/517,151
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/386,985
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: WO PCT/JPO3/07070
; PRIOR FILING DATE: 2003-06-04
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-517-151-4

Query Match 45.2%; Score 33; DB 6; Length 500;
Best Local Similarity 46.7%; Pred. No. 1e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
| | | | |
Db 328 SSSRLVSHRRVHSGE 342

RESULT 17
US-11-152-697-3
; Sequence 3, Application US/11152697
; Publication No. US20060003367A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL HUMAN KUPFFER CELL RECEPTOR
; FILE REFERENCE: D0242 NP
; CURRENT APPLICATION NUMBER: US/11/152,697
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/580,006
; PRIOR FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3

```
; LENGTH: 548
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-152-697-3

Query Match      45.2%; Score 33; DB 7; Length 548;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSS 15
Db 104 VAIQRLRDYEENSS 118
   :::||| | :|||
   :::||| | :|||

RESULT 18
US-11-080-991-54
; Sequence 54, Application US/11080991
; Publication No. US20050266437A1
; GENERAL INFORMATION:
; APPLICANT: Veiby, Petter Ole
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
; TITLE OF INVENTION: AND OVARIAN CANCER
; FILE REFERENCE: MRI-039
; CURRENT APPLICATION NUMBER: US/11/080.991
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: US/10/176.847
; PRIOR FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 2828
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-080-991-54

Query Match      45.2%; Score 33; DB 7; Length 2828;
Best Local Similarity 46.7%; Pred. No. 6.5e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSS 15
Db 2137 LNVQRAAANARITGT 2151
   :::||| | :|||
   :::||| | :|||

RESULT 19
US-11-186-284-49
; Sequence 49, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-029P2RMW
; CURRENT APPLICATION NUMBER: US/11/186.284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301.822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
```

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 2828
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-49

Query Match      45.2%; Score 33; DB 7; Length 2828;
Best Local Similarity 46.7%; Pred. No. 6.5e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSS 15
Db 2137 LNVQRAAANARITGT 2151
   :::||| | :|||
   :::||| | :|||

RESULT 20
US-10-957-887B-215
; Sequence 215, Application US/10957887B
; Publication No. US20050272677A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Robert H. E.
; APPLICANT: Leenhouts, Cornelius J.
; APPLICANT: Hektor, Harm
; APPLICANT: van Esch, Johannes H.
; APPLICANT: Heeres, Andre
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
; FILE REFERENCE: 2183-6668US
; CURRENT APPLICATION NUMBER: US/10/957.887B
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/NL/00256
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Listeria innocua
US-10-957-887B-215

Query Match      43.8%; Score 32; DB 6; Length 43;
Best Local Similarity 40.0%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASYYRITSS 15
Db 18 VSVQDINSWNHLSS 32
   :::||| | :|||
   :::||| | :|||

RESULT 21
US-10-957-887B-225
; Sequence 225, Application US/10957887B
; Publication No. US20050272677A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Robert H. E.
; APPLICANT: Leenhouts, Cornelius J.
; APPLICANT: Hektor, Harm
; APPLICANT: van Esch, Johannes H.
; APPLICANT: Heeres, Andre
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
; FILE REFERENCE: 2183-6668US
; CURRENT APPLICATION NUMBER: US/10/957.887B
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/NL/00256
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-957-887B-225
```

```
Query Match      43.8%; Score 32; DB 6; Length 43;
Best Local Similarity 40.0%; Pred. No. 11;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 ISVQRLASVRRRTSS 15
    :||| :| :|||
Db 18 VSVQDIMSWNNLSSS 32

RESULT 22
US-11-156-084-358
; Sequence 358, Application US/11156084
; Publication No. US20060010515A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: Controlled expression of cytokinin biosynthetic genes leads to
; FILE OF INVENTION: agronomically interesting phenotypes
; FILE REFERENCE: (38-21)
; CURRENT APPLICATION NUMBER: US/11/156,084
; CURRENT FILING DATE: 2005-06-17
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 358
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Geobacter sulfurreducens PCA
US-11-156-084-358

Query Match      43.8%; Score 32; DB 7; Length 311;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ISVQRLASVRRRI 12
    |||:| ||||
Db 202 ISVERDDLYRRI 213

RESULT 23
US-11-217-562-3
; Sequence 3, Application US/11217562
; Publication No. US2006002952A1
; GENERAL INFORMATION:
; APPLICANT: WANG, LI
; APPLICANT: BABIUK, LORNE A.
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: WILLSON, PHILIP
; TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM
; FILE OF INVENTION: PIGS
; FILE REFERENCE: 9000-0040
; CURRENT APPLICATION NUMBER: US/11/217,562
; CURRENT FILING DATE: 2005-09-01
; PRIOR APPLICATION NUMBER: US/09/209,961
; PRIOR FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: 60/069,233
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069,750
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Porcine Circovirus Type II
US-11-217-562-3

Query Match      43.8%; Score 32; DB 7; Length 314;
Best Local Similarity 87.5%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ASVRRITS 14
    |||||
Db 273 ALYRRITS 280
```

```
RESULT 24
US-10-454-437-140
; Sequence 140, Application US/10454437
; Publication No. US2005027115A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
; FILE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
; FILE REFERENCE: BGI-128PCPN
; CURRENT APPLICATION NUMBER: US/10/454,437
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: DE 19931636.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932125.6
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932126.4
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932127.2
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932128.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932129.9
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: DE 19932226.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932920.6
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19932922.2
; PRIOR FILING DATE: 1999-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 442
; SEQ ID NO 140
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-10-454-437-140

Query Match      43.8%; Score 32; DB 6; Length 432;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 VQRLASVRRITS 14
    :||| ||| |
Db 33 IERLGSVTRTVS 44

RESULT 25
US-11-055-822-184
; Sequence 184, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
; APPLICANT: Pompeius, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
; FILE REFERENCE: BGI-121PCPN
; CURRENT APPLICATION NUMBER: US/11/055,822
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: 09/606,740
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141,031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142,101
```

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; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/148,613
; PRIOR FILING DATE: 1999-08-12
; PRIOR APPLICATION NUMBER: 60/187,970
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: DE 19930476.9
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931415.2
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931418.7
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931419.5
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931420.9
; PRIOR FILING DATE: 1999-07-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 184
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-11-055-822-184

Query Match      43.8%; Score 32; DB 7; Length 432;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 VORLASVRRITS 14
   :||| ||| |
Db 33 IERLGSYTRTVS 44

RESULT 26
US-11-127-877-39
; Sequence 39, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merchiers, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittaels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-127-877-39

Query Match      43.8%; Score 32; DB 7; Length 472;
Best Local Similarity 42.9%; Pred. No. 1.4e+02;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 ISVORLASVRRITS 14
   ||| :||| :
Db 216 ISIHRLPAYKRIVT 229

RESULT 27
US-11-182-016-33
; Sequence 33, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
```

```
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tks 118
; US-11-182-016-33

Query Match      43.8%; Score 32; DB 7; Length 496;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVORLASVRRITSS 15
   |.:|.:|.:|.:|
Db 294 SARFSSRRFSSS 307

RESULT 28
US-10-467-962B-37
; Sequence 37, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000_857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn Vers. 2.0
; SEQ ID NO 37
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-467-962B-37

Query Match      43.8%; Score 32; DB 6; Length 566;
Best Local Similarity 60.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 RLASVRRITS 14
   ||| ||| :|
Db 465 RLGYRTLTA 474

RESULT 29
US-10-957-887B-222
; Sequence 222, Application US/10957887B
; Publication No. US20050272677A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Robert H. E.
; APPLICANT: Leenhouts, Cornelius J.
; APPLICANT: Hektor, Harm
; APPLICANT: van Bsch, Johannes H.
; APPLICANT: Heeres, Andre
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
; FILE REFERENCE: 2183-6668US
; CURRENT APPLICATION NUMBER: US/10/957,887B
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/NL/00256
; PRIOR FILING DATE: 2003-04-04
```

; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 222
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Listeria ivanovii
US-10-957-887B-222

Query Match 42.5%; Score 31; DB 6; Length 43;
Best Local Similarity 42.9%; Pred. No. 16;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 SVQRLSYRRITSS 15
||| | : : :
DB 19 SVQNLMSWNLSSS 32

RESULT 30

US-10-957-887B-233
; Sequence 233, Application US/10957887B
; Publication No. US20050272677A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Robert H. E.
; APPLICANT: Leenhouts, Cornelius J.
; APPLICANT: Hektor, Harm
; APPLICANT: van Esch, Johannes H.
; APPLICANT: Heeres, Andre
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
; FILE REFERENCE: 2183-6668US
; CURRENT APPLICATION NUMBER: US/10/957,887B
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/NL/00256
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 233
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Listeria seeligeri
US-10-957-887B-233

Query Match 42.5%; Score 31; DB 6; Length 43;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SVQRLSYRRITSS 15
||| | : : :
DB 19 SVQDLMSWNLSSS 32

RESULT 31

US-10-957-887B-236
; Sequence 236, Application US/10957887B
; Publication No. US20050272677A1
; GENERAL INFORMATION:
; APPLICANT: Friesen, Robert H. E.
; APPLICANT: Leenhouts, Cornelius J.
; APPLICANT: Hektor, Harm
; APPLICANT: van Esch, Johannes H.
; APPLICANT: Heeres, Andre
; TITLE OF INVENTION: DELIVERY OF A SUBSTANCE TO A PRE-DETERMINED SITE
; FILE REFERENCE: 2183-6668US
; CURRENT APPLICATION NUMBER: US/10/957,887B
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/NL/00256
; PRIOR FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 236
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Listeria welshimeri
US-10-957-887B-236

Query Match 42.5%; Score 31; DB 6; Length 43;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SVQRLSYRRITSS 15
||| | : : :
DB 19 SVQDLMSWNLSSS 32

RESULT 32

US-10-793-626-894
; Sequence 894, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 894
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-894

Query Match 42.5%; Score 31; DB 6; Length 110;
Best Local Similarity 60.0%; Pred. No. 45;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 ASYRRITSSK 16
||| | : : :
DB 43 ASFRKSTSSR 52

RESULT 33

US-11-054-515-1584
; Sequence 1584, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.

```
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1584
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1584

Query Match          42.5%; Score 31; DB 7; Length 254;
Best Local Similarity 56.2%; Pred. No. 1.1e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy 1 ISVQRLAS--YRRITS 14
Db 70 ISVDRLTSVAYMELTS 85

RESULT 34
US-11-129-143-103
; Sequence 103, Application US/11129143
; Publication No. US20050266518A1
; GENERAL INFORMATION:
; APPLICANT: BERRY, Alan
; APPLICANT: BRETZEL, Werner
; APPLICANT: HUMBELIN, Markus
; APPLICANT: LOPEZ-ULIBARRI, Rual
; APPLICANT: MAYER, Anne F.
; APPLICANT: VELISEV, Alexei A.
; TITLE OF INVENTION: IMPROVED ISOPRENOID PRODUCTION
; FILE REFERENCE: C38435/121966
; CURRENT APPLICATION NUMBER: US/11/129,143
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Streptomyces griseolosporeus
US-11-129-143-103

Query Match          42.5%; Score 31; DB 7; Length 334;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ISVQRLASVRRITSS 15
Db 81 VTAQALDGLRLITAS 95

RESULT 35
US-11-196-976-4
; Sequence 4, Application US/11196976
; Publication No. US20050272091A1
; GENERAL INFORMATION:
; APPLICANT: Ruelle, Jean-Louis
; TITLE OF INVENTION: Polynucleotides and Polypeptides BASB033
; TITLE OF INVENTION: from Neisseria Meningitidis and Their Uses
; FILE REFERENCE: BM45331
; CURRENT APPLICATION NUMBER: US/11/196,976
; CURRENT FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: US/10/417,885
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: US/09/787,084
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: PCT/EP99/06718
; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: GB 9820003.3
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Neisseria meningitidis

US-11-196-976-4
Query Match          42.5%; Score 31; DB 7; Length 374;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
Db 33 NVTRLACYDRIFAQAQ 47

RESULT 36
US-11-103-957-95
; Sequence 95, Application US/11103957
; Publication No. US20050281847A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/11/103,957
; CURRENT FILING DATE: 2005-04-12
; PRIOR APPLICATION NUMBER: US/10/467,534
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-11-103-957-95

Query Match          42.5%; Score 31; DB 7; Length 375;
Best Local Similarity 46.7%; Pred. No. 1.7e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
Db 34 NVTRLACYDRIFAQAQ 48

RESULT 37
US-10-467-657-7076
; Sequence 7076, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7076
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7076

Query Match          42.5%; Score 31; DB 6; Length 386;
Best Local Similarity 46.7%; Pred. No. 1.8e+02;
```

Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SVQRLASYRRITSSK 16
:|||||:|:|:
Db 45 NVTRLACYDRIPAAQ 59

RESULT 38

US-10-821-234-1463
; Sequence 1463, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt SEQ_genes Version 1.0
; SEQ ID NO 1463
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1463

Query Match 42.5%; Score 31; DB 6; Length 432;
Best Local Similarity 55.6%; Pred. No. 2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QRLASYRRI 12
|:|:|:|:
Db 379 QEIATYRRL 387

RESULT 39

US-11-024-959-287
; Sequence 287, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 287
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Eucalyptus sp.
US-11-024-959-287

Query Match 42.5%; Score 31; DB 7; Length 465;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRI 12
|:|:|:|:|:
Db 301 IDVQRLLSFDKV 312

RESULT 40
US-11-024-959-288
; Sequence 288, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
; APPLICANT: FORSTER, RICHARD L.
; APPLICANT: CONNETT, MARIE B.
; APPLICANT: EMERSON, SARAH JANE
; APPLICANT: GRIGOR, MURRAY ROBERT
; APPLICANT: HIGGINS, COLLEEN M.
; APPLICANT: LUND, STEVEN TROY
; APPLICANT: MAGUSIN, ANDREAS
; APPLICANT: KODRZYCKI, BOB
; TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
; FILE REFERENCE: 044463-0360
; CURRENT APPLICATION NUMBER: US/11/024,959
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: 60/533,036
; PRIOR FILING DATE: 2003-12-30
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 288
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Eucalyptus sp.
US-11-024-959-288

Query Match 42.5%; Score 31; DB 7; Length 465;
Best Local Similarity 50.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ISVQRLASYRRI 12
|:|:|:|:|:
Db 301 IDVQRLLSFDKV 312

RESULT 41

US-11-065-943-65
; Sequence 65, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-65

Query Match 42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VQRLASYRRITSSK 16
|:|:|:|:|:
Db 240 VEKILQYRELTKLK 253

RESULT 42
US-11-065-943-67

; Sequence 67, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-67

Query Match 42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VQRLASYRRITSSK 16
|::||:|
Db 240 VEKIQYRELTKLK 253

RESULT 43
US-11-065-943-69
; Sequence 69, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-69

Query Match 42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VQRLASYRRITSSK 16
|::||:|
Db 240 VEKIQYRELTKLK 253

RESULT 44
US-11-065-943-73
; Sequence 73, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I

; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-73

Query Match 42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VQRLASYRRITSSK 16
|::||:|
Db 240 VEKIQYRELTKLK 253

RESULT 45
US-11-065-943-75
; Sequence 75, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-75

Query Match 42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 3 VQRLASYRRITSSK 16
|::||:|
Db 240 VEKIQYRELTKLK 253

RESULT 46
US-11-065-943-77
; Sequence 77, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; CURRENT FILING DATE: 2005-02-25
; PRIOR FILING DATE: 2004-02-27


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; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-77

Query Match      42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      3 VORLASYRRITSSK 16
Db      240 VEKILQYRELTKLK 253

RESULT 47
US-11-065-943-79
; Sequence 79, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 79
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-79

Query Match      42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      3 VORLASYRRITSSK 16
Db      240 VEKILQYRELTKLK 253

RESULT 48
US-11-065-943-81
; Sequence 81, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 81
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-81
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Query Match      42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      3 VORLASYRRITSSK 16
Db      240 VEKILQYRELTKLK 253

RESULT 49
US-11-065-943-83
; Sequence 83, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-83

Query Match      42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      3 VORLASYRRITSSK 16
Db      240 VEKILQYRELTKLK 253

RESULT 50
US-11-065-943-85
; Sequence 85, Application US/11065943
; Publication No. US20050250131A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, JEAN-LUC
; APPLICANT: VICHIER-GUERRE, SOPHIE
; APPLICANT: FERRIS, STEPHANE
; TITLE OF INVENTION: METHODS FOR OBTAINING THERMOSTABLE ENZYMES, DNA POLYMERASE I
; TITLE OF INVENTION: VARIANTS FROM THERMUS AQUATICUS HAVING NEW CATALYTIC ACTIVITIES,
; TITLE OF INVENTION: METHODS FOR OBTAINING THE SAME, AND APPLICATIONS OF THE SAME
; FILE REFERENCE: 266426USOXCIP
; CURRENT APPLICATION NUMBER: US/11/065,943
; PRIOR FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 10/787,219
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Thermus aquaticus
US-11-065-943-85

Query Match      42.5%; Score 31; DB 7; Length 545;
Best Local Similarity 35.7%; Pred. No. 2.6e+02;
Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      3 VORLASYRRITSSK 16
Db      240 VEKILQYRELTKLK 253
```

Db 240 VEKILQYRELTKLK 253

Search completed: February 6, 2006, 14:34:05
Job time : 21 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:43:53 ; Search time 5.68063 Seconds
(without alignment)
1287.264 Million cell updates/sec

Title: US-10-644-277-149
Perfect score: 405
Sequence: 1 QPDAINAPVTCCYNFTNRKI.....QKWVQDSMDHLDKQTQTPKT 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	405	100.0	99	2	A60299 monocyte chemoattr
2	337	83.2	99	2	JC2136 monocyte chemoattr
3	315	77.8	99	1	A39296 monocyte chemoattr
4	315	77.8	99	2	JC2336 monocyte chemoattr
5	314	77.5	125	2	I46857 monocyte chemoattr
6	288	71.1	72	2	A55984 monocyte chemoattr
7	287	70.9	109	2	A54678 monocyte chemoattr
8	270	66.7	97	2	JC4912 eotaxin precursor
9	268	66.2	99	2	JC5295 monocyte chemoattr
10	261	64.4	99	2	JC2417 monocyte chemoattr
11	252	62.2	148	1	A30209 PGPf-inducible JE
12	241	59.5	148	1	S07723 immediate-early se
13	236	58.3	120	2	I48147 monocyte chemoattr
14	214	52.8	96	2	I48099 eotaxin precursor
15	207	51.1	96	2	JC2478 monocyte chemoattr
16	200	49.4	97	2	A48093 monocyte precursor
17	145.5	35.9	93	2	B35673 LD78-beta protein
18	142.5	35.2	92	2	A30574 macrophage inflam
19	135.5	33.5	92	1	A31767 macrophage inflam
20	133.5	33.0	92	2	I46730 immune activation
21	127.5	31.5	92	2	C30552 macrophage inflam
22	123	30.4	92	2	I52322 macrophage inflam
23	119	29.4	92	2	A32393 macrophage inflam
24	108.5	26.8	91	1	A46539 monocyte chemoattr
25	106	26.2	120	2	JE0177 lymphocyte and mon
26	105.5	26.0	91	1	A28815 monocyte chemoattr
27	99.5	24.6	96	2	A37236 I-309 protein prec
28	99.5	24.6	114	1	ETHUL lymphotactin prec
29	98	24.2	50	2	C60407 monocyte adherence

30	94	23.2	103	2	A53096 interleukin-8 prec
31	93.5	23.1	92	2	S24236 TC3A3 protein - mou
32	91.5	22.6	114	1	ETMSL lymphotactin precu
33	83	20.5	101	2	I48148 Neutrophil attract
34	79	19.5	101	2	S42496 interleukin-8 prec
35	79	19.5	101	2	I46871 interleukin-8 - ra
36	75	18.5	95	2	JN0841 interleukin-8 - do
37	73.5	18.1	116	2	I49555 gene C10 protein -
38	70	17.3	99	2	A37034 interleukin-8 prec
39	66	16.3	2867	2	AG3481 cellobiose-phospho
40	65.5	16.2	143	2	S76162 hypothetical prote
41	65	16.0	282	2	S44825 F54F2.8 protein -
42	64.5	15.9	363	2	T26700 hypothetical prote
43	64	15.8	1019	2	E90037 hypothetical prote
44	64	15.8	1076	2	F96831 hypothetical prote
45	62.5	15.4	853	2	AB2020 hypothetical prote

ALIGNMENTS

RESULT 1

A60299
monocyte chemoattractant protein 1 precursor - human
N;Alternate names: GDCF-1; glioma-derived monocyte chemotactic factor 1; MCAF; MCP-1; monocyte chemoattractant factor 2 (GDCF-2)
N;Contains: glioma-derived chemotactic factor 2 (GDCF-2)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1993 #sequence, revision 20-Feb-1993 #text change 09-Jul-2004
C;Accession: A35474; A33476; S03339; I51841; A60299; A32300; A32396; A34561; 157488; JCI: R;Shyy, Y.J.; Li, Y.S.; Kolattukudy, P.E.
Biochem. Biophys. Res. Commun. 169, 346-351, 1990
A;Title: Structure of human monocyte chemotactic protein gene and its regulation by TPA.
A;Reference number: A35474; MUID:90290466; PMID:2357211
A;Accession: A35474
A;Molecule type: DNA
A;Residues: 1-99 <SH>
A;Cross-references: UNIPROT:P13500; UNIPARC:UPI00000000DC9; GB:M37719; NID:gl87447; PIDN: R;Rollins, B.J.; Stier, P.; Ernst, T.; Wong, G.G.
Mol. Cell. Biol. 9, 4687-4695, 1989
A;Title: The human homolog of the JE gene encodes a monocyte secretory protein.
A;Reference number: A33476; MUID:90097880; PMID:2513477
A;Accession: A33476
A;Molecule type: mRNA
A;Residues: 1-99 <ROL>
A;Cross-references: UNIPARC:UPI00000000DC9; GB:M30816; GB:M31625; GB:M31626; NID:gl88701; R;Yoshimura, T.; Yuhki, N.; Moore, S.K.; Appella, E.; Lerman, M.I.; Leonard, E.J.
FEBS Lett. 244, 487-493, 1989
A;Title: Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, exp

A;Reference number: S03339; MUID:89153605; PMID:2465924
A;Accession: S03339
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-99 <YOS>
A;Cross-references: UNIPARC:UPI00000000DC9; GB:X14768; NID:g34513; PIDN:CAA32876.1; PID:9
A;Experimental source: glioma cell line U-105MG
R;Yoshimura, T.; Leonard, E.J.
Adv. Exp. Med. Biol. 305, 47-56, 1991
A;Title: Human monocyte chemoattractant protein-1 (MCP-1).
A;Reference number: I51841; MUID:92095166; PMID:1661560
A;Accession: I51841
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-99 <Y02>
A;Cross-references: UNIPARC:UPI00000000DC9; GB:S71513; NID:g240867; PIDN:AAB20651.1; PID:9
R;Bottazzi, B.; Colotta, F.; Sica, A.; Nobili, N.; Mantovani, A.
Int. J. Cancer 45, 795-797, 1990
A;Title: A chemoattractant expressed in human sarcoma cells (tumor-derived chemotactic factor-1/MCAF).
A;Reference number: A60299; MUID:90216082; PMID:2182547
A;Accession: A60299
A;Status: not compared with conceptual translation
A;Molecule type: mRNA

Tue Feb 7 10:19:31 2006

A:Residues: 1-99 <BOT>
A:Cross-references: UNIPARC:UPI00000000DC9
R:J.Furutani, Y.; Nomura, H.; Notoke, M.; Oyama, Y.; Fukui, T.; Yamada, M.; Larsen, C.G.;
Biochem. Biophys. Res. Commun. 159, 249-255, 1989
A:Title: Cloning and sequencing of the cDNA for human monocyte chemoattractant and activator
A:Reference number: A32300; MUID:89165862; PMID:2923622
A:Accession: A32300
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-99 <FUR>
A:Cross-references: UNIPARC:UPI00000000DC9; GB:M24545; NID:g187434; PIDN:AAA18164.1; PID:
R:Robinson, E.A.; Yoshimura, T.; Leonard, E.J.; Tanaka, S.; Griffin, P.R.; Shabanowitz,
Proc. Natl. Acad. Sci. U.S.A. 86, 1850-1854, 1989
A:Title: Complete amino acid sequence of a human monocyte chemoattractant, a putative me
A:Reference number: A32396; MUID:89184525; PMID:2648385
A:Accession: A32396
A:Molecule type: protein
A:Residues: 'X', 25-99 <ROB>
A:Cross-references: UNIPARC:UPI00001429D5
R:Decock, B.; Conings, R.; Lenaerts, J.P.; Billiau, A.; Van Damme, J.
Biochem. Biophys. Res. Commun. 167, 904-909, 1990
A:Title: Identification of the monocyte chemoattractant protein from human osteosarcoma cell
A:Reference number: A34561; MUID:90211336; PMID:2322286
A:Accession: A34561
A:Molecule type: protein
A:Residues: 29-33, 'XX', 36-52; 82-92 <DEC>
A:Cross-references: UNIPARC:UPI000017674D; UNIPARC:UPI000017674E
R:Li, Y.S.; Shyy, Y.J.; Wright, J.G.; Valente, A.J.; Cornhill, J.F.; Kolattukudy, P.E.
Mol. Cell. Biochem. 126, 61-68, 1993
A:Title: The expression of monocyte chemoattractant protein (MCP-1) in human vascular endoth
A:Reference number: I57488; MUID:94150478; PMID:8107650
A:Accession: I57488
A:Molecule type: mRNA
A>Status: translated from GB/EMBL/DBJ
A:Residues: 1-99
A:Cross-references: UNIPARC:UPI00000000DC9; GB:S69738; NID:g545464; PIDN:AAB29926.1; PID:
R:Ye, Q.N.; Su, G.F.; Yuan, Y.; Huang, C.F.
Chinese J. Microbiol. Immunol. 14, 29-32, 1994
A:Title: The PCR, cloning and sequencing of human monocyte chemoattractant protein-1 (MCP
A:Reference number: JC1096
A:Accession: JC1096
A:Molecule type: mRNA
A:Residues: 24-28, 'Q', 30-99 <YEQ>
A:Cross-references: UNIPARC:UPI000017674F
C:Genetics:
A:Gene: GDB:SCVA2
A:Cross-references: GDB:125279; OMIM:158105
A:Map position: 17q11.2-17q12
C:Superfamily: macrophage inflammatory protein
C:Keywords: cytokine; glycoprotein; inflammation; pyroglutamic acid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemoattractant protein 1 #status experimental <MAT>
F:29-99/Product: monocyte chemoattractant protein 1, short form #status experimental <M
F:24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimen
F:37/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	100.0%	Score 405;	DB 2;	Length 99;
Best Local Similarity	100.0%	Pred. No. 3-2e-39;		
Matches	76;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

Qy 1 QPDAINAPVTCYNTFTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKETICADPKQKWV 60
Db 24 QPDAINAPVTCYNTFTNRKISVQRLASVYRRITSSKCPKEAVIFKTIIVAKETICADPKQKWV 83
Qy 61 QDSMDHLDKQTQTPKT 76
Db 84 QDSMDHLDKQTQTPKT 99

RESULT 2
JC2136
monocyte chemoattractant protein-1 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)

A;Title: Purification, sequence analysis, and biological characterization of a second b

A;Reference number: A55984; MUID:95034774; PMID:7947749

A;Accession: A55984

A>Status: preliminary

A:Molecule type: protein

A;Residues: 1-72 <PRO>

A;Cross-references: UNIPARC:UPI000017674C

C;Superfamily: macrophage inflammatory protein

Query Match 71.1%; Score 288; DB 2; Length 72;
Best Local Similarity 74.0%; Pred. No. 5.7e-26;
Matches 54; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

Qy 3 DAINAPVTCYNFTNRKISVORLASYYRITSSKCPKEAVIFKTIVAKEICADPKQKWVD 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DAINSPTVCYTLTSSKKISMORLMSYRRVTSSKCPKEAVIFKTIVAGKEIXAEP--KWVD 58

Qy 63 SMDHLDKOTQTPK 75
|||:|||||:|||||:
Db 59 SISHLDRKNQXPK 71

RESULT 7
A54678
monocyte chemotactic protein 3 precursor - human
N;Alternate names: monocyte chemoattractant protein MCP-3
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text_change 16-Jul-1999
C;Accession: A54678; JCI478; S32222
R;Opdenakker, G.; Fiten, P.; Nyg, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys, G.
Genomics 21, 403-408, 1994
A;Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the
A;Reference number: A54678; MUID:94375065; PMID:7916328
A;Accession: A54678
A:Molecule type: DNA
A;Residues: 1-109 <OPD>
A;Cross-references: UNIPARC:UPI00000006BD; GB:X72309
R;Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.
Biochem. Biophys. Res. Commun. 191, 535-542, 1993
A;Title: Human monocyte chemotactic protein-3 (MCP-3): Molecular cloning of the cDNA and
A;Reference number: JCI478; MUID:93213290; PMID:8461011
A;Accession: JCI478
A:Molecule type: mRNA
A;Residues: 1-109 <OP2>
A;Cross-references: UNIPARC:UPI00000006BD; GB:X72308; GB:S57464; NID:G3928270; PIDN:CAAS
R;Winty, A.; Chalon, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Miloux,
submitted to the EMBL Data Library, March 1993
A;Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoattrac
A;Reference number: S32222
A;Accession: S32222
A:Molecule type: mRNA
A;Residues: 1-109 <MLN>
A;Cross-references: UNIPARC:UPI00000006BD; EMBL:X71087; NID:G288396; PIDN:CAAS0405.1; PI
C;Comment: This protein induces proteinase secretion and chemotaxis by macrophages and m
C;Genetics:
A;Gene: GDB:SCYA7; SCYA6; MCP-3
A;Cross-references: GDB:I38473; OMIM:158106
A;Map position: 17q11-17q12
A;Introns: 36/1; 75/2
C;Superfamily: macrophage inflammatory protein
C;Keywords: cytokine; glycoprotein; inflammation
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-109/Product: monocyte chemotactic protein 3 #status predicted <MAT>
F;39/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.9%; Score 287; DB 2; Length 109;
Best Local Similarity 72.0%; Pred. No. 1.1e-25;
Matches 54; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 OPDAINAPVTCYNFTNRKISVORLASYYRITSSKCPKEAVIFKTIVAKEICADPKQKW 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 34 QPVGINTTCCVRFINKKIPKQLSYYRRTSSHCPREAVIFKTIKLDKEICADPTQKW 93

Qy 61 QDSMDHLDKQTQTPK 75
Db 94 QDFMKHLDDKKTQTPK 108

RESULT 8
JC4912
eotaxin precursor - human
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: JC4912
R:Bartels, J.; Schluster, C.; Richter, E.; Noso, N.; Kulke, R.; Christophers, E.; Schroe
Biochem. Biophys. Res. Commun. 225, 1045-1051, 1996
A:Title: Human dermal fibroblasts express eotaxin: Molecular cloning, mRNA expression, a
A:Reference number: JC4912; MUID:96374440; PMID:8780731
A:Accession: JC4912
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-97 <BAR>
A:Cross-references: UNIPROT:P51671; UNIPARC:UPI0000016A67B; EMBL:Z75668; NID:gl531982; P
A:Experimental source: dermal fibroblast
C:Comment: This protein has eosinophil specific chemotactic activity.
C:Superfamily: macrophage inflammatory protein
C:Keywords: fibroblast
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-97/Product: eotaxin #status predicted <MAT>

Query Match 66.7%; Score 270; DB 2; Length 97;
Best Local Similarity 67.1%; Pred. No. 8.8e-24;
Matches 47; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 6 NAPVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWQDSMD 65
Db 27 SVPTTCCFNLANRKIPQLRLESYRRITSGKCPQKAVIFKTKLAKDICKADPKRWQDSMK 86

Qy 66 HLDKQTQTPK 75
Db 87 YLDQKSPTPK 96

RESULT 9
JC5295
monocyte chemotactic protein-2 precursor - human
C:Species: Homo sapiens (man)
C>Date: 02-May-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: JC5295
R:Van Coillie, E.; Froyen, G.; Nomiya, H.; Miura, R.; Fiten, P.; Van Aelst, I.; Van Da
Biochem. Biophys. Res. Commun. 231, 726-730, 1997
A:Title: Human monocyte chemotactic protein-2: cDNA cloning and regulated expression of
A:Reference number: JC5295; MUID:97224420; PMID:9070881
A:Accession: JC5295
A:Molecule type: mRNA
A:Residues: 1-99 <VAN>
A:Cross-references: UNIPROT:P80075; UNIPARC:UPI0000030FC6; GB:Y10802; NID:g1924937; PIDN
A:Experimental source: bone marrow
C:Comment: This protein belongs to the beta-chemokine family which is one of the major h
tis and in tumor biology, and contribute to the trafficking and recruitment of the respon
C:Genetics:
A:Gene: mcp-2
C:Superfamily: macrophage inflammatory protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemotactic protein-2 #status predicted <MAT>

Query Match 66.2%; Score 268; DB 2; Length 99;
Best Local Similarity 62.7%; Pred. No. 1.5e-23;
Matches 47; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

Qy 1 QPDAINAVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 24 QPDSVSIPTCCFNLANRKIPQLRLESYRRITNQCPKEAVIFKTRGKQKVCADPKRWV 83

Qy 61 QDSMDHLDKQTQTPK 75
Db 87 YLDQKSPTPK 96

Db 84 RDSMKHLDDKQTQTPK 98

RESULT 10
JC2417
monocyte chemoattractant protein-2 precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: JC2417
R:Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 205, 148-153, 1994
A:Title: Porcine luteal cells express monocyte chemoattractant protein-2 (MCP-2): Analys
A:Reference number: JC2417; MUID:95091716; PMID:7999015
A:Accession: JC2417
A:Molecule type: mRNA
A:Residues: 1-99 <HOS>
A:Cross-references: UNIPROT:P49873; UNIPARC:UPI000001362D6; GB:Z48480; NID:g683718; PIDN:
A:Experimental source: corpus luteum
C:Superfamily: macrophage inflammatory protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-99/Product: monocyte chemoattractant protein-2 #status predicted <MAT>

Query Match 64.4%; Score 261; DB 2; Length 99;
Best Local Similarity 60.0%; Pred. No. 9.6e-23;
Matches 45; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 1 QPDAINAVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 24 QPDSVSIPTCCFNLANRKIPQLRLESYRRITNQCPKEAVIFKTRKADKEVCADPKQKWV 83

Qy 61 QDSMDHLDKQTQTPK 75
Db 84 QNSMKLLDQKSPTPK 98

RESULT 11
A30209
PDGF-inducible JE glycoprotein precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A30209; A44771; A30861
R:Rollins, B.J.; Morrison, E.D.; Stiles, C.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988
A:Title: Cloning and expression of JE, a gene inducible by platelet-derived growth facto
A:Reference number: A30209; MUID:88234503; PMID:3287374
A:Accession: A30209
A:Molecule type: DNA
A:Residues: 1-148 <ROL>
A:Cross-references: UNIPROT:P10148; UNIPARC:UPI0000020A69; GB:M19681; NID:g193486; PIDN:
R:Kawahara, R.S.; Deuel, T.F.
J. Biol. Chem. 264, 679-682, 1989
A:Title: Platelet-derived growth factor-inducible gene JE is a member of a family of sma
A:Reference number: A44771; MUID:89093129; PMID:2910858
A:Accession: A44771
A:Molecule type: DNA
A:Residues: 1-148 <KAZ>
A:Cross-references: UNIPARC:UPI0000020A69; GB:J04467; NID:g193488; PIDN:AAA37685.1; PID:
C:Genetics:
A:Gene: JE
A:Introns: 26/1; 65/2
C:Superfamily: macrophage inflammatory protein
C:Keywords: cytokine; glycoprotein
F:126/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.2%; Score 252; DB 1; Length 148;
Best Local Similarity 60.9%; Pred. No. 1.5e-21;
Matches 42; Conservative 17; Mismatches 10; Indels 0; Gaps 0;

Qy 1 QPDAINAVTCCYNFTNRKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
Db 24 QPDSVSIPTCCFNLANRKIPQLRLESYRRITNQCPKEAVIFKTRKADKEVCADPKQKWV 83

Qy 61 QDSMDHLDK 69

```

Db      24  QPDGVNTP-TCCVTP-NKQIPLKRVKGYERITSSRCPCQEAIVFRTLKNKEVCADPTQKKV 8
Qy      61  QDSMDHLDKQQT 72
      || : |||:|
Db      82  QDVIAXLQDRTQ 93

RESULT 14
I48099
eotaxin precursor - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I48099
J:Rothenberg, M.E.; Luter, A.D.; Lilly, C.M.; Drazen, J.M.; Leder, P.
J. Exp. Med. 181, 1211-1216, 1995
A:Title: Constitutive and allergen-induced expression of eotaxin mRNA in the
A:Reference number: I48099; MUID:95173589; PMID:7869037
A:Accession: I48099
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-96 <RES>
A:Cross-references: UNIPROT:P80325; UNIPARC:UPI000012A065; EMBL:UI8941; NID:g
C:Superfamily: macrophage inflammatory protein

Query Match      52.8%; Score 214; DB 2; Length 96;
Best Local Similarity 57.4%; Pred. No. 2.2e-17;
Matches 39; Conservative 12; Mismatches 17; Indels 0; Gaps

Qy      8  PVTCCYNFTNRKISVORLASYYRRTSSKCPKEAVIFKTIVAKEICADPKQKWQDSMDHL 67
Db      28  PSACCFRVTNKILSFORLKSXYKIITSSKCPQTAVIFEIKPDKMICADPKKRWQDAKKYL 87
Qy      68  DKQQTQPK 75
      || : |||:|
Db      88  DQISQTTK 95

RESULT 15
JC2478
eotaxin precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 16-Jul-1999
C:Accession: JC2478
R:Jose, P.J.; Adcock, I.M.; Griffiths-Johnson, D.A.; Berkman, N.; Wells, T.N.
Biochem. Biophys. Res. Commun. 205, 788-794, 1994
A:Title: Botaxin: Cloning of an eosinophil chemoattractant cytokine and incre
A:Reference number: JC2478; MUID:95091818; PMID:7999113
A:Accession: JC2478
A:Molecule type: mRNA
A:Residues: 1-96 <JOS>
A:Cross-references: UNIPARC:UPI000017074E; EMBL:X77603; NID:g602551; PIDN:CAA
C:Comment: This protein is identified as a potent eosinophil chemoattractant.
C:Superfamily: macrophage inflammatory protein
C:Keywords: Glycoprotein
F:1-23/Domain: signal sequence #status predicted <STG>
F:24-96/Product: eotaxin #status predicted <MAT>
F:93/Binding site: carbohydrate (Thr) (covalent) #status predicted

Query Match      51.1%; Score 207; DB 2; Length 96;
Best Local Similarity 55.9%; Pred. No. 1.4e-16;
Matches 38; Conservative 12; Mismatches 18; Indels 0; Gaps

Qy      8  PVTCCYNFTNRKISVORLASYYRRTSSKCPKEAVIFKTIVAKEICADPKQKWQDSMDHL 67
Db      28  PSACCFRVTNKILSFORLKSXYKIITSSKCPQTAVIFEIKPDKMICADPKKRWQDAKKYL 87
Qy      68  DKQQTQPK 75
      || : |||:|
Db      88  GQISQTTK 95

Search completed: February 3, 2006, 09:59:42
Job time : 6.68063 secs

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QY 1 QPDAINAPVTCCYNFTNRKISVQRLASRYRITSSKCPKEAVIFKTIVAKEICADPKQKW 60

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 3, 2006, 09:43:44 ; Search time 34.6863 Seconds
(without alignment)
1545.860 Million cell updates/sec

Title: US-10-644-277-149

Perfect score: 405

Sequence: 1 QPDAINAPVTCYCNFTNRKI.....QKVVQDSMDHLKQTQTPKT 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	405	100.0	99	1	CCL2_HUMAN
2	395	97.5	99	1	CCL2_PONPY
3	394	97.3	99	1	CCL2_MACFA
4	394	97.3	99	1	CCL2_MACMU
5	394	97.3	99	2	O6XV5_MACNE
6	394	97.3	99	2	O7LME7_MACMU
7	337	83.2	99	1	CCL2_PIG
8	331	81.7	101	1	CCL2_CANFA
9	330	81.5	99	1	CCL2_HORSE
10	315	77.8	99	1	MCPA_BOVIN
11	314	77.5	125	1	CCL2_RABIT
12	308	76.0	74	1	MCPB_BOVIN
13	297	73.3	99	2	O51F8_CANFA
14	297	73.3	109	2	O865F3_MACNE
15	292	72.1	99	2	O5K57_CANFA
16	287	70.9	99	1	CCL7_HUMAN
17	287	70.9	99	2	O569J6_HUMAN
18	287	70.9	109	2	O727Q8_HUMAN
19	284	70.1	104	1	CCL12_MOUSE
20	284	70.1	104	2	O5SVB4_MOUSE
21	277	68.4	99	2	O8MKC8_HORSE
22	274.5	67.8	99	1	CCL13_CANFA
23	274	67.7	99	2	O865F4_MACNE
24	273	67.4	97	1	CCL11_HUMAN
25	273	67.4	97	2	O619T4_HUMAN
26	273	67.4	99	1	CCL8_CANFA
27	271	66.9	99	2	O8HYQ0_MACMU
28	268	66.2	99	1	CCL8_HUMAN
29	261	64.4	97	1	CCL11_MACMU
30	261	64.4	97	2	O8HXZ5_MACMU
31	261	64.4	99	1	CCL8_PIG

32	260	64.2	150	2	O8CGM5_SIGHI	O8CGM5 sigmodon hi
33	253.5	62.6	98	1	CCL13_HUMAN	Q99616 h small ind
34	253.5	62.6	98	2	O6IC06_HUMAN	Q6IC06 homo sapien
35	252	62.2	100	1	CCL11_HORSE	Q9TTQ4 equus cabal
36	252	62.2	148	1	CCL2_MOUSE	P10148 mus musculus
37	252	62.2	148	2	O5SVU3_MOUSE	Q92VU3 mus musculus
38	249	61.5	97	2	O92318_CAVPO	Q92318 cavia porce
39	247	61.0	99	1	CCL8_BOVIN	Q09141 bos taurus
40	241	59.5	148	1	CCL5_RAT	P14844 rattus norv
41	241	59.5	148	2	O549R5_RAT	Q549R5 rattus norv
42	236	58.3	120	1	CCL2_CAVPO	Q08782 cavia porce
43	235	58.0	97	2	O9TT56_BOVIN	Q9TT56 bos taurus
44	221	54.6	97	1	CCL11_RAT	P97545 rattus norv
45	218	53.8	97	1	CCL11_MOUSE	P48298 mus musculus

ALIGNMENTS

RESULT 1						
CCL2_HUMAN						
ID	CCL2_HUMAN	STANDARD;	PRT;	99 AA.		
AC	P13500; Q9UDF3;					
DT	01-JAN-1990 (Rel. 13, Created)					
DT	01-JAN-1990 (Rel. 13, Last sequence update)					
DT	13-SEP-2005 (Rel. 48, Last annotation update)					
DE	Small inducible cytokine A2 precursor (CCL2) (Monocyte chemoattractant protein 1) (MCP-1) (Monocyte chemotactic and activating factor) (MCAF) (Monocyte secretory protein JB) (HC11).					
GN	Names=CCL2; Synonyms=MCP1, SCYA2;					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;					
OC	Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RX	MEDLINE=89165862; PubMed=2923622;					
RA	Furutani Y., Nomura H., Notake M., Oyama Y., Fukui T., Yamada M.,					
RA	Larsen C.G., Oppenheim J.J., Matsushima K.;					
RT	"Cloning and sequencing of the cDNA for human monocyte chemoattractant and activating factor (MCAF).";					
RL	Biochem. Biophys. Res. Commun. 159:249-255(1989).					
RP	NUCLEOTIDE SEQUENCE.					
RX	MEDLINE=90097880; PubMed=2513477;					
RA	Rollins B.J., Stier P., Ernst T., Wong G.G.;					
RT	"The human homolog of the JB gene encodes a monocyte secretory protein.";					
RL	Mol. Cell. Biol. 9:4687-4695(1989).					
RP	NUCLEOTIDE SEQUENCE.					
RX	MEDLINE=89153605; PubMed=2465924; DOI=10.1016/0014-5793(89)80590-3;					
RA	Yoshimura T., Fukui N., Moore S.K., Appella E., Lerman M.I.,					
RA	Leonard E.J.;					
RT	"Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expression in mitogen-stimulated blood mononuclear leukocytes, and sequence similarity to mouse competence gene JB.";					
RL	FEBS Lett. 244:487-493(1989).					
RP	NUCLEOTIDE SEQUENCE.					
RX	MEDLINE=90290466; PubMed=2357211;					
RA	Shyy Y.J., Li Y.S., Kolattukudy P.E.;					
RT	"Structure of human monocyte chemoattractant protein gene and its regulation by TPA.";					
RL	Biochem. Biophys. Res. Commun. 169:346-351(1990).					
RP	NUCLEOTIDE SEQUENCE.					
RX	MEDLINE=91207938; PubMed=2518762;					
RA	Chang H.C., Hsu F., Freeman G.J., Griffin J.D., Reinherz E.L.;					
RT	"Cloning and expression of a gamma-interferon-inducible gene in monocytes: a new member of a cytokine gene family.";					

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RL Int. Immunol. 1:388-399(1989).
RN [6]
RX NUCLEOTIDE SEQUENCE.
RP MEDLINE=94150478; PubMed=8107690;
RA Li Y.S., Shyy Y.J., Wright J.G., Valente A.J., Cornhill J.F.,
RA Kolattukudy P.E.;
RT "The expression of monocyte chemotactic protein (MCP-1) in human
RT vascular endothelium in vitro and in vivo.";
RL Mol. Cell. Biochem. 126:61-68(1993).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92095166; PubMed=1661560;
RA Yoshimura T., Leonard E.J.;
RT "Human monocyte chemoattractant protein-1 (MCP-1).";
RL Adv. Exp. Med. Biol. 305:47-56(1991).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91301709; PubMed=2071154;
RA Rollins B.J., Morton C.C., Ledbetter D.H., Eddy R.L. Jr., Shows T.B.;
RT "Assignment of the human small inducible cytokine A2 gene, SCYA2
RT (encoding JE or MCP-1), to 17q11.2-12: evolutionary relatedness of
RT cytokines clustered at the same locus.";
RL Genomics 10:489-492(1991).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20374005; PubMed=10918580; DOI=10.1038/sj.onc.1203643;
RA Finzer P., Soto U., Delius H., Patzelt A., Poustka A., Coy J.F.,
RA zur Hausen H., Roel F.;
RT "Differential transcriptional regulation of the monocyte-
RT chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-
RT tumorigenic HPV 18 positive cells: the role of the chromatin structure
RT and AP-1 composition.";
RL Oncogene 19:3235-3244(2000).
RN [10]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA Kalline N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
RA Phelan M., Farmer A.;
RT "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT vector.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [11]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-
RT FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [12]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Pancreas;
RX MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grummond J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [13]
RP PROTEIN SEQUENCE OF 24-99.
RX MEDLINE=89184525; PubMed=2648385;
RA Robinson E.A., Yoshimura T., Leonard E.J., Tanaka S., Griffin P.R.,
RA Shabanowitz J., Hunt D.F., Appella E.;
RT "Complete amino acid sequence of a human monocyte chemoattractant, a
RT putative mediator of cellular immune reactions.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:1850-1854(1989).
RN [14]
RP PROTEIN SEQUENCE OF 29-53 AND 82-92.
RX MEDLINE=90211336; PubMed=2322286;
RA Decock B., Conings R., Lenaerts J.-P., Biliau A., van Damme J.;
RT "Identification of the monocyte chemotactic protein from human
RT osteosarcoma cells and monocytes: detection of a novel N-terminally
RT processed form.";
RL Biochem. Biophys. Res. Commun. 167:904-909(1990).
RN [15]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=91312872; PubMed=1857712;
RA Gronenborn A.M., Clore G.M.;
RT "Modeling the three-dimensional structure of the monocyte chemo-
RT attractant and activating protein MCP-1 on the basis of the
RT solution structure of interleukin-8.";
RL Protein Eng. 4:263-269(1991).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
RX MEDLINE=97143315; PubMed=8989326;
RA Lubkowski J., Bujacz G., Domaille P.J., Handel T.M., Wlodawer A.;
RT "The structure of MCP-1 in two crystal forms provides a rare example
RT of variable quaternary interactions.";
RL Nat. Struct. Biol. 4:64-69(1997).
RN [17]
RP STRUCTURE BY NMR.
RX MEDLINE=96234959; PubMed=8639605; DOI=10.1021/bi9602270;
RA Handel T.M., Domaille P.J.;
RT "Heteronuclear (1H, 13C, 15N) NMR assignments and solution structure
RT of the monocyte chemoattractant protein-1 (MCP-1) dimer.";
RL Biochemistry 35:6569-6584(1996).
RN [18]
RP EFFECT OF DELETION OF N-TERMINAL RESIDUES.
RX MEDLINE=96195223; PubMed=8627182; DOI=10.1084/jem.183.2.681;
RA Weber M., Ugucioni M., Baggiolini M., Clark-Lewis I., Dahinden C.A.;
RT "Deletion of the NH2-terminal residue converts monocyte chemotactic
RT protein 1 from an activator of basophil mediator release to an
RT eosinophil chemoattractant.";
RL J. Exp. Med. 183:681-685(1996).
RN [19]
RP MUTAGENESIS.
RX MEDLINE=94253189; PubMed=8195247;
RA Zhang Y.J., Rutledge B.J., Rollins B.J.;
RT "Structure/activity analysis of human monocyte chemoattractant
RT protein-1 (MCP-1) by mutagenesis. Identification of a mutated protein
RT that inhibits MCP-1-mediated monocyte chemotaxis.";
RL J. Biol. Chem. 269:15918-15924(1994).
RN [20]
RP SUBUNIT.
RX MEDLINE=97053697; PubMed=8898111; DOI=10.1016/0014-5793(96)01024-1;
RA Kim K.-S., Rajaratnam K., Clark-Lewis I., Sykes B.D.;
RT "Structural characterization of a monomeric chemokine: monocyte
RT chemoattractant protein-3.";
RL FEBS Lett. 395:277-282(1996).
RN [21]
RP FUNCTION: Chemotactic factor that attracts monocytes and basophils
CC but not neutrophils or eosinophils. Augments monocyte anti-tumor
CC activity. Has been implicated in the pathogenesis of diseases
CC characterized by monocyte infiltrates, like psoriasis, rheumatoid
CC arthritis or atherosclerosis. May be involved in the recruitment
CC of monocytes into the arterial wall during the disease process of
CC atherosclerosis. Binds to CCR2 and CCR4.
CC SUBCELLULAR LOCATION: Secreted.
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium.
CC -1- PTM: Processing at the N-terminus can regulate receptor and target
CC cell selectivity. Deletion of the N-terminal residue converts it
CC from an activator of basophil to an eosinophil chemoattractant.
CC -1- SIMILARITY: Belongs to the interleukin beta (chemokine CC) family.

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CC
Query Match 100.0%; Score 405; DB 1; Length 99;
Best Local Similarity 100.0%; Pred. No. 7.6e-38;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLKQQTPTKT 76
Db 84 QDSMDHLKQQTPTKT 99

RESULT 2
CCL2_PONPY STANDARD; PRT; 99 AA.
AC Q5RA36;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DE Small inducible cytokine A2 precursor (CCL2).
GN Name=CCL2;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC Tissue=Kidney;
RG The German cDNA consortium;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemotactic factor that attracts monocytes and basophils
CC but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By
CC similarity).
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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use as long as its content is in no way modified and this statement is not
removed.
EMBL; CR859186; CAH91374.1; -, mRNA.
SMR; Q5RA36; 24-94.
InterPro; IPR000827; CC chemokine sm1.
InterPro; IPR001811; Chemokine IL8.
Pfam; PF000048; IL8; 1.
PRINTS; PR01721; FRACTALKINE.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
Pyrrolidone carboxylic acid; Sensory transduction; Signal.
SIGNAL 1 23 By similarity.
CHAIN 24 99 Small inducible cytokine A2.
MOD_RES 24 24 Pyrrolidone carboxylic acid (By
similarity).
CARBOHYD 37 37 N-linked (GlcNAc...) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 11015 MW; 45FCA8CC64FF8A4F CRC64;

Query Match 97.5%; Score 395; DB 1; Length 99;
Best Local Similarity 98.7%; Pred. No. 1e-36;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLKQQTPTKT 76
Db 84 QDSMDHLKQQTPTKT 99

RESULT 3
CCL2_MACFA STANDARD; PRT; 99 AA.
AC P61274; Q9MYN4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 48, Last sequence update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
protein 1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=MCPI, SCY2;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Studer C., Ufer R.;
RT "Cloning and expression of cynomolgus monkey chemoattractant protein-
1.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemotactic factor that attracts monocytes and basophils
CC but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By
CC similarity).
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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use as long as its content is in no way modified and this statement is not
removed.
EMBL; AF276081; AAP81899.1; -, mRNA.
HSSP; P13500; 1DOK.
SMR; P61274; 24-93.
InterPro; IPR000827; CC chemokine sm1.
InterPro; IPR001811; Chemokine IL8.
InterPro; IPR008097; Fractalkine.
Pfam; PF000048; IL8; 1.
PRINTS; PR01721; FRACTALKINE.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
Pyrrolidone carboxylic acid; Sensory transduction; Signal.
SIGNAL 1 23 By similarity.
CHAIN 24 99 Small inducible cytokine A2.
MOD_RES 24 24 Pyrrolidone carboxylic acid (By
similarity).
CARBOHYD 37 37 N-linked (GlcNAc...) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 11007 MW; 433CB88C64EE7A4F CRC64;

Query Match 97.3%; Score 394; DB 1; Length 99;
Best Local Similarity 98.7%; Pred. No. 1.3e-36;
Matches 74; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLKQQTPTKT 76
Db 84 QDSMDHLKQQTPTKT 99
```

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Db 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLKQQTPTKT 76
Db 84 QDSMDHLKQQTPTKT 99

RESULT 3
CCL2_MACFA STANDARD; PRT; 99 AA.
AC P61274; Q9MYN4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 48, Last sequence update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
protein 1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=MCPI, SCY2;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Studer C., Ufer R.;
RT "Cloning and expression of cynomolgus monkey chemoattractant protein-
1.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Chemotactic factor that attracts monocytes and basophils
CC but not neutrophils or eosinophils. Binds to CCR2 and CCR4 (By
CC similarity).
CC -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
CC
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removed.
EMBL; AF276081; AAP81899.1; -, mRNA.
HSSP; P13500; 1DOK.
SMR; P61274; 24-93.
InterPro; IPR000827; CC chemokine sm1.
InterPro; IPR001811; Chemokine IL8.
InterPro; IPR008097; Fractalkine.
Pfam; PF000048; IL8; 1.
PRINTS; PR01721; FRACTALKINE.
SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
Pyrrolidone carboxylic acid; Sensory transduction; Signal.
SIGNAL 1 23 By similarity.
CHAIN 24 99 Small inducible cytokine A2.
MOD_RES 24 24 Pyrrolidone carboxylic acid (By
similarity).
CARBOHYD 37 37 N-linked (GlcNAc...) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 99 AA; 11007 MW; 433CB88C64EE7A4F CRC64;

Query Match 97.3%; Score 394; DB 1; Length 99;
Best Local Similarity 98.7%; Pred. No. 1.3e-36;
Matches 74; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 60
Db 24 QPDAINAPVTCYNTNRKISVQRLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKW 83
QY 61 QDSMDHLKQQTPTKT 76
Db 84 QDSMDHLKQQTPTKT 99
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Best Local Similarity 73.3%; Pred. No. 1.1e-27;
Matches 55; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

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Db 24 QPDAVNSPVTCCTYFTNKTISVQRLMSYRRINSTKCPKEAVIFMTKLAKGICADPKQKWV 83
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 QDSMDHLDKQQTPTK 75
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Db 84 QDSINYLKKNQTPK 98
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```

RESULT 11

```
ID _CCL2_RABIT STANDARD; PRT; 125 AA.
AC P28292;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic
protein 1) (MCP-1) (Monocyte chemoattractant protein 1).
GN Name=CCL2; Synonyms=SCYA2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=New Zealand white; TISSUE=Spleen;
RX MEDLINE=91225489; PubMed=2026877;
RA Yoshimura T., Yuhki N.;
RT "Neutrophil attractant/activation protein-1 and monocyte
chemoattractant protein-1 in rabbit. cDNA cloning and their expression
in spleen cells.";
RL J. Immunol. 146:3483-3488(1991).
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, but not
neutrophils.
CC -1- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
```

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CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; M57440; AAA31386.1; -; mRNA.
DR PIR; I46857; I46857.
DR HSP; P13500; IDOM.
DR SMR; P28292; 24-99.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Glycoprotein; Inflammatory response;
KW Pyrilidone carboxylic acid; Sensory transduction; Signal.
FT SIGNAL 1 23 By similarity.
FT CHAIN 24 125 Small inducible cytokine A2. (By
FT MOD_RES 24 24 Pyrrolidone carboxylic acid (By
FT CARBOHYD 40 40 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 55 55 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 112 112 N-linked (GlcNAc. .) (Potential).
FT DISULFID 34 59 By similarity.
FT DISULFID 35 75 By similarity.
SQ SEQUENCE 125 AA; 13776 MW; 24C3A542CB6A47BE CRC64;
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DR Query Match 77.5%; Score 314; DB 1; Length 125;
DR Best Local Similarity 75.0%; Pred. No. 1.9e-27;
DR Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;
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Qy 1 OPDAINAVTCCYNTFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24 QPDAVNSPVTCCTYFTNKTISVQRLMSYRRINSTKCPKEAVIFMTKLAKGICADPKQKWV 83
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 QDSMDHLDKQQTPTK 75
    |||||:|||||:|||||
Db 84 QDSINYLKKNQTPK 98
    |||||:|||||:|||||
```

Query Match

Best Local Similarity 77.5%; Score 314; DB 1; Length 125;
Matches 57; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

```
Qy 1 OPDAINAVTCCYNTFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWV 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24 QPDAVNSPVTCCTYFTNKTISVQRLMSYRRINSTKCPKEAVIFMTKLAKGICADPKQKWV 83
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 QDSMDHLDKQQTPTK 76
    |||||:|||||:|||||
Db 84 QDAIANLDKKNQTPK 99
    |||||:|||||:|||||
```

RESULT 12

```
MCPB_BOVIN
ID _MCPB_BOVIN STANDARD; PRT; 74 AA.
AC P80343;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Monocyte chemotactic protein 1B (MCP-1B) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=95034774; PubMed=7947749;
RA Proost P., Wuyts A., Lenaerts J.-P., van Damme J.;
RT "Purification, sequence analysis, and biological characterization of a
second bovine monocyte chemotactic protein-1 (Bo MCP-1B).";
RL Biochemistry 33:13406-13412(1994).
CC -1- FUNCTION: Chemotactic factor that attracts monocytes, but not
neutrophils. Augments monocyte anti-tumor activity. Also induces
the release of gelatinase B. This protein can bind heparin.
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
DR HSP; P13500; IDOK.
DR SMR; P80343; 1-68.
DR InterPro; IPR000827; CC chemokine sm1.
DR InterPro; IPR001811; Chemokine_IL8.
DR Pfam; PF00048; IL8; 1.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
KW Chemotaxis; Cytokine; Direct protein sequencing; Heparin-binding;
KW Sensory transduction.
FT DISULFID 9 34 By similarity.
FT DISULFID 10 50 By similarity.
FT NON_TER 1 1
SQ SEQUENCE 74 AA; 8363 MW; FAAF72B970EB16E3 CRC64;
```

```
-----
DR Query Match 76.0%; Score 308; DB 1; Length 74;
DR Best Local Similarity 75.3%; Pred. No. 5.2e-27;
DR Matches 55; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
-----
Qy 3 DAINAPVTCYNTFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWVD 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DAINSPVTCCTYFTNKTISVQRLMSYRRITSSKCPKEAVIFKTIAGKEICAEPPKXWVD 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 63 SMDHLDKQQTPTK 75
    |||||:|||||:|||||
Db 61 STHLDKKNQXPX 73
    |||||:|||||:|||||
```

Query Match 76.0%; Score 308; DB 1; Length 74;
Best Local Similarity 75.3%; Pred. No. 5.2e-27;
Matches 55; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

```
Qy 3 DAINAPVTCYNTFNKISVORLASVRRITSSKCPKEAVIFKTIIVAKEICADPKQKWVD 62
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DAINSPVTCCTYFTNKTISVQRLMSYRRITSSKCPKEAVIFKTIAGKEICAEPPKXWVD 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 63 SMDHLDKQQTPTK 75
    |||||:|||||:|||||
Db 61 STHLDKKNQXPX 73
    |||||:|||||:|||||
```

RESULT 13

Q516F8_CANPA
ID Q516F8_CANPA PRELIMINARY; PRT; 99 AA.

Search completed: February 3, 2006, 09:57:26
Job time : 36.6863 secs

Search completed: February 3, 2006, 09:57:26
Job time : 36.6863 secs